

# Dan Knights

## List of Publications by Year in descending order

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100  
papers

84,824  
citations

26630

56  
h-index

32842

100  
g-index

110  
all docs

110  
docs citations

110  
times ranked

74584  
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	19.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
3	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	17.5	8,049
4	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	27.8	6,247
5	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. <i>Science</i> , 2011, 334, 105-108.	12.6	5,253
6	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.0	2,582
7	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	9.8	2,280
8	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	12.6	1,712
9	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	19.0	1,284
10	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. <i>Science</i> , 2013, 339, 548-554.	12.6	1,012
11	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	9.6	934
12	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	6.0	801
13	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
14	Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. <i>Nature Biotechnology</i> , 2016, 34, 942-949.	17.5	623
15	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
16	US Immigration Westernizes the Human Gut Microbiome. <i>Cell</i> , 2018, 175, 962-972.e10.	28.9	511
17	Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. <i>Cell Host and Microbe</i> , 2019, 25, 789-802.e5.	11.0	441
18	Antibiotics, Pediatric Dysbiosis, and Disease. <i>Cell Host and Microbe</i> , 2015, 17, 553-564.	11.0	428

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19	Advances in inflammatory bowel disease pathogenesis: linking host genetics and the microbiome. <i>Gut</i> , 2013, 62, 1505-1510.	12.1	387
20	Supervised classification of human microbiota. <i>FEMS Microbiology Reviews</i> , 2011, 35, 343-359.	8.6	377
21	Captivity humanizes the primate microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10376-10381.	7.1	369
22	Stable Engraftment of <i>Bifidobacterium longum</i> AH1206 in the Human Gut Depends on Individualized Features of the Resident Microbiome. <i>Cell Host and Microbe</i> , 2016, 20, 515-526.	11.0	337
23	Chemotherapy-driven dysbiosis in the intestinal microbiome. <i>Alimentary Pharmacology and Therapeutics</i> , 2015, 42, 515-528.	3.7	334
24	Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.	8.2	322
25	Rethinking "Enterotypes". <i>Cell Host and Microbe</i> , 2014, 16, 433-437.	11.0	321
26	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018, 3, .	3.8	293
27	Antibiotic-mediated gut microbiome perturbation accelerates development of type 1 diabetes in mice. <i>Nature Microbiology</i> , 2016, 1, 16140.	13.3	275
28	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <i>Microbiome</i> , 2015, 3, 10.	11.1	218
29	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	28.9	217
30	Substituting whole grains for refined grains in a 6-wk randomized trial has a modest effect on gut microbiota and immune and inflammatory markers of healthy adults. <i>American Journal of Clinical Nutrition</i> , 2017, 105, 635-650.	4.7	203
31	Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. <i>Genome Medicine</i> , 2015, 7, 55.	8.2	197
32	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	197
33	Insights from Characterizing Extinct Human Gut Microbiomes. <i>PLoS ONE</i> , 2012, 7, e51146.	2.5	178
34	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
35	Small intestinal microbial dysbiosis underlies symptoms associated with functional gastrointestinal disorders. <i>Nature Communications</i> , 2019, 10, 1012.	12.8	168
36	Pretreatment gut microbiome predicts chemotherapy-related bloodstream infection. <i>Genome Medicine</i> , 2016, 8, 49.	8.2	136

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37	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	9.6	134
38	Human-Associated Microbial Signatures: Examining Their Predictive Value. <i>Cell Host and Microbe</i> , 2011, 10, 292-296.	11.0	134
39	Development of the Human Mycobiome over the First Month of Life and across Body Sites. <i>MSystems</i> , 2018, 3, .	3.8	132
40	Intergenerational transfer of antibiotic-perturbed microbiota enhances colitis in susceptible mice. <i>Nature Microbiology</i> , 2018, 3, 234-242.	13.3	118
41	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. <i>American Journal of Primatology</i> , 2018, 80, e22867.	1.7	100
42	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018, 8, 6219.	3.3	99
43	Effects of Diet-Modulated Autologous Fecal Microbiota Transplantation on Weight Regain. <i>Gastroenterology</i> , 2021, 160, 158-173.e10.	1.3	95
44	High-Fat Diet Changes Fungal Microbiomes and Interkingdom Relationships in the Murine Gut. <i>MSphere</i> , 2017, 2, .	2.9	94
45	Patterns of seasonality and group membership characterize the gut microbiota in a longitudinal study of wild Verreaux's sifakas ( <i>Propithecus verreauxi</i> ). <i>Ecology and Evolution</i> , 2017, 7, 5732-5745.	1.9	90
46	Gut microbiota modulation with long-chain corn bran arabinoxylan in adults with overweight and obesity is linked to an individualized temporal increase in fecal propionate. <i>Microbiome</i> , 2020, 8, 118.	11.1	81
47	A Guide to Diet-Microbiome Study Design. <i>Frontiers in Nutrition</i> , 2020, 7, 79.	3.7	78
48	Substituting whole grains for refined grains in a 6-wk randomized trial favorably affects energy-balance metrics in healthy men and postmenopausal women. <i>American Journal of Clinical Nutrition</i> , 2017, 105, 589-599.	4.7	74
49	Functional Genomics of Host-Microbiome Interactions in Humans. <i>Trends in Genetics</i> , 2018, 34, 30-40.	6.7	73
50	An Increased Abundance of Clostridiaceae Characterizes Arthritis in Inflammatory Bowel Disease and Rheumatoid Arthritis: A Cross-sectional Study. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 902-913.	1.9	72
51	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. <i>ELife</i> , 2018, 7, .	6.0	70
52	Infant fungal communities: current knowledge and research opportunities. <i>BMC Medicine</i> , 2017, 15, 30.	5.5	67
53	SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. <i>MSystems</i> , 2018, 3, .	3.8	66
54	NINJA-OPS: Fast Accurate Marker Gene Alignment Using Concatenated Ribosomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004658.	3.2	66

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55	Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. PLoS Genetics, 2018, 14, e1007376.	3.5	65
56	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	28.9	64
57	Supplementation with a probiotic mixture accelerates gut microbiome maturation and reduces intestinal inflammation in extremely preterm infants. Cell Host and Microbe, 2022, 30, 696-711.e5.	11.0	63
58	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. Scientific Reports, 2018, 8, 11159.	3.3	60
59	Identification of shared and disease-specific host gene-microbiome associations across human diseases using multi-omic integration. Nature Microbiology, 2022, 7, 780-795.	13.3	57
60	Microbiome Learning Repo (ML Repo): A public repository of microbiome regression and classification tasks. GigaScience, 2019, 8, .	6.4	54
61	Temporal Relationships Exist Between Cecum, Ileum, and Litter Bacterial Microbiomes in a Commercial Turkey Flock, and Subtherapeutic Penicillin Treatment Impacts Ileum Bacterial Community Establishment. Frontiers in Veterinary Science, 2015, 2, 56.	2.2	48
62	SplinctomeR Enables Group Comparisons in Longitudinal Microbiome Studies. Frontiers in Microbiology, 2018, 9, 785.	3.5	48
63	A Microbiome Foundation for the Study of Crohn's Disease. Cell Host and Microbe, 2017, 21, 301-304.	11.0	46
64	The effects of the Green-Mediterranean diet on cardiometabolic health are linked to gut microbiome modifications: a randomized controlled trial. Genome Medicine, 2022, 14, 29.	8.2	46
65	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. PLoS ONE, 2015, 10, e0116705.	2.5	45
66	Supervised classification of microbiota mitigates mislabeling errors. ISME Journal, 2011, 5, 570-573.	9.8	42
67	Multi-omics analysis of inflammatory bowel disease. Immunology Letters, 2014, 162, 62-68.	2.5	42
68	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. Bioinformatics, 2020, 36, 4088-4090.	4.1	42
69	Genetic effects on the commensal microbiota in inflammatory bowel disease patients. PLoS Genetics, 2019, 15, e1008018.	3.5	35
70	Antibiotics and Host-Tailored Probiotics Similarly Modulate Effects on the Developing Avian Microbiome, Mycobiome, and Host Gene Expression. MBio, 2019, 10, .	4.1	33
71	Elucidating the role of the gut microbiota in the physiological effects of dietary fiber. Microbiome, 2022, 10, 77.	11.1	31
72	Diverse bacterial communities exist on canine skin and are impacted by cohabitation and time. PeerJ, 2017, 5, e3075.	2.0	30

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73	Obesity induces gut microbiota alterations and augments acute graft-versus-host disease after allogeneic stem cell transplantation. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	29
74	Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. <i>Gastroenterology</i> , 2021, 161, 1194-1207.e8.	1.3	28
75	Functional genomics identifies negative regulatory nodes controlling phagocyte oxidative burst. <i>Nature Communications</i> , 2015, 6, 7838.	12.8	26
76	Sex Bias in Gut Microbiome Transmission in Newly Paired Marmosets ( <i>Callithrix jacchus</i> ). <i>MSystems</i> , 2020, 5, .	3.8	26
77	Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. <i>Clinical Transplantation</i> , 2018, 32, e13436.	1.6	24
78	A Potential Role for Stress-Induced Microbial Alterations in IgA-Associated Irritable Bowel Syndrome with Diarrhea. <i>Cell Reports Medicine</i> , 2020, 1, 100124.	6.5	24
79	Moving beyond <i>de novo</i> clustering in fungal community ecology. <i>New Phytologist</i> , 2017, 216, 629-634.	7.3	17
80	Toward revision of antimicrobial therapies in hematopoietic stem cell transplantation: target the pathogens, but protect the indigenous microbiota. <i>Translational Research</i> , 2017, 179, 116-125.	5.0	16
81	CLOUD: a non-parametric detection test for microbiome outliers. <i>Microbiome</i> , 2018, 6, 137.	11.1	16
82	Pretransplant Gut Colonization with Intrinsically Vancomycin-Resistant Enterococci ( <i>E. gallinarum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Blood and Marrow Transplantation, 2018, 24, 1260-1263.	2.0	15
83	Placentas delivered by preëpregnant obese women have reduced abundance and diversity in the microbiome. <i>FASEB Journal</i> , 2021, 35, e21524.	0.5	14
84	Bacterial communities associated with wood rot fungi that use distinct decomposition mechanisms. <i>ISME Communications</i> , 2022, 2, .	4.2	13
85	Bygiene: The New Paradigm of Bidirectional Hygiene. <i>Yale Journal of Biology and Medicine</i> , 2015, 88, 359-65.	0.2	12
86	Metagenomic Information Recovery from Human Stool Samples Is Influenced by Sequencing Depth and Profiling Method. <i>Genes</i> , 2020, 11, 1380.	2.4	11
87	Saliva Testing Is Accurate for Early-Stage and Presymptomatic COVID-19. <i>Microbiology Spectrum</i> , 2021, 9, e0008621.	3.0	11
88	US Immigration Is Associated With Rapid and Persistent Acquisition of Antibiotic Resistance Genes in the Gut. <i>Clinical Infectious Diseases</i> , 2020, 71, 419-421.	5.8	10
89	HOMINID: a framework for identifying associations between host genetic variation and microbiome composition. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	9
90	Bacterial community structure and function distinguish gut sites in captive redâ€shanked doucs ( <i>Pygathrix nemaeus</i> ). <i>American Journal of Primatology</i> , 2019, 81, e22977.	1.7	9

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91	High-Throughput flaA Short Variable Region Sequencing to Assess Campylobacter Diversity in Fecal Samples From Birds. <i>Frontiers in Microbiology</i> , 2018, 9, 2201.	3.5	8
92	The guts of obesity: progress and challenges in linking gut microbes to obesity. <i>Discovery Medicine</i> , 2015, 19, 81-8.	0.5	8
93	Wild primate microbiomes prevent weight gain in germ-free mice. <i>Animal Microbiome</i> , 2020, 2, 16.	3.8	7
94	Gut microbiota from metabolic disease-resistant, macrophage-specific RIP140 knockdown mice improves metabolic phenotype and gastrointestinal integrity. <i>Scientific Reports</i> , 2016, 6, 38599.	3.3	5
95	Early <i>E. casseliflavus</i> gut colonization and outcomes of allogeneic hematopoietic cell transplantation. <i>PLoS ONE</i> , 2019, 14, e0220850.	2.5	4
96	Shotgun sequencing of the faecal microbiome to predict response to steroids in patients with lower gastrointestinal acute graft-versus-host disease: An exploratory analysis. <i>British Journal of Haematology</i> , 2021, 192, e69-e73.	2.5	3
97	Whole Wheat and Bran Cereal Affects Microbiome Stability. <i>Current Developments in Nutrition</i> , 2021, 5, 1162.	0.3	2
98	Pre-Engraftment Gut Colonization with <i>Enterococcus Casseliflavus</i> Improves Survival after Allogeneic Hematopoietic Cell Transplantation. <i>Blood</i> , 2018, 132, 813-813.	1.4	0
99	Obesity-Induced Microbiome Alterations Result in Severe Gastrointestinal Graft-Versus-Host Disease Following Allogeneic Hematopoietic Stem Cell Transplantation. <i>Blood</i> , 2019, 134, 1922-1922.	1.4	0
100	Nutrition As a Predictor of Microbiome Injury in Allo-HCT. <i>Blood</i> , 2021, 138, 746-746.	1.4	0