

# Dan Knights

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6321948/publications.pdf>

Version: 2024-02-01

100  
papers

84,824  
citations

30551

56  
h-index

37326

100  
g-index

110  
all docs

110  
docs citations

110  
times ranked

80783  
citing authors

#	ARTICLE	IF	CITATIONS
1	The effects of the Green-Mediterranean diet on cardiometabolic health are linked to gut microbiome modifications: a randomized controlled trial. <i>Genome Medicine</i> , 2022, 14, 29.	3.6	46
2	Bacterial communities associated with wood rot fungi that use distinct decomposition mechanisms. <i>ISME Communications</i> , 2022, 2, .	1.7	13
3	Supplementation with a probiotic mixture accelerates gut microbiome maturation and reduces intestinal inflammation in extremely preterm infants. <i>Cell Host and Microbe</i> , 2022, 30, 696-711.e5.	5.1	63
4	Elucidating the role of the gut microbiota in the physiological effects of dietary fiber. <i>Microbiome</i> , 2022, 10, 77.	4.9	31
5	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
6	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.	1.2	3
7	Effects of Diet-Modulated Autologous Fecal Microbiota Transplantation on Weight Regain. <i>Gastroenterology</i> , 2021, 160, 158-173.e10.	0.6	95
8	Placentas delivered by pre-pregnant obese women have reduced abundance and diversity in the microbiome. <i>FASEB Journal</i> , 2021, 35, e21524.	0.2	14
9	Whole Wheat and Bran Cereal Affects Microbiome Stability. <i>Current Developments in Nutrition</i> , 2021, 5, 1162.	0.1	2
10	Saliva Testing Is Accurate for Early-Stage and Presymptomatic COVID-19. <i>Microbiology Spectrum</i> , 2021, 9, e0008621.	1.2	11
11	Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. <i>Gastroenterology</i> , 2021, 161, 1194-1207.e8.	0.6	28
12	Nutrition As a Predictor of Microbiome Injury in Allo-HCT. <i>Blood</i> , 2021, 138, 746-746.	0.6	0
13	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
14	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.	2.9	10
15	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	13.5	217
16	A Potential Role for Stress-Induced Microbial Alterations in IgA-Associated Irritable Bowel Syndrome with Diarrhea. <i>Cell Reports Medicine</i> , 2020, 1, 100124.	3.3	24
17	Metagenomic Information Recovery from Human Stool Samples Is Influenced by Sequencing Depth and Profiling Method. <i>Genes</i> , 2020, 11, 1380.	1.0	11
18	Obesity induces gut microbiota alterations and augments acute graft-versus-host disease after allogeneic stem cell transplantation. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	29

#	ARTICLE	IF	CITATIONS
19	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.	4.9	81
20	Sex Bias in Gut Microbiome Transmission in Newly Paired Marmosets ( <i>Callithrix jacchus</i> ). <i>MSystems</i> , 2020, 5, .	1.7	26
21	SHOGLIN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , 2020, 36, 4088-4090.	1.8	42
22	Wild primate microbiomes prevent weight gain in germ-free mice. <i>Animal Microbiome</i> , 2020, 2, 16.	1.5	7
23	A Guide to Diet-Microbiome Study Design. <i>Frontiers in Nutrition</i> , 2020, 7, 79.	1.6	78
24	Early <i>E. casseliflavus</i> gut colonization and outcomes of allogeneic hematopoietic cell transplantation. <i>PLoS ONE</i> , 2019, 14, e0220850.	1.1	4
25	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
26	Antibiotics and Host-Tailored Probiotics Similarly Modulate Effects on the Developing Avian Microbiome, Mycobiome, and Host Gene Expression. <i>MBio</i> , 2019, 10, .	1.8	33
27	Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. <i>Cell Host and Microbe</i> , 2019, 25, 789-802.e5.	5.1	441
28	Bacterial community structure and function distinguish gut sites in captive red-shanked doucs ( <i>Pygathrix nemaeus</i> ). <i>American Journal of Primatology</i> , 2019, 81, e22977.	0.8	9
29	Microbiome Learning Repo (ML Repo): A public repository of microbiome regression and classification tasks. <i>GigaScience</i> , 2019, 8, .	3.3	54
30	Small intestinal microbial dysbiosis underlies symptoms associated with functional gastrointestinal disorders. <i>Nature Communications</i> , 2019, 10, 2012.	5.8	168
31	Genetic effects on the commensal microbiota in inflammatory bowel disease patients. <i>PLoS Genetics</i> , 2019, 15, e1008018.	1.5	35
32	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
33	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.	0.9	72
34	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.	0.6	0
35	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018, 8, 6219.	1.6	99
36	Pretransplant Gut Colonization with Intrinsically Vancomycin-Resistant Enterococci ( <i>E. gallinarum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 00 Blood and Marrow Transplantation, 2018, 24, 1260-1263.	2.0	15

#	ARTICLE	IF	CITATIONS
37	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
38	Development of the Human Mycobiome over the First Month of Life and across Body Sites. <i>MSystems</i> , 2018, 3, .	1.7	132
39	Functional Genomics of Host-Microbiome Interactions in Humans. <i>Trends in Genetics</i> , 2018, 34, 30-40.	2.9	73
40	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018, 3, .	1.7	293
41	SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. <i>MSystems</i> , 2018, 3, .	1.7	66
42	High-Throughput <i>flaA</i> Short Variable Region Sequencing to Assess <i>Campylobacter</i> Diversity in Fecal Samples From Birds. <i>Frontiers in Microbiology</i> , 2018, 9, 2201.	1.5	8
43	Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. <i>Clinical Transplantation</i> , 2018, 32, e13436.	0.8	24
44	US Immigration Westernizes the Human Gut Microbiome. <i>Cell</i> , 2018, 175, 962-972.e10.	13.5	511
45	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
46	Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. <i>Scientific Reports</i> , 2018, 8, 11159.	1.6	60
47	SplinctomeR Enables Group Comparisons in Longitudinal Microbiome Studies. <i>Frontiers in Microbiology</i> , 2018, 9, 785.	1.5	48
48	CLOUD: a non-parametric detection test for microbiome outliers. <i>Microbiome</i> , 2018, 6, 137.	4.9	16
49	The gut microbiome of nonhuman primates: Lessons in ecology and evolution. <i>American Journal of Primatology</i> , 2018, 80, e22867.	0.8	100
50	Intergenerational transfer of antibiotic-perturbed microbiota enhances colitis in susceptible mice. <i>Nature Microbiology</i> , 2018, 3, 234-242.	5.9	118
51	Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. <i>PLoS Genetics</i> , 2018, 14, e1007376.	1.5	65
52	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. <i>ELife</i> , 2018, 7, .	2.8	70
53	Pre-Engraftment Gut Colonization with <i>Enterococcus Casseliflavus</i> Improves Survival after Allogeneic Hematopoietic Cell Transplantation. <i>Blood</i> , 2018, 132, 813-813.	0.6	0
54	A Microbiome Foundation for the Study of Crohn's Disease. <i>Cell Host and Microbe</i> , 2017, 21, 301-304.	5.1	46

#	ARTICLE	IF	CITATIONS
55	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.	2.2	74
56	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.	2.2	203
57	High-Fat Diet Changes Fungal Microbiomes and Interkingdom Relationships in the Murine Gut. <i>MSphere</i> , 2017, 2, .	1.3	94
58	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.	0.8	90
59	Moving beyond <i>de novo</i> clustering in fungal community ecology. <i>New Phytologist</i> , 2017, 216, 629-634.	3.5	17
60	Infant fungal communities: current knowledge and research opportunities. <i>BMC Medicine</i> , 2017, 15, 30.	2.3	67
61	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.	2.2	16
62	HOMINID: a framework for identifying associations between host genetic variation and microbiome composition. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	9
63	Diverse bacterial communities exist on canine skin and are impacted by cohabitation and time. <i>PeerJ</i> , 2017, 5, e3075.	0.9	30
64	Gut microbiota from metabolic disease-resistant, macrophage-specific RIP140 knockdown mice improves metabolic phenotype and gastrointestinal integrity. <i>Scientific Reports</i> , 2016, 6, 38599.	1.6	5
65	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.	5.1	337
66	Captivity humanizes the primate microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10376-10381.	3.3	369
67	Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. <i>Nature Biotechnology</i> , 2016, 34, 942-949.	9.4	623
68	Antibiotic-mediated gut microbiome perturbation accelerates development of type 1 diabetes in mice. <i>Nature Microbiology</i> , 2016, 1, 16140.	5.9	275
69	Pretreatment gut microbiome predicts chemotherapy-related bloodstream infection. <i>Genome Medicine</i> , 2016, 8, 49.	3.6	136
70	NINJA-OPS: Fast Accurate Marker Gene Alignment Using Concatenated Ribosomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004658.	1.5	66
71	Chemotherapy-driven dysbiosis in the intestinal microbiome. <i>Alimentary Pharmacology and Therapeutics</i> , 2015, 42, 515-528.	1.9	334
72	Temporal Relationships Exist Between Cecum, Ileum, and Litter Bacterial Microbiomes in a Commercial Turkey Flock, and Subtherapeutic Penicillin Treatment Impacts Ileum Bacterial Community Establishment. <i>Frontiers in Veterinary Science</i> , 2015, 2, 56.	0.9	48

#	ARTICLE	IF	CITATIONS
73	Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. <i>Genome Medicine</i> , 2015, 7, 55.	3.6	197
74	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.	4.9	218
75	Antibiotics, Pediatric Dysbiosis, and Disease. <i>Cell Host and Microbe</i> , 2015, 17, 553-564.	5.1	428
76	Functional genomics identifies negative regulatory nodes controlling phagocyte oxidative burst. <i>Nature Communications</i> , 2015, 6, 7838.	5.8	26
77	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. <i>PLoS ONE</i> , 2015, 10, e0116705.	1.1	45
78	Bygiene: The New Paradigm of Bidirectional Hygiene. <i>Yale Journal of Biology and Medicine</i> , 2015, 88, 359-65.	0.2	12
79	The guts of obesity: progress and challenges in linking gut microbes to obesity. <i>Discovery Medicine</i> , 2015, 19, 81-8.	0.5	8
80	Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.	3.6	322
81	Multi-omics analysis of inflammatory bowel disease. <i>Immunology Letters</i> , 2014, 162, 62-68.	1.1	42
82	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
83	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	13.5	64
84	Rethinking "Enterotypes". <i>Cell Host and Microbe</i> , 2014, 16, 433-437.	5.1	321
85	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
86	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. <i>Science</i> , 2013, 339, 548-554.	6.0	1,012
87	Advances in inflammatory bowel disease pathogenesis: linking host genetics and the microbiome. <i>Gut</i> , 2013, 62, 1505-1510.	6.1	387
88	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	2.8	801
89	Insights from Characterizing Extinct Human Gut Microbiomes. <i>PLoS ONE</i> , 2012, 7, e51146.	1.1	178
90	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	13.7	6,247

#	ARTICLE	IF	CITATIONS
91	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712
92	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	13.9	934
93	Human-Associated Microbial Signatures: Examining Their Predictive Value. <i>Cell Host and Microbe</i> , 2011, 10, 292-296.	5.1	134
94	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. <i>Science</i> , 2011, 334, 105-108.	6.0	5,253
95	Supervised classification of human microbiota. <i>FEMS Microbiology Reviews</i> , 2011, 35, 343-359.	3.9	377
96	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	4.4	2,280
97	Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , 2011, 5, 570-573.	4.4	42
98	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	9.0	1,284
99	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
100	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	13.9	134