

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

109321

35
h-index

118850

62
g-index

82
all docs

82
docs citations

82
times ranked

13678
citing authors

#	ARTICLE	IF	CITATIONS
1	Public human microbiome data are dominated by highly developed countries. <i>PLoS Biology</i> , 2022, 20, e3001536.	5.6	78
2	<i>BiomeHorizon</i> : Visualizing Microbiome Time Series Data in R. <i>MSystems</i> , 2022, 7, e0138021.	3.8	2
3	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.	13.3	57
4	Synchrony and idiosyncrasy in the gut microbiome of wild baboons. <i>Nature Ecology and Evolution</i> , 2022, 6, 955-964.	7.8	18
5	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021, 373, 181-186.	12.6	126
6	The gut microbiome in konzo. <i>Nature Communications</i> , 2021, 12, 5371.	12.8	8
7	Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. <i>Gastroenterology</i> , 2021, 161, 1194-1207.e8.	1.3	28
8	Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057.	6.4	9
9	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	28.9	217
10	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.	4.0	12
11	Interactions between the gut microbiome and host gene regulation in cystic fibrosis. <i>Genome Medicine</i> , 2020, 12, 12.	8.2	73
12	International authorship and collaboration across bioRxiv preprints. <i>ELife</i> , 2020, 9, .	6.0	17
13	Traditional Human Populations and Nonhuman Primates Show Parallel Gut Microbiome Adaptations to Analogous Ecological Conditions. <i>MSystems</i> , 2020, 5, .	3.8	13
14	Population dynamics of the human gut microbiome: change is the only constant. <i>Genome Biology</i> , 2019, 20, 150.	8.8	33
15	Challenges and recommendations to improve the installability and archival stability of omics computational tools. <i>PLoS Biology</i> , 2019, 17, e3000333.	5.6	54
16	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. <i>MSphere</i> , 2019, 4, .	2.9	40
17	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	13.3	141
18	Mapping gastrointestinal gene expression patterns in wild primates and humans via fecal RNA-seq. <i>BMC Genomics</i> , 2019, 20, 493.	2.8	8

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19	Rxiv.org: Sorting biology preprints using social media and readership metrics. PLoS Biology, 2019, 17, e3000269.	5.6	10
20	Genes, geology and germs: gut microbiota across a primate hybrid zone are explained by site soil properties, not host species. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190431.	2.6	82
21	Improving the usability and archival stability of bioinformatics software. Genome Biology, 2019, 20, 47.	8.8	62
22	Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. MSystems, 2019, 4, .	3.8	74
23	Integrating tumor genomics into studies of the microbiome in colorectal cancer. Gut Microbes, 2019, 10, 547-552.	9.8	14
24	Tracking the popularity and outcomes of all bioRxiv preprints. ELife, 2019, 8, .	6.0	138
25	Functional Genomics of Host-Microbiome Interactions in Humans. Trends in Genetics, 2018, 34, 30-40.	6.7	73
26	Crowdsourcing Our National Gut. MSystems, 2018, 3, .	3.8	3
27	Gut microbiota diversity across ethnicities in the United States. PLoS Biology, 2018, 16, e2006842.	5.6	216
28	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. Genome Medicine, 2018, 10, 78.	8.2	107
29	Transposon mutagenesis screen in mice identifies TM9SF2 as a novel colorectal cancer oncogene. Scientific Reports, 2018, 8, 15327.	3.3	17
30	Interaction between Host MicroRNAs and the Gut Microbiota in Colorectal Cancer. MSystems, 2018, 3, .	3.8	97
31	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. American Journal of Primatology, 2018, 80, e22867.	1.7	100
32	Host microbe interactions in the primate gut: Implications for human origins. FASEB Journal, 2018, 32, 101.1-101.1.	0.5	1
33	Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. PLoS Genetics, 2018, 14, e1007376.	3.5	65
34	Host microbe interactions in the primate gut: Implications for human origins. FASEB Journal, 2018, 32, 101.1.	0.5	0
35	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. Molecular Biology and Evolution, 2017, 34, 2704-2715.	8.9	57
36	HOMINID: a framework for identifying associations between host genetic variation and microbiome composition. GigaScience, 2017, 6, 1-7.	6.4	9

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37	Atopic Dermatitis Susceptibility Variants in Filaggrin Hitchhike Hornerin Selective Sweep. <i>Genome Biology and Evolution</i> , 2016, 8, 3240-3255.	2.5	35
38	Genetic and Transcriptional Analysis of Human Host Response to Healthy Gut Microbiota. <i>MSystems</i> , 2016, 1, .	3.8	28
39	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.	3.3	63
40	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	28.9	419
41	Recent evolution of the salivary mucin MUC7. <i>Scientific Reports</i> , 2016, 6, 31791.	3.3	30
42	Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. <i>Cell Reports</i> , 2016, 14, 2142-2153.	6.4	231
43	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.	9.8	84
44	Social networks predict gut microbiome composition in wild baboons. <i>ELife</i> , 2015, 4, .	6.0	403
45	Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. <i>Genome Medicine</i> , 2015, 7, 55.	8.2	197
46	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	8.8	612
47	Comparative metabolomics in primates reveals the effects of diet and gene regulatory variation on metabolic divergence. <i>Scientific Reports</i> , 2015, 4, 5809.	3.3	24
48	Variation in Rural African Gut Microbiota Is Strongly Correlated with Colonization by <i>Entamoeba</i> and Subsistence. <i>PLoS Genetics</i> , 2015, 11, e1005658.	3.5	171
49	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. <i>PLoS ONE</i> , 2015, 10, e0121644.	2.5	13
50	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	28.9	2,523
51	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. <i>Genetics</i> , 2011, 187, 1225-1234.	2.9	89
52	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	5.5	239
53	Functional Comparison of Innate Immune Signaling Pathways in Primates. <i>PLoS Genetics</i> , 2010, 6, e1001249.	3.5	94
54	Segmental Duplications Contribute to Gene Expression Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2009, 182, 627-630.	2.9	26

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55	Natural Selection on Genes that Underlie Human Disease Susceptibility. <i>Current Biology</i> , 2008, 18, 883-889.	3.9	207
56	A Signature of Evolutionary Constraint on a Subset of Ectopically Expressed Olfactory Receptor Genes. <i>Molecular Biology and Evolution</i> , 2008, 26, 491-494.	8.9	59
57	Selective Constraints in Experimentally Defined Primate Regulatory Regions. <i>PLoS Genetics</i> , 2008, 4, e1000157.	3.5	20
58	Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271.	3.5	143
59	An Evolutionarily Conserved Sexual Signature in the Primate Brain. <i>PLoS Genetics</i> , 2008, 4, e1000100.	3.5	81
60	A Combination of Genomic Approaches Reveals the Role of FOXO1a in Regulating an Oxidative Stress Response Pathway. <i>PLoS ONE</i> , 2008, 3, e1670.	2.5	41
61	Using Reporter Gene Assays to Identify cis Regulatory Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2007, 176, 2069-2076.	2.9	15
62	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.	8.9	70