

# Alexander Kurilshchikov

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

14,016  
citations

117625

34  
h-index

102487

66  
g-index

83  
all docs

83  
docs citations

83  
times ranked

16936  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of the gut microbiome in mediating lactose intolerance symptoms. <i>Gut</i> , 2022, 71, 215-217.	12.1	18
2	Discovery, diversity, and functional associations of crAss-like phages in human gut metagenomes from four Dutch cohorts. <i>Cell Reports</i> , 2022, 38, 110204.	6.4	30
3	Yoghurt consumption is associated with changes in the composition of the human gut microbiome and metabolome. <i>BMC Microbiology</i> , 2022, 22, 39.	3.3	31
4	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. <i>Nature Genetics</i> , 2022, 54, 143-151.	21.4	132
5	Challenges and future directions for studying effects of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2022, 54, 100-106.	21.4	46
6	Environmental factors shaping the gut microbiome in a Dutch population. <i>Nature</i> , 2022, 604, 732-739.	27.8	239
7	Integrated fecal microbiomeâ€“metabolome signatures reflect stress and serotonin metabolism in irritable bowel syndrome. <i>Gut Microbes</i> , 2022, 14, 2063016.	9.8	28
8	Genetic, parental and lifestyle factors influence telomere length. <i>Communications Biology</i> , 2022, 5, .	4.4	23
9	Whole exome sequencing analyses reveal geneâ€“microbiota interactions in the context of IBD. <i>Gut</i> , 2021, 70, gutjnl-2019-319706.	12.1	26
10	An association between chronic widespread pain and the gut microbiome. <i>Rheumatology</i> , 2021, 60, 3727-3737.	1.9	40
11	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
12	The long-term genetic stability and individual specificity of the human gut microbiome. <i>Cell</i> , 2021, 184, 2302-2315.e12.	28.9	166
13	Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Gut</i> , 2021, 70, 1287-1298.	12.1	246
14	P006 Host-genetics, dysbiosis, and clinical history explains fecal metabolic alterations in patients with Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2021, 15, S128-S128.	1.3	0
15	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021, 35, 109132.	6.4	34
16	Gut Microbiota Composition of Biliary Atresia Patients Before Kasai Portoenterostomy Associates With Long-term Outcome. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2021, 73, 485-490.	1.8	10
17	Association of Insulin Resistance and Type 2 Diabetes With Gut Microbial Diversity. <i>JAMA Network Open</i> , 2021, 4, e2118811.	5.9	119
18	A combination of fecal calprotectin and human beta-defensin 2 facilitates diagnosis and monitoring of inflammatory bowel disease. <i>Gut Microbes</i> , 2021, 13, 1943288.	9.8	4

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19	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. <i>Cell Genomics</i> , 2021, 1, 100069.	6.5	15
20	ImmunoChip meta-analysis in European and Argentinian populations identifies two novel genetic loci associated with celiac disease. <i>European Journal of Human Genetics</i> , 2020, 28, 313-323.	2.8	21
21	Genetic and Microbial Associations to Plasma and Fecal Bile Acids in Obesity Relate to Plasma Lipids and Liver Fat Content. <i>Cell Reports</i> , 2020, 33, 108212.	6.4	55
22	Gut microbial co-abundance networks show specificity in inflammatory bowel disease and obesity. <i>Nature Communications</i> , 2020, 11, 4018.	12.8	80
23	A Two-Sample Mendelian Randomization Analysis Investigates Associations Between Gut Microbiota and Celiac Disease. <i>Nutrients</i> , 2020, 12, 1420.	4.1	26
24	Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. <i>Nature Communications</i> , 2020, 11, 362.	12.8	416
25	A novel thermophilic <i>Aeribacillus</i> bacteriophage AP45 isolated from the Valley of Geysers, Kamchatka: genome analysis suggests the existence of a new genus within the Siphoviridae family. <i>Extremophiles</i> , 2019, 23, 599-612.	2.3	7
26	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
27	Intestinal microbiome composition and its relation to joint pain and inflammation. <i>Nature Communications</i> , 2019, 10, 4881.	12.8	176
28	Studying the gut virome in the metagenomic era: challenges and perspectives. <i>BMC Biology</i> , 2019, 17, 84.	3.8	113
29	Gut microbiome composition and its relation to joint pain and inflammation. <i>Osteoarthritis and Cartilage</i> , 2019, 27, S26.	1.3	0
30	Structural variation in the gut microbiome associates with host health. <i>Nature</i> , 2019, 568, 43-48.	27.8	244
31	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , 2019, 124, 1808-1820.	4.5	137
32	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. <i>Nature Genetics</i> , 2019, 51, 600-605.	21.4	854
33	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019, 4, 623-632.	13.3	1,206
34	Relationship between gut microbiota and circulating metabolites in population-based cohorts. <i>Nature Communications</i> , 2019, 10, 5813.	12.8	168
35	Shared gut, but distinct oral microbiota composition in primary Sjögren's syndrome and systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2019, 97, 77-87.	6.5	147
36	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019, 10, 358-366.	9.8	118

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37	Marked Changes in Gut Microbiota in Cardio-Surgical Intensive Care Patients: A Longitudinal Cohort Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 467.	3.9	32
38	IBD Genetics and the Gut Microbiome. , 2019, , 231-248.		1
39	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018, 555, 210-215.	27.8	1,958
40	Isolation and characterization of a group of new <i>Proteus</i> bacteriophages. <i>Archives of Virology</i> , 2018, 163, 2189-2197.	2.1	18
41	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	351
42	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	21.4	97
43	Microbiome Responses to an Uncontrolled Short-Term Diet Intervention in the Frame of the Citizen Science Project. <i>Nutrients</i> , 2018, 10, 576.	4.1	96
44	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	11.1	109
45	Role of gut microbiota in chronic low-grade inflammation as potential driver for atherosclerotic cardiovascular disease: a systematic review of human studies. <i>Obesity Reviews</i> , 2018, 19, 1719-1734.	6.5	169
46	Microbial Impact on Plasma Metabolites is Linked to the Cardiovascular Risk and Phenotypes. <i>Atherosclerosis Supplements</i> , 2018, 32, 118-119.	1.2	2
47	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	2.0	48
48	Host Genetics and Gut Microbiome: Challenges and Perspectives. <i>Trends in Immunology</i> , 2017, 38, 633-647.	6.8	219
49	The systemic tumor response to RNase A treatment affects the expression of genes involved in maintaining cell malignancy. <i>Oncotarget</i> , 2017, 8, 78796-78810.	1.8	19
50	Alteration of the exDNA profile in blood serum of LLC-bearing mice under the decrease of tumour invasion potential by bovine pancreatic DNase I treatment. <i>PLoS ONE</i> , 2017, 12, e0171988.	2.5	19
51	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	12.6	1,398
52	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	12.6	1,716
53	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016, 48, 1407-1412.	21.4	672
54	Lytic bacteriophage PM16 specific for <i>Proteus mirabilis</i> : a novel member of the genus Phikmvirus. <i>Archives of Virology</i> , 2016, 161, 2457-2472.	2.1	20

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55	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	28.9	806
56	Human bocavirus in hospitalized children with acute gastroenteritis in Russia from 2010 to 2012. <i>Infection, Genetics and Evolution</i> , 2016, 37, 143-149.	2.3	16
57	Comparative Metagenomic Profiling of Symbiotic Bacterial Communities Associated with <i>Ixodes persulcatus</i> , <i>Ixodes pavlovskyi</i> and <i>Dermacentor reticulatus</i> Ticks. <i>PLoS ONE</i> , 2015, 10, e0131413.	2.5	41
58	Genetic diversity of <i>Ixodes pavlovskyi</i> and <i>I. persulcatus</i> (Acari: Ixodidae) from the sympatric zone in the south of Western Siberia and Kazakhstan. <i>Experimental and Applied Acarology</i> , 2015, 67, 441-456.	1.6	19
59	Complete Genome Sequencing of <i>Borrelia valaisiana</i> and <i>Borrelia afzelii</i> Isolated from <i>Ixodes persulcatus</i> Ticks in Western Siberia. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
60	Evolutionary time-scale of primate bocaviruses. <i>Infection, Genetics and Evolution</i> , 2013, 14, 265-274.	2.3	25
61	MicroRNA Drop in the Bloodstream and MicroRNA Boost in the Tumour Caused by Treatment with Ribonuclease A Leads to an Attenuation of Tumour Malignancy. <i>PLoS ONE</i> , 2013, 8, e83482.	2.5	18
62	Whole-Genome Sequencing of <i>Borrelia garinii</i> BgVir, Isolated from Taiga Ticks ( <i>Ixodes persulcatus</i> ). <i>Journal of Bacteriology</i> , 2012, 194, 5713-5713.	2.2	16
63	Genetic diversity of group a rotavirus isolates found in Western Siberia in 2007-2011. <i>Molecular Genetics, Microbiology and Virology</i> , 2012, 27, 174-183.	0.3	12
64	Unbiased approach to profile the variety of small non-coding RNA of human blood plasma with massively parallel sequencing technology. <i>Expert Opinion on Biological Therapy</i> , 2012, 12, S43-S51.	3.1	29
65	A comparative study of cell-free apoptotic and genomic DNA using FISH and massive parallel sequencing. <i>Expert Opinion on Biological Therapy</i> , 2012, 12, S11-S17.	3.1	14