

# Ran Blekhman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8721562/publications.pdf>

Version: 2024-02-01

62  
papers

8,038  
citations

109137

35  
h-index

118652

62  
g-index

82  
all docs

82  
docs citations

82  
times ranked

13678  
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
2	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	3.8	612
3	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	13.5	419
4	Social networks predict gut microbiome composition in wild baboons. <i>ELife</i> , 2015, 4, .	2.8	403
5	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239
6	Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. <i>Cell Reports</i> , 2016, 14, 2142-2153.	2.9	231
7	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	13.5	217
8	Gut microbiota diversity across ethnicities in the United States. <i>PLoS Biology</i> , 2018, 16, e2006842.	2.6	216
9	Natural Selection on Genes that Underlie Human Disease Susceptibility. <i>Current Biology</i> , 2008, 18, 883-889.	1.8	207
10	Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. <i>Genome Medicine</i> , 2015, 7, 55.	3.6	197
11	Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by <i>Entamoeba</i> and Subsistence. <i>PLoS Genetics</i> , 2015, 11, e1005658.	1.5	171
12	Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271.	1.5	143
13	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
14	Tracking the popularity and outcomes of all bioRxiv preprints. <i>ELife</i> , 2019, 8, .	2.8	138
15	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021, 373, 181-186.	6.0	126
16	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. <i>Genome Medicine</i> , 2018, 10, 78.	3.6	107
17	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. <i>American Journal of Primatology</i> , 2018, 80, e22867.	0.8	100
18	Interaction between Host MicroRNAs and the Gut Microbiota in Colorectal Cancer. <i>MSystems</i> , 2018, 3, .	1.7	97

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19	Functional Comparison of Innate Immune Signaling Pathways in Primates. <i>PLoS Genetics</i> , 2010, 6, e1001249.	1.5	94
20	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. <i>Genetics</i> , 2011, 187, 1225-1234.	1.2	89
21	Temporal variation selects for diet-“microbe co-metabolic traits in the gut of <i>Gorilla</i> spp. <i>ISME Journal</i> , 2016, 10, 514-526.	4.4	84
22	Genes, geology and germs: gut microbiota across a primate hybrid zone are explained by site soil properties, not host species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190431.	1.2	82
23	An Evolutionarily Conserved Sexual Signature in the Primate Brain. <i>PLoS Genetics</i> , 2008, 4, e1000100.	1.5	81
24	Public human microbiome data are dominated by highly developed countries. <i>PLoS Biology</i> , 2022, 20, e3001536.	2.6	78
25	Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. <i>MSystems</i> , 2019, 4, .	1.7	74
26	Functional Genomics of Host-“Microbiome Interactions in Humans. <i>Trends in Genetics</i> , 2018, 34, 30-40.	2.9	73
27	Interactions between the gut microbiome and host gene regulation in cystic fibrosis. <i>Genome Medicine</i> , 2020, 12, 12.	3.6	73
28	The “Domino Theory” of Gene Death: Gradual and Mass Gene Extinction Events in Three Lineages of Obligate Symbiotic Bacterial Pathogens. <i>Molecular Biology and Evolution</i> , 2006, 23, 310-316.	3.5	70
29	Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. <i>PLoS Genetics</i> , 2018, 14, e1007376.	1.5	65
30	Common methods for fecal sample storage in field studies yield consistent signatures of individual identity in microbiome sequencing data. <i>Scientific Reports</i> , 2016, 6, 31519.	1.6	63
31	Improving the usability and archival stability of bioinformatics software. <i>Genome Biology</i> , 2019, 20, 47.	3.8	62
32	A Signature of Evolutionary Constraint on a Subset of Ectopically Expressed Olfactory Receptor Genes. <i>Molecular Biology and Evolution</i> , 2008, 26, 491-494.	3.5	59
33	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. <i>Molecular Biology and Evolution</i> , 2017, 34, 2704-2715.	3.5	57
34	Identification of shared and disease-specific host gene-“microbiome associations across human diseases using multi-omic integration. <i>Nature Microbiology</i> , 2022, 7, 780-795.	5.9	57
35	Challenges and recommendations to improve the installability and archival stability of omics computational tools. <i>PLoS Biology</i> , 2019, 17, e3000333.	2.6	54
36	A Combination of Genomic Approaches Reveals the Role of FOXO1a in Regulating an Oxidative Stress Response Pathway. <i>PLoS ONE</i> , 2008, 3, e1670.	1.1	41

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37	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. <i>MSphere</i> , 2019, 4, .	1.3	40
38	Atopic Dermatitis Susceptibility Variants in Filaggrin Hitchhike Hornerin Selective Sweep. <i>Genome Biology and Evolution</i> , 2016, 8, 3240-3255.	1.1	35
39	Population dynamics of the human gut microbiome: change is the only constant. <i>Genome Biology</i> , 2019, 20, 150.	3.8	33
40	Recent evolution of the salivary mucin MUC7. <i>Scientific Reports</i> , 2016, 6, 31791.	1.6	30
41	Genetic and Transcriptional Analysis of Human Host Response to Healthy Gut Microbiota. <i>MSystems</i> , 2016, 1, .	1.7	28
42	Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. <i>Gastroenterology</i> , 2021, 161, 1194-1207.e8.	0.6	28
43	Segmental Duplications Contribute to Gene Expression Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2009, 182, 627-630.	1.2	26
44	Comparative metabolomics in primates reveals the effects of diet and gene regulatory variation on metabolic divergence. <i>Scientific Reports</i> , 2015, 4, 5809.	1.6	24
45	Selective Constraints in Experimentally Defined Primate Regulatory Regions. <i>PLoS Genetics</i> , 2008, 4, e1000157.	1.5	20
46	Synchrony and idiosyncrasy in the gut microbiome of wild baboons. <i>Nature Ecology and Evolution</i> , 2022, 6, 955-964.	3.4	18
47	Transposon mutagenesis screen in mice identifies TM9SF2 as a novel colorectal cancer oncogene. <i>Scientific Reports</i> , 2018, 8, 15327.	1.6	17
48	International authorship and collaboration across bioRxiv preprints. <i>ELife</i> , 2020, 9, .	2.8	17
49	Using Reporter Gene Assays to Identify cis Regulatory Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2007, 176, 2069-2076.	1.2	15
50	Integrating tumor genomics into studies of the microbiome in colorectal cancer. <i>Gut Microbes</i> , 2019, 10, 547-552.	4.3	14
51	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. <i>PLoS ONE</i> , 2015, 10, e0121644.	1.1	13
52	Traditional Human Populations and Nonhuman Primates Show Parallel Gut Microbiome Adaptations to Analogous Ecological Conditions. <i>MSystems</i> , 2020, 5, .	1.7	13
53	Microbial control of host gene regulation and the evolution of host-microbiome interactions in primates. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190598.	1.8	12
54	Rxivist.org: Sorting biology preprints using social media and readership metrics. <i>PLoS Biology</i> , 2019, 17, e3000269.	2.6	10

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55	HOMINID: a framework for identifying associations between host genetic variation and microbiome composition. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	9
56	Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057.	2.9	9
57	Mapping gastrointestinal gene expression patterns in wild primates and humans via fecal RNA-seq. <i>BMC Genomics</i> , 2019, 20, 493.	1.2	8
58	The gut microbiome in konzo. <i>Nature Communications</i> , 2021, 12, 5371.	5.8	8
59	Crowdsourcing Our National Gut. <i>MSystems</i> , 2018, 3, .	1.7	3
60	<i>BiomeHorizon</i> : Visualizing Microbiome Time Series Data in R. <i>MSystems</i> , 2022, 7, e0138021.	1.7	2
61	Host microbe interactions in the primate gut: Implications for human origins. <i>FASEB Journal</i> , 2018, 32, 101.1-101.1.	0.2	1
62	Host microbe interactions in the primate gut: Implications for human origins. <i>FASEB Journal</i> , 2018, 32, 101.1.	0.2	0