# Dan Knights

List of Publications by Year
in descending order

| | |
|---|---|
| 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 | QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336. | 9.0 | 31,818 |
| 2 | Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857. | 9.4 | 11,167 |
| 3 | Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821. | 9.4 | 8,049 |
| 4 | Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227. | 13.7 | 6,247 |
| 5 | Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. Science, 2011, 334, 105-108. | 6.0 | 5,253 |
| 6 | The Treatment-Naive Microbiome in New-Onset Crohn's Disease. Cell Host and Microbe, 2014, 15, 382-392. | 5.1 | 2,582 |
| 7 | UniFrac: an effective distance metric for microbial community comparison. ISME Journal, 2011, 5, 169-172. | 4.4 | 2,280 |
| 8 | Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. Science, 2011, 332, 970-974. | 6.0 | 1,712 |
| 9 | Bayesian community-wide culture-independent microbial source tracking. Nature Methods, 2011, 8, 761-763. | 9.0 | 1,284 |
| 10 | Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. Science, 2013, 339, 548-554. | 6.0 | 1,012 |
| 11 | Moving pictures of the human microbiome. Genome Biology, 2011, 12, R50. | 13.9 | 934 |
| 12 | Cohabiting family members share microbiota with one another and with their dogs. ELife, 2013, 2, e00458. | 2.8 | 801 |
| 13 | Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16. | 5.9 | 717 |
| 14 | Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. Nature Biotechnology, 2016, 34, 942-949. | 9.4 | 623 |
| 15 | American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, . | 1.7 | 604 |
| 16 | US Immigration Westernizes the Human Gut Microbiome. Cell, 2018, 175, 962-972.e10. | 13.5 | 511 |
| 17 | Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. Cell Host and Microbe, 2019, 25, 789-802.e5. | 5.1 | 441 |
| 18 | Antibiotics, Pediatric Dysbiosis, and Disease. Cell Host and Microbe, 2015, 17, 553-564. | 5.1 | 428 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | Advances in inflammatory bowel disease pathogenesis: linking host genetics and the microbiome. Gut, 2013, 62, 1505-1510. | 6.1 | 387 |
| 20 | Supervised classification of human microbiota. FEMS Microbiology Reviews, 2011, 35, 343-359. | 3.9 | 377 |
| 21 | Captivity humanizes the primate microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10376-10381. | 3.3 | 369 |
| 22 | Stable Engraftment of Bifidobacterium longum AH1206 in the Human Gut Depends on Individualized Features of the Resident Microbiome. Cell Host and Microbe, 2016, 20, 515-526. | 5.1 | 337 |
| 23 | Chemotherapyâ€driven dysbiosis in the intestinal microbiome. Alimentary Pharmacology and Therapeutics, 2015, 42, 515-528. | 1.9 | 334 |
| 24 | Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Medicine, 2014, 6, 107. | 3.6 | 322 |
| 25 | Rethinking â€œEnterotypesâ€. Cell Host and Microbe, 2014, 16, 433-437. | 5.1 | 321 |
| 26 | Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, . | 1.7 | 293 |
| 27 | Antibiotic-mediated gut microbiome perturbation accelerates development of type 1 diabetes in mice. Nature Microbiology, 2016, 1, 16140. | 5.9 | 275 |
| 28 | Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection. Microbiome, 2015, 3, 10. | 4.9 | 218 |
| 29 | Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. Cell, 2020, 182, 1460-1473.e17. | 13.5 | 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. American Journal of Clinical Nutrition, 2017, 105, 635-650. | 2.2 | 203 |
| 31 | Virulence genes are a signature of the microbiome in the colorectal tumor microenvironment. Genome Medicine, 2015, 7, 55. | 3.6 | 197 |
| 32 | Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477. | 5.8 | 197 |
| 33 | Insights from Characterizing Extinct Human Gut Microbiomes. PLoS ONE, 2012, 7, e51146. | 1.1 | 178 |
| 34 | Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892. | 15.2 | 170 |
| 35 | Small intestinal microbial dysbiosis underlies symptoms associated with functional gastrointestinal disorders. Nature Communications, 2019, 10, 2012. | 5.8 | 168 |
| 36 | Pretreatment gut microbiome predicts chemotherapy-related bloodstream infection. Genome Medicine, 2016, 8, 49. | 3.6 | 136 |

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|---|---------|-----|-----------|
| 37 | Direct sequencing of the human microbiome readily reveals community differences. Genome Biology, 2010, 11, 210. | 13.9 | 134 |
| 38 | Human-Associated Microbial Signatures: Examining Their Predictive Value. Cell Host and Microbe, 2011, 10, 292-296. | 5.1 | 134 |
| 39 | Development of the Human Mycobiome over the First Month of Life and across Body Sites. MSystems, 2018, 3, . | 1.7 | 132 |
| 40 | Intergenerational transfer of antibiotic-perturbed microbiota enhances colitis in susceptible mice. Nature Microbiology, 2018, 3, 234-242. | 5.9 | 118 |
| 41 | The gut microbiome of nonhuman primates: Lessons in ecology and evolution. American Journal of Primatology, 2018, 80, e22867. | 0.8 | 100 |
| 42 | Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. Scientific Reports, 2018, 8, 6219. | 1.6 | 99 |
| 43 | Effects of Diet-Modulated Autologous Fecal Microbiota Transplantation on Weight Regain. Gastroenterology, 2021, 160, 158-173.e10. | 0.6 | 95 |
| 44 | High-Fat Diet Changes Fungal Microbiomes and Interkingdom Relationships in the Murine Gut. MSphere, 2017, 2, . | 1.3 | 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>). Ecology and Evolution, 2017, 7, 5732-5745. | 0.8 | 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. Microbiome, 2020, 8, 118. | 4.9 | 81 |
| 47 | A Guide to Diet-Microbiome Study Design. Frontiers in Nutrition, 2020, 7, 79. | 1.6 | 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. American Journal of Clinical Nutrition, 2017, 105, 589-599. | 2.2 | 74 |
| 49 | Functional Genomics of Host–Microbiome Interactions in Humans. Trends in Genetics, 2018, 34, 30-40. | 2.9 | 73 |
| 50 | An Increased Abundance of Clostridiaceae Characterizes Arthritis in Inflammatory Bowel Disease and Rheumatoid Arthritis: A Cross-sectional Study. Inflammatory Bowel Diseases, 2019, 25, 902-913. | 0.9 | 72 |
| 51 | Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. ELife, 2018, 7, . | 2.8 | 70 |
| 52 | Infant fungal communities: current knowledge and research opportunities. BMC Medicine, 2017, 15, 30. | 2.3 | 67 |
| 53 | SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. MSystems, 2018, 3, . | 1.7 | 66 |
| 54 | NINJA-OPS: Fast Accurate Marker Gene Alignment Using Concatenated Ribosomes. PLoS Computational Biology, 2016, 12, e1004658. | 1.5 | 66 |

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|---|---------|-----|-----------|
| 55 | Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment. PLoS Genetics, 2018, 14, e1007376. | 1.5 | 65 |
| 56 | Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230. | 13.5 | 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. | 5.1 | 63 |
| 58 | Associations Between Nutrition, Gut Microbiome, and Health in A Novel Nonhuman Primate Model. Scientific Reports, 2018, 8, 11159. | 1.6 | 60 |
| 59 | Identification of shared and disease-specific host geneâ€"microbiome associations across human diseases using multi-omic integration. Nature Microbiology, 2022, 7, 780-795. | 5.9 | 57 |
| 60 | Microbiome Learning Repo (ML Repo): A public repository of microbiome regression and classification tasks. GigaScience, 2019, 8, . | 3.3 | 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. | 0.9 | 48 |
| 62 | SplinectomeR Enables Group Comparisons in Longitudinal Microbiome Studies. Frontiers in Microbiology, 2018, 9, 785. | 1.5 | 48 |
| 63 | A Microbiome Foundation for the Study of Crohnâ€™s Disease. Cell Host and Microbe, 2017, 21, 301-304. | 5.1 | 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. | 3.6 | 46 |
| 65 | Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. PLoS ONE, 2015, 10, e0116705. | 1.1 | 45 |
| 66 | Supervised classification of microbiota mitigates mislabeling errors. ISME Journal, 2011, 5, 570-573. | 4.4 | 42 |
| 67 | Multi-omics analysis of inflammatory bowel disease. Immunology Letters, 2014, 162, 62-68. | 1.1 | 42 |
| 68 | SHOGUN: a modular, accurate and scalable framework for microbiome quantification. Bioinformatics, 2020, 36, 4088-4090. | 1.8 | 42 |
| 69 | Genetic effects on the commensal microbiota in inflammatory bowel disease patients. PLoS Genetics, 2019, 15, e1008018. | 1.5 | 35 |
| 70 | Antibiotics and Host-Tailored Probiotics Similarly Modulate Effects on the Developing Avian Microbiome, Mycobiome, and Host Gene Expression. MBio, 2019, 10, . | 1.8 | 33 |
| 71 | Elucidating the role of the gut microbiota in the physiological effects of dietary fiber. Microbiome, 2022, 10, 77. | 4.9 | 31 |
| 72 | Diverse bacterial communities exist on canine skin and are impacted by cohabitation and time. PeerJ, 2017, 5, e3075. | 0.9 | 30 |

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|---|---------|----|-----------|
| 73 | Obesity induces gut microbiota alterations and augments acute graft-versus-host disease after allogeneic stem cell transplantation. Science Translational Medicine, 2020, 12, . | 5.8 | 29 |
| 74 | Multi-Omics Analyses Show Disease, Diet, and Transcriptome Interactions With the Virome. Gastroenterology, 2021, 161, 1194-1207.e8. | 0.6 | 28 |
| 75 | Functional genomics identifies negative regulatory nodes controlling phagocyte oxidative burst. Nature Communications, 2015, 6, 7838. | 5.8 | 26 |
| 76 | Sex Bias in Gut Microbiome Transmission in Newly Paired Marmosets (Callithrix jacchus). MSystems, 2020, 5, . | 1.7 | 26 |
| 77 | Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. Clinical Transplantation, 2018, 32, e13436. | 0.8 | 24 |
| 78 | A Potential Role for Stress-Induced Microbial Alterations in IgA-Associated Irritable Bowel Syndrome with Diarrhea. Cell Reports Medicine, 2020, 1, 100124. | 3.3 | 24 |
| 79 | Moving beyond <i>de novo</i> clustering in fungal community ecology. New Phytologist, 2017, 216, 629-634. | 3.5 | 17 |
| 80 | Toward revision of antimicrobial therapies in hematopoietic stem cell transplantation: target the pathogens, but protect the indigenous microbiota. Translational Research, 2017, 179, 116-125. | 2.2 | 16 |
| 81 | CLOUD: a non-parametric detection test for microbiome outliers. Microbiome, 2018, 6, 137. | 4.9 | 16 |
| 82 | Pretransplant Gut Colonization with Intrinsically Vancomycin-Resistant Enterococci (E. gallinarum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Blood and Marrow Transplantation, 2018, 24, 1260-1263. | 2.0 | 15 |
| 83 | Placentas delivered by pre–pregnant obese women have reduced abundance and diversity in the microbiome. FASEB Journal, 2021, 35, e21524. | 0.2 | 14 |
| 84 | Bacterial communities associated with wood rot fungi that use distinct decomposition mechanisms. ISME Communications, 2022, 2, . | 1.7 | 13 |
| 85 | Bygiene: The New Paradigm of Bidirectional Hygiene. Yale Journal of Biology and Medicine, 2015, 88, 359-65. | 0.2 | 12 |
| 86 | Metagenomic Information Recovery from Human Stool Samples Is Influenced by Sequencing Depth and Profiling Method. Genes, 2020, 11, 1380. | 1.0 | 11 |
| 87 | Saliva Testing Is Accurate for Early-Stage and Presymptomatic COVID-19. Microbiology Spectrum, 2021, 9, e0008621. | 1.2 | 11 |
| 88 | US Immigration Is Associated With Rapid and Persistent Acquisition of Antibiotic Resistance Genes in the Gut. Clinical Infectious Diseases, 2020, 71, 419-421. | 2.9 | 10 |
| 89 | HOMINID: a framework for identifying associations between host genetic variation and microbiome composition. GigaScience, 2017, 6, 1-7. | 3.3 | 9 |
| 90 | Bacterial community structure and function distinguish gut sites in captive red–shanked doucs (Pygathrix nemaeus). American Journal of Primatology, 2019, 81, e22977. | 0.8 | 9 |

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|---|---------|----|-----------|
| 91 | High-Throughput flaA Short Variable Region Sequencing to Assess Campylobacter Diversity in Fecal Samples From Birds. Frontiers in Microbiology, 2018, 9, 2201. | 1.5 | 8 |
| 92 | The guts of obesity: progress and challenges in linking gut microbes to obesity. Discovery Medicine, 2015, 19, 81-8. | 0.5 | 8 |
| 93 | Wild primate microbiomes prevent weight gain in germ-free mice. Animal Microbiome, 2020, 2, 16. | 1.5 | 7 |
| 94 | Gut microbiota from metabolic disease-resistant, macrophage-specific RIP140 knockdown mice improves metabolic phenotype and gastrointestinal integrity. Scientific Reports, 2016, 6, 38599. | 1.6 | 5 |
| 95 | Early E. casseliflavus gut colonization and outcomes of allogeneic hematopoietic cell transplantation. PLoS ONE, 2019, 14, e0220850. | 1.1 | 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. British Journal of Haematology, 2021, 192, e69-e73. | 1.2 | 3 |
| 97 | Whole Wheat and Bran Cereal Affects Microbiome Stability. Current Developments in Nutrition, 2021, 5, 1162. | 0.1 | 2 |
| 98 | Pre-Engraftment Gut Colonization with Enterococcus Casseliflavus Improves Survival after Allogeneic Hematopoietic Cell Transplantation. Blood, 2018, 132, 813-813. | 0.6 | 0 |
| 99 | Obesity-Induced Microbiome Alterations Result in Severe Gastrointestinal Graft-Versus-Host Disease Following Allogeneic Hematopoietic Stem Cell Transplantation. Blood, 2019, 134, 1922-1922. | 0.6 | 0 |
| 100 | Nutrition As a Predictor of Microbiome Injury in Allo-HCT. Blood, 2021, 138, 746-746. | 0.6 | 0 |