

Ran Blekhman

List of Publications by Year in descending order

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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 | Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799. | 28.9 | 2,523 |
| 2 | Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191. | 8.8 | 612 |
| 3 | Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21. | 28.9 | 419 |
| 4 | Social networks predict gut microbiome composition in wild baboons. <i>ELife</i> , 2015, 4, . | 6.0 | 403 |
| 5 | Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189. | 5.5 | 239 |
| 6 | 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 |
| 7 | Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17. | 28.9 | 217 |
| 8 | Gut microbiota diversity across ethnicities in the United States. <i>PLoS Biology</i> , 2018, 16, e2006842. | 5.6 | 216 |
| 9 | Natural Selection on Genes that Underlie Human Disease Susceptibility. <i>Current Biology</i> , 2008, 18, 883-889. | 3.9 | 207 |
| 10 | Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. <i>Genome Medicine</i> , 2015, 7, 55. | 8.2 | 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. | 3.5 | 171 |
| 12 | Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. <i>PLoS Genetics</i> , 2008, 4, e1000271. | 3.5 | 143 |
| 13 | Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700. | 13.3 | 141 |
| 14 | Tracking the popularity and outcomes of all bioRxiv preprints. <i>ELife</i> , 2019, 8, . | 6.0 | 138 |
| 15 | Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021, 373, 181-186. | 12.6 | 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. | 8.2 | 107 |
| 17 | The gut microbiome of nonhuman primates: Lessons in ecology and evolution. <i>American Journal of Primatology</i> , 2018, 80, e22867. | 1.7 | 100 |
| 18 | Interaction between Host MicroRNAs and the Gut Microbiota in Colorectal Cancer. <i>MSystems</i> , 2018, 3, . | 3.8 | 97 |

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|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | Functional Comparison of Innate Immune Signaling Pathways in Primates. PLoS Genetics, 2010, 6, e1001249. | 3.5 | 94 |
| 20 | Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. Genetics, 2011, 187, 1225-1234. | 2.9 | 89 |
| 21 | Temporal variation selects for diet- <i>microbe</i> co-metabolic traits in the gut of <i>Gorilla</i> spp. ISME Journal, 2016, 10, 514-526. | 9.8 | 84 |
| 22 | 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 |
| 23 | An Evolutionarily Conserved Sexual Signature in the Primate Brain. PLoS Genetics, 2008, 4, e1000100. | 3.5 | 81 |
| 24 | Public human microbiome data are dominated by highly developed countries. PLoS Biology, 2022, 20, e3001536. | 5.6 | 78 |
| 25 | Gut Microbiota Has a Widespread and Modifiable Effect on Host Gene Regulation. MSystems, 2019, 4, . | 3.8 | 74 |
| 26 | Functional Genomics of Host- <i>Microbiome</i> Interactions in Humans. Trends in Genetics, 2018, 34, 30-40. | 6.7 | 73 |
| 27 | Interactions between the gut microbiome and host gene regulation in cystic fibrosis. Genome Medicine, 2020, 12, 12. | 8.2 | 73 |
| 28 | The <i>“Domino Theory”</i> of Gene Death: Gradual and Mass Gene Extinction Events in Three Lineages of Obligate Symbiotic Bacterial Pathogens. Molecular Biology and Evolution, 2006, 23, 310-316. | 8.9 | 70 |
| 29 | Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. PLoS Genetics, 2018, 14, e1007376. | 3.5 | 65 |
| 30 | Common methods for fecal sample storage in field studies yield consistent signatures of individual identity in microbiome sequencing data. Scientific Reports, 2016, 6, 31519. | 3.3 | 63 |
| 31 | Improving the usability and archival stability of bioinformatics software. Genome Biology, 2019, 20, 47. | 8.8 | 62 |
| 32 | A Signature of Evolutionary Constraint on a Subset of Ectopically Expressed Olfactory Receptor Genes. Molecular Biology and Evolution, 2008, 26, 491-494. | 8.9 | 59 |
| 33 | Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. Molecular Biology and Evolution, 2017, 34, 2704-2715. | 8.9 | 57 |
| 34 | Identification of shared and disease-specific host <i>gene-<i>microbiome</i></i> associations across human diseases using multi-omic integration. Nature Microbiology, 2022, 7, 780-795. | 13.3 | 57 |
| 35 | Challenges and recommendations to improve the installability and archival stability of omics computational tools. PLoS Biology, 2019, 17, e3000333. | 5.6 | 54 |
| 36 | A Combination of Genomic Approaches Reveals the Role of FOXO1a in Regulating an Oxidative Stress Response Pathway. PLoS ONE, 2008, 3, e1670. | 2.5 | 41 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. <i>MSphere</i> , 2019, 4, . | 2.9 | 40 |
| 38 | Atopic Dermatitis Susceptibility Variants in Filaggrin Hitchhike Hornerin Selective Sweep. <i>Genome Biology and Evolution</i> , 2016, 8, 3240-3255. | 2.5 | 35 |
| 39 | Population dynamics of the human gut microbiome: change is the only constant. <i>Genome Biology</i> , 2019, 20, 150. | 8.8 | 33 |
| 40 | Recent evolution of the salivary mucin MUC7. <i>Scientific Reports</i> , 2016, 6, 31791. | 3.3 | 30 |
| 41 | Genetic and Transcriptional Analysis of Human Host Response to Healthy Gut Microbiota. <i>MSystems</i> , 2016, 1, . | 3.8 | 28 |
| 42 | Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. <i>Gastroenterology</i> , 2021, 161, 1194-1207.e8. | 1.3 | 28 |
| 43 | Segmental Duplications Contribute to Gene Expression Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2009, 182, 627-630. | 2.9 | 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. | 3.3 | 24 |
| 45 | Selective Constraints in Experimentally Defined Primate Regulatory Regions. <i>PLoS Genetics</i> , 2008, 4, e1000157. | 3.5 | 20 |
| 46 | Synchrony and idiosyncrasy in the gut microbiome of wild baboons. <i>Nature Ecology and Evolution</i> , 2022, 6, 955-964. | 7.8 | 18 |
| 47 | Transposon mutagenesis screen in mice identifies TM9SF2 as a novel colorectal cancer oncogene. <i>Scientific Reports</i> , 2018, 8, 15327. | 3.3 | 17 |
| 48 | International authorship and collaboration across bioRxiv preprints. <i>ELife</i> , 2020, 9, . | 6.0 | 17 |
| 49 | Using Reporter Gene Assays to Identify cis Regulatory Differences Between Humans and Chimpanzees. <i>Genetics</i> , 2007, 176, 2069-2076. | 2.9 | 15 |
| 50 | Integrating tumor genomics into studies of the microbiome in colorectal cancer. <i>Gut Microbes</i> , 2019, 10, 547-552. | 9.8 | 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. | 2.5 | 13 |
| 52 | Traditional Human Populations and Nonhuman Primates Show Parallel Gut Microbiome Adaptations to Analogous Ecological Conditions. <i>MSystems</i> , 2020, 5, . | 3.8 | 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. | 4.0 | 12 |
| 54 | Rxivist.org: Sorting biology preprints using social media and readership metrics. <i>PLoS Biology</i> , 2019, 17, e3000269. | 5.6 | 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. | 6.4 | 9 |
| 56 | Interspecies variation in hominid gut microbiota controls host gene regulation. <i>Cell Reports</i> , 2021, 37, 110057. | 6.4 | 9 |
| 57 | Mapping gastrointestinal gene expression patterns in wild primates and humans via fecal RNA-seq. <i>BMC Genomics</i> , 2019, 20, 493. | 2.8 | 8 |
| 58 | The gut microbiome in konzo. <i>Nature Communications</i> , 2021, 12, 5371. | 12.8 | 8 |
| 59 | Crowdsourcing Our National Gut. <i>MSystems</i> , 2018, 3, . | 3.8 | 3 |
| 60 | <i>BiomeHorizon</i> : Visualizing Microbiome Time Series Data in R. <i>MSystems</i> , 2022, 7, e0138021. | 3.8 | 2 |
| 61 | Host microbe interactions in the primate gut: Implications for human origins. <i>FASEB Journal</i> , 2018, 32, 101.1-101.1. | 0.5 | 1 |
| 62 | Host microbe interactions in the primate gut: Implications for human origins. <i>FASEB Journal</i> , 2018, 32, 101.1. | 0.5 | 0 |