

# Rob Knight

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

780  
papers

207,290  
citations

182  
h-index

451  
g-index

893  
ext. papers

267,170  
ext. citations

12.9  
avg, IF

8.95  
L-index

| #   | Paper  | IF   | Citations |
|-----|--|------|-----------|
| 780 | A gut-derived metabolite alters brain activity and anxiety behaviour in mice.. <i>Nature</i> , <b>2022</b> ,   | 47.5 | 7         |
| 779 | Cancer's second genome: Microbial cancer diagnostics and redefining clonal evolution as a multispecies process: Humans and their tumors are not aseptic, and the multispecies nature of cancer modulates clinical care and clonal evolution: Humans and their tumors are not aseptic, and the multispecies nature of cancer modulates clinical care and clonal evolution.. <i>BioEssays</i> , <b>2022</b> , e2100252 | 3.9  | 0         |
| 778 | Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting.. <i>Cell Metabolism</i> , <b>2022</b> ,   | 23.7 | 1         |
| 777 | Salivary bacterial signatures in depression-obesity comorbidity are associated with neurotransmitters and neuroactive dipeptides.. <i>BMC Microbiology</i> , <b>2022</b> , 22, 75  | 4.3  | 0         |
| 776 | The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction.. <i>Scientific Reports</i> , <b>2022</b> , 12, 5077   | 4.7  | 0         |
| 775 | Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases.. <i>MSystems</i> , <b>2022</b> , e0137821  | 7.4  |           |
| 774 | Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , <b>2022</b> , e0016722  | 7.4  | 0         |
| 773 | Wastewater sequencing uncovers early, cryptic SARS-CoV-2 variant transmission. <b>2022</b> ,   |      | 1         |
| 772 | Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS.. <i>Npj Biofilms and Microbiomes</i> , <b>2022</b> , 8, 30   | 8    | 0         |
| 771 | The impact of maternal asthma on the preterm infants' gut metabolome and microbiome (MAP study).. <i>Scientific Reports</i> , <b>2022</b> , 12, 6437   | 4.7  |           |
| 770 | Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity.. <i>Nature Microbiology</i> , <b>2022</b> ,  | 25.8 | 4         |
| 769 | Using all our genomes: Blood-based liquid biopsies for the early detection of cancer. <i>View</i> , <b>2022</b> , 3, 20209118  |      |           |
| 768 | Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians.. <i>Molecular Ecology</i> , <b>2022</b> ,  | 5.5  | 1         |
| 767 | Genomic mutations within the host microbiome: Adaptive evolution or purifying selection. <i>Engineering</i> , <b>2022</b> ,  | 9.3  |           |
| 766 | Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort.. <i>Nature Genetics</i> , <b>2022</b> , 54, 134-142   | 35.2 | 5         |
| 765 | Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype.. <i>MSystems</i> , <b>2022</b> , e0005022   | 7.4  | 0         |
| 764 | Nitrite Generating and Depleting Capacity of the Oral Microbiome and Cardiometabolic Risk: Results from ORIGINS.. <i>Journal of the American Heart Association</i> , <b>2022</b> , 11, e023038   | 5.7  | 0         |

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|-----|---|------|----|
| 763 | SARS-CoV-2 Distribution in Residential Housing Suggests Contact Deposition and Correlates with sp.. <i>MSystems</i> , <b>2022</b> , e0141121  | 7.4  |    |
| 762 | Gut microbiome in serious mental illnesses: A systematic review and critical evaluation. <i>Schizophrenia Research</i> , <b>2021</b> , 234, 24-40   | 3.6  | 30 |
| 761 | Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 169-173   | 43.2 | 34 |
| 760 | Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. <i>Gastroenterology</i> , <b>2021</b> , 160, 183-192.e3      | 7.8  | 38 |
| 759 | Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , <b>2021</b> , 27, 603-616           | 2.8  | 6  |
| 758 | Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. <i>Genome Research</i> , <b>2021</b> , 31, 64-74        | 9.4  | 19 |
| 757 | Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 146-151  | 11.3 | 26 |
| 756 | Current Concepts, Opportunities, and Challenges of Gut Microbiome-Based Personalized Medicine in Nonalcoholic Fatty Liver Disease. <i>Cell Metabolism</i> , <b>2021</b> , 33, 21-32       | 23.7 | 36 |
| 755 | Coinfection and infection duration shape how pathogens affect the African buffalo gut microbiota. <i>ISME Journal</i> , <b>2021</b> , 15, 1359-1371                                       | 11.6 | 0  |
| 754 | High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , <b>2021</b> , 18, 165-169                       | 21   | 57 |
| 753 | Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. <i>Brain, Behavior, and Immunity</i> , <b>2021</b> , 91, 245-256      | 16.2 | 16 |
| 752 | Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 165-168   | 43.2 | 20 |
| 751 | Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2327, 87-92   | 1.4  |    |
| 750 | Nonalcoholic Steatohepatitis and HCC in a Hyperphagic Mouse Accelerated by Western Diet. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , <b>2021</b> , 12, 891-920        | 7.6  | 2  |
| 749 | Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , <b>2021</b> , 18, 40-41  | 1.1  | 2  |
| 748 | Early life gut microbiota is associated with rapid infant growth in Hispanics from Southern California. <i>Gut Microbes</i> , <b>2021</b> , 13, 1961203                                   | 8.4  | 4  |
| 747 | Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , <b>2021</b> , 9, 25 | 16.2 | 7  |
| 746 | A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , <b>2021</b> , 19,                                     | 5.7  | 4  |

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| 745 | Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , <b>2021</b> , 53, 156-165  | 35.2 | 69  |
| 744 | METTL3 regulates viral m6A RNA modification and host cell innate immune responses during SARS-CoV-2 infection. <i>Cell Reports</i> , <b>2021</b> , 35, 109091  | 10.3 | 26  |
| 743 | Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , <b>2021</b> , 184, 2587-2594  | 54.5 | 124 |
| 742 | Insight into the function and evolution of the Wood-Ljungdahl pathway in Actinobacteria. <i>ISME Journal</i> , <b>2021</b> , 15, 3005-3018   | 11.6 | 8   |
| 741 | Structure-based protein function prediction using graph convolutional networks. <i>Nature Communications</i> , <b>2021</b> , 12, 3168  | 16.9 | 36  |
| 740 | Taxonomic signatures of cause-specific mortality risk in human gut microbiome. <i>Nature Communications</i> , <b>2021</b> , 12, 2671   | 16.9 | 13  |
| 739 | Candidate probiotic <i>Lactiplantibacillus plantarum</i> HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. <i>Microbiome</i> , <b>2021</b> , 9, 151 | 16.2 | 3   |
| 738 | Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009056   | 4.8  | 0   |
| 737 | Intermittent Hypoxia and Hypercapnia Alter Diurnal Rhythms of Luminal Gut Microbiome and Metabolome. <i>MSystems</i> , <b>2021</b> , e0011621  | 7.4  | 3   |
| 736 | Effects of processed meat and drinking water nitrate on oral and fecal microbial populations in a controlled feeding study. <i>Environmental Research</i> , <b>2021</b> , 197, 111084  | 7.8  | 4   |
| 735 | Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , <b>2021</b> , 15, 3399-3411   | 11.6 | 6   |
| 734 | Host and gut microbial tryptophan metabolism and type 2 diabetes: an integrative analysis of host genetics, diet, gut microbiome and circulating metabolites in cohort studies. <i>Gut</i> , <b>2021</b> ,                             | 18.6 | 13  |
| 733 | SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , <b>2021</b> , 9, 132   | 16.2 | 14  |
| 732 | Comparison of heat-inactivated and infectious SARS-CoV-2 across indoor surface materials shows comparable RT-qPCR viral signal intensity and persistence <b>2021</b> ,   |      | 2   |
| 731 | The microbiome and prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , <b>2021</b> ,  | 5.9  | 3   |
| 730 | Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , <b>2021</b> , 41, 479-510  | 51.0 | 4   |
| 729 | A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. <i>MSystems</i> , <b>2021</b> , 6, e0039421  | 7.4  | 1   |
| 728 | Rapid, Large-Scale Wastewater Surveillance and Automated Reporting System Enable Early Detection of Nearly 85% of COVID-19 Cases on a University Campus. <i>MSystems</i> , <b>2021</b> , 6, e0079321                                   | 7.4  | 10  |

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|-----|--|------|----|
| 727 | Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding.. <i>Med</i> , <b>2021</b> , 2, 951-964.e5   | 30.9 | 6  |
| 726 | Individuals with substance use disorders have a distinct oral microbiome pattern. <i>Brain, Behavior, &amp; Immunity - Health</i> , <b>2021</b> , 15, 100271   | 5    | 2  |
| 725 | A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. <i>MSphere</i> , <b>2021</b> , 6, e0045521   | 4.9  | 0  |
| 724 | Systems Analysis Reveals Ageing-Related Perturbations in Retinoids and Sex Hormones in Alzheimer's and Parkinson's Diseases. <i>Biomedicines</i> , <b>2021</b> , 9,  | 4.6  | 2  |
| 723 | Markers of Gut Barrier Function and Microbial Translocation Associate with Lower Gut Microbial Diversity in People with HIV. <i>Viruses</i> , <b>2021</b> , 13,  | 6    | 3  |
| 722 | Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , <b>2021</b> , 184, 4939-4952.e15   | 54.5 | 2  |
| 721 | Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , <b>2021</b> , 31, 2131-2137  | 9.4  | 3  |
| 720 | Emergence of an early SARS-CoV-2 epidemic in the United States <b>2021</b> ,   |      | 3  |
| 719 | Absence of CCR2 reduces spontaneous intestinal tumorigenesis in the Apc mouse model. <i>International Journal of Cancer</i> , <b>2021</b> , 148, 2594  | 7.3  | 4  |
| 718 | Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , <b>2021</b> , 6,  | 7.4  | 7  |
| 717 | Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States <b>2021</b> ,  |      | 44 |
| 716 | Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. <i>International Journal of Cancer</i> , <b>2021</b> , 148, 2712-2723  | 7.3  | 3  |
| 715 | The microbiome and human cancer. <i>Science</i> , <b>2021</b> , 371,   | 32.2 | 68 |
| 714 | A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. <i>BioTechniques</i> , <b>2021</b> , 70, 149-159   | 2.4  | 4  |
| 713 | Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) screening among symptom-free healthcare workers. <i>Infection Control and Hospital Epidemiology</i> , <b>2021</b> , 1-4  | 2    | 5  |
| 712 | Association of Loneliness and Wisdom With Gut Microbial Diversity and Composition: An Exploratory Study. <i>Frontiers in Psychiatry</i> , <b>2021</b> , 12, 648475   | 4.9  | 9  |
| 711 | Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. <i>Environmental Science &amp; Technology</i> , <b>2021</b> , 55, 4899-4913   | 10.2 | 18 |
| 710 | Dietary factors, gut microbiota, and serum trimethylamine-N-oxide associated with cardiovascular disease in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Clinical Nutrition</i> , <b>2021</b> , 113, 1503-1514 | 6.6  | 8  |

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|-----|---|------|----|
| 709 | High-Throughput Wastewater SARS-CoV-2 Detection Enables Forecasting of Community Infection Dynamics in San Diego County. <i>MSystems</i> , <b>2021</b> , 6,   | 7.4  | 28 |
| 708 | Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , <b>2021</b> , 6,   | 7.4  | 3  |
| 707 | Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , <b>2021</b> , 9, 92  | 16.2 | 7  |
| 706 | Influence of Intermittent Hypoxia/Hypercapnia on Atherosclerosis, Gut Microbiome, and Metabolome. <i>Frontiers in Physiology</i> , <b>2021</b> , 12, 663950   | 4.4  | 4  |
| 705 | EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , <b>2021</b> , 6,  | 7.4  | 11 |
| 704 | Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , <b>2021</b> , 18, 618-626   | 2.1  | 10 |
| 703 | A semiparametric model for between-subject attributes: Applications to beta-diversity of microbiome data. <i>Biometrics</i> , <b>2021</b> ,   | 1.7  | 1  |
| 702 | Associations of healthy food choices with gut microbiota profiles. <i>American Journal of Clinical Nutrition</i> , <b>2021</b> , 114, 605-616   | 6.6  | 7  |
| 701 | Intratumoral bacteria generate a new class of therapeutically relevant tumor antigens in melanoma. <i>Cancer Cell</i> , <b>2021</b> , 39, 601-603   | 23.1 | 2  |
| 700 | Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. <i>Genome Biology</i> , <b>2021</b> , 22, 336   | 17.7 | 1  |
| 699 | Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. <i>MSystems</i> , <b>2021</b> , e0113621   | 7.4  | 1  |
| 698 | The Gut Microbiome Modifies the Association between a Mediterranean Diet and Diabetes in US Hispanic / Latino Population. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2021</b> ,   | 5.4  | 1  |
| 697 | The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , <b>2021</b> , e0100621   | 7.4  | 1  |
| 696 | Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , <b>2021</b> , 27, 1885-1892  | 49.3 | 10 |
| 695 | Comparison of fecal and oral collection methods for studies of the human microbiota in two Iranian cohorts. <i>BMC Microbiology</i> , <b>2021</b> , 21, 324   | 4.3  |    |
| 694 | Clean room microbiome complexity impacts planetary protection bioburden. <i>Microbiome</i> , <b>2021</b> , 9, 238   | 16.2 | 2  |
| 693 | <i>Ruminiclostridium 5</i> , <i>Parabacteroides distasonis</i> , and bile acid profile are modulated by prebiotic diet and associate with facilitated sleep/clock realignment after chronic disruption of rhythms. <i>Brain, Behavior, and Immunity</i> , <b>2021</b> , 97, 150-166 | 16.2 | 4  |
| 692 | Links between gut microbiome composition and fatty liver disease in a large population sample. <i>Gut Microbes</i> , <b>2021</b> , 13, 1-22   | 8.4  | 10 |

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|-----|---|------|----|
| 691 | Fecal Microbiome Composition Does Not Predict Diet-Induced TMAO Production in Healthy Adults. <i>Journal of the American Heart Association</i> , <b>2021</b> , 10, e021934  | 5.7  | 0  |
| 690 | Development of a Rapid and Sensitive CasRx-Based Diagnostic Assay for SARS-CoV-2. <i>ACS Sensors</i> , <b>2021</b> , 6, 3957-3966   | 9    | 1  |
| 689 | Skin inflammation activates intestinal stromal fibroblasts and promotes colitis. <i>Journal of Clinical Investigation</i> , <b>2021</b> , 131,  | 15.3 | 3  |
| 688 | Wastewater and surface monitoring to detect COVID-19 in elementary school settings: The Safer at School Early Alert project <b>2021</b> ,   |      | 4  |
| 687 | Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , <b>2021</b> , 6, e0069121  | 7.4  | 3  |
| 686 | IL-4R $\beta$ Blockade by Dupilumab Decreases <i>Staphylococcus aureus</i> Colonization and Increases Microbial Diversity in Atopic Dermatitis. <i>Journal of Investigative Dermatology</i> , <b>2020</b> , 140, 191-202.e7 | 1.1  | 57 |
| 685 | Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , <b>2020</b> , 65, 103738  | 4.9  | 32 |
| 684 | Mass spectrometry searches using MASST. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 23-26   | 43.2 | 68 |
| 683 | Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , <b>2020</b> , 82, 26-41   | 12.3 | 33 |
| 682 | Using microbiome tools for estimating the postmortem interval <b>2020</b> , 171-191   |      | 1  |
| 681 | The emergence of microbiome centres. <i>Nature Microbiology</i> , <b>2020</b> , 5, 2-3  | 25.8 | 6  |
| 680 | Three-dimensional culture of oral progenitor cells: Effects on small extracellular vesicles production and proliferative function. <i>Journal of Oral Pathology and Medicine</i> , <b>2020</b> , 49, 342-349                | 3.1  | 7  |
| 679 | Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , <b>2020</b> , 5, 108-115  | 25.8 | 35 |
| 678 | Altered Gut Microbiota and Host Metabolite Profiles in Women With Human Immunodeficiency Virus. <i>Clinical Infectious Diseases</i> , <b>2020</b> , 71, 2345-2353   | 11.3 | 9  |
| 677 | 48: Oral probiotic versus placebo and the maternal microbiome during pregnancy: A randomized controlled trial. <i>American Journal of Obstetrics and Gynecology</i> , <b>2020</b> , 222, S41-S42                            | 1.9  |    |
| 676 | Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. <i>Cell</i> , <b>2020</b> , 183, 666-683.e17   | 54.5 | 58 |
| 675 | Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , <b>2020</b> , 5,  | 4.9  | 6  |
| 674 | A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. <i>MBio</i> , <b>2020</b> , 11,   | 7.6  | 5  |



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|-----|--|-------|----|
| 673 | Evaluating Organism-Wide Changes in the Metabolome and Microbiome following a Single Dose of Antibiotic. <i>MSystems</i> , <b>2020</b> , 5,  | 7.4   | 3  |
| 672 | Early-life gut dysbiosis linked to juvenile mortality in ostriches. <i>Microbiome</i> , <b>2020</b> , 8, 147   | 16.2  | 9  |
| 671 | Leveling up citizen science. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1124-1126   | 43.2  | 2  |
| 670 | The Urinary Tract Microbiome in Older Women Exhibits Host Genetic and Environmental Influences. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 298-305.e3  | 22.8  | 13 |
| 669 | Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , <b>2020</b> , 11, 5997   | 16.9  | 28 |
| 668 | Triclosan leads to dysregulation of the metabolic regulator FGF21 exacerbating high fat diet-induced nonalcoholic fatty liver disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 31259-31266 | 11.1  | 12 |
| 667 | Handwashing and Detergent Treatment Greatly Reduce SARS-CoV-2 Viral Load on Halloween Candy Handled by COVID-19 Patients. <i>MSystems</i> , <b>2020</b> , 5,   | 7.4   | 6  |
| 666 | The Gut Microbiome, Aging, and Longevity: A Systematic Review. <i>Nutrients</i> , <b>2020</b> , 12,  | 6.4   | 35 |
| 665 | Association Between the Gut Microbiota and Blood Pressure in a Population Cohort of 6953 Individuals. <i>Journal of the American Heart Association</i> , <b>2020</b> , 9, e016641  | 5.7   | 22 |
| 664 | Microbiome and Metagenome Analyses of a Closed Habitat during Human Occupation. <i>MSystems</i> , <b>2020</b> , 5,   | 7.4   | 3  |
| 663 | Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , <b>2020</b> , 8, 152   | 16.2  | 18 |
| 662 | Type I IFNs and CD8 T cells increase intestinal barrier permeability after chronic viral infection. <i>Journal of Experimental Medicine</i> , <b>2020</b> , 217,   | 16.2  | 11 |
| 661 | Two hundred and fifty-four metagenome-assembled bacterial genomes from the bank vole gut microbiota. <i>Scientific Data</i> , <b>2020</b> , 7, 312   | 8     | 3  |
| 660 | CD8 T cells drive anorexia, dysbiosis, and blooms of a commensal with immunosuppressive potential after viral infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 24998-25007               | 11.1  | 2  |
| 659 | Fructose stimulated de novo lipogenesis is promoted by inflammation. <i>Nature Metabolism</i> , <b>2020</b> , 2, 1034-1045   | 10.45 | 61 |
| 658 | Association of Body Mass Index with Fecal Microbial Diversity and Metabolites in the Northern Finland Birth Cohort. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2020</b> , 29, 2289-2299   | 3.6   | 5  |
| 657 | Mortality Risk Profiling of Staphylococcus aureus Bacteremia by Multi-omic Serum Analysis Reveals Early Predictive and Pathogenic Signatures. <i>Cell</i> , <b>2020</b> , 182, 1311-1327.e14   | 54.5  | 16 |
| 656 | ReDU: a framework to find and reanalyze public mass spectrometry data. <i>Nature Methods</i> , <b>2020</b> , 17, 901-904   | 20    | 25 |



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|-----|--|------|-----|
| 655 | Effects of Diet versus Gastric Bypass on Metabolic Function in Diabetes. <i>New England Journal of Medicine</i> , <b>2020</b> , 383, 721-732   | 57.2 | 78  |
| 654 | Host variables confound gut microbiota studies of human disease. <i>Nature</i> , <b>2020</b> , 587, 448-454  | 47.5 | 103 |
| 653 | The Southern Bluefin Tuna Mucosal Microbiome Is Influenced by Husbandry Method, Net Pen Location, and Anti-parasite Treatment. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 2015   | 5.5  | 1   |
| 652 | SHOGUN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , <b>2020</b> , 36, 4088-4090  | 6.8  | 10  |
| 651 | Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , <b>2020</b> , 11, 2500   | 16.9 | 89  |
| 650 | Visualizing genomic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa023   | 3.5  | 42  |
| 649 | Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. <i>Genome Research</i> , <b>2020</b> , 30, 898-909 | 9.4  | 12  |
| 648 | Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, <i>Scomber japonicus</i> . <i>MSphere</i> , <b>2020</b> , 5,  | 4.9  | 10  |
| 647 | Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , <b>2020</b> , 8, 82  | 16.2 | 76  |
| 646 | Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , <b>2020</b> , 579, 567-574  | 47.5 | 211 |
| 645 | Enhanced Characterization of Drug Metabolism and the Influence of the Intestinal Microbiome: A Pharmacokinetic, Microbiome, and Untargeted Metabolomics Study. <i>Clinical and Translational Science</i> , <b>2020</b> , 13, 972-984                     | 4.8  | 7   |
| 644 | Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , <b>2020</b> , 21, 55   | 17.7 | 35  |
| 643 | Air pollution exposure is associated with the gut microbiome as revealed by shotgun metagenomic sequencing. <i>Environment International</i> , <b>2020</b> , 138, 105604   | 12.8 | 40  |
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| 641 | Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. <i>Frontiers in Psychiatry</i> , <b>2020</b> , 11, 518  | 4.9  | 3   |
| 640 | Patterns of Oral Microbiota Diversity in Adults and Children: A Crowdsourced Population Study. <i>Scientific Reports</i> , <b>2020</b> , 10, 2133  | 4.7  | 27  |
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| 638 | Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. <i>PLoS ONE</i> , <b>2020</b> , 15, e0229001  | 3.6  | 18  |

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| 637 | OP31 MetaOmics reveals microbiome-driven proteolysis as a contributing factor to the severity of ulcerative colitis disease activity. <i>Journal of Crohns and Colitis</i> , <b>2020</b> , 14, S030-S031               | 1.4  | 0  |
| 636 | Organ-level protein networks as a reference for the host effects of the microbiome. <i>Genome Research</i> , <b>2020</b> , 30, 276-286   | 9.4  | 5  |
| 635 | Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , <b>2020</b> , 5,  | 7.4  | 29 |
| 634 | Differing salivary microbiome diversity, community and diurnal rhythmicity in association with affective state and peripheral inflammation in adults. <i>Brain, Behavior, and Immunity</i> , <b>2020</b> , 87, 591-602 | 16.2 | 4  |
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| 632 | Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , <b>2020</b> , 11,  | 7.6  | 71 |
| 631 | QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , <b>2020</b> , 70, e100                 | 23.1 | 50 |
| 630 | Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , <b>2020</b> , 5,  | 7.4  | 27 |
| 629 | Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , <b>2020</b> , 5,   | 7.4  | 11 |
| 628 | Microbial Ecology of Atlantic Salmon ( <i>Salmo salar</i> ) Hatcheries: Impacts of the Built Environment on Fish Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , <b>2020</b> , 86,                 | 4.6  | 24 |
| 627 | Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. <i>MSystems</i> , <b>2020</b> , 5,  | 7.4  | 7  |
| 626 | Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , <b>2020</b> , 1352458520924594                              | 4.9  | 5  |
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| 624 | Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment <b>2020</b> ,   |      | 3  |
| 623 | SARS-CoV-2 Screening Among Symptom-Free Healthcare Workers <b>2020</b> ,   |      | 2  |
| 622 | Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity <b>2020</b> ,  |      | 14 |
| 621 | A Sensitive, Rapid, and Portable CasRx-based Diagnostic Assay for SARS-CoV-2 <b>2020</b> ,   |      | 7  |
| 620 | A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities <b>2020</b> ,   |      | 1  |

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| 619 | Microbial context predicts SARS-CoV-2 prevalence in patients and the hospital built environment <b>2020,</b>  |      | 10  |
| 618 | A gut bacterial amyloid promotes $\beta$ -synuclein aggregation and motor impairment in mice. <i>ELife,</i> <b>2020,</b> 9,   | 8.6  | 107 |
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| 616 | Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome <b>2020,</b> 15, e0229001   |      |     |
| 615 | Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome <b>2020,</b> 15, e0229001   |      |     |
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| 610 | Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology,</i> <b>2019,</b> 20, 226   | 17.7 | 21  |
| 609 | Learning representations of microbe-metabolite interactions. <i>Nature Methods,</i> <b>2019,</b> 16, 1306-1314  | 21   | 71  |
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| 607 | Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems,</i> <b>2019,</b> 4,   | 7.4  | 14  |
| 606 | A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. <i>MSystems,</i> <b>2019,</b> 4,  | 7.4  | 11  |
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| 593 | Triplicate PCR reactions for 16S rRNA gene amplicon sequencing are unnecessary. <i>BioTechniques</i> , <b>2019</b> , 67, 29-32  | 2.4  | 24  |
| 592 | Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , <b>2019</b> , 177, 1600-1618.e17  | 54.5 | 364 |
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| 589 | Gut microbiota in wild and captive Guizhou snub-nosed monkeys, <i>Rhinopithecus brelichi</i> . <i>American Journal of Primatology</i> , <b>2019</b> , 81, e22989                      | 2.4  | 21  |
| 588 | Trait-like vulnerability of higher-order cognition and ability to maintain wakefulness during combined sleep restriction and circadian misalignment. <i>Sleep</i> , <b>2019</b> , 42, | 1    | 6   |
| 587 | Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , <b>2019</b> , 4,  | 7.4  | 100 |
| 586 | Consent insufficient for data release-Response. <i>Science</i> , <b>2019</b> , 364, 446   | 32.2 | 4   |
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| 584 | Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , <b>2019</b> , 6, 43                                     | 8    | 3   |

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| 583 | Red Sea SAR11 and Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,   | 4.6  | 7    |
| 582 | Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , <b>2019</b> , 4,  | 7.4  | 20   |
| 581 | Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1 month. <i>Microbiome</i> , <b>2019</b> , 7, 34                            | 16.2 | 57   |
| 580 | The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006213  | 4.8  | 12   |
| 579 | Major shifts in gut microbiota during development and its relationship to growth in ostriches. <i>Molecular Ecology</i> , <b>2019</b> , 28, 2653-2667  | 5.5  | 30   |
| 578 | Links between environment, diet, and the hunter-gatherer microbiome. <i>Gut Microbes</i> , <b>2019</b> , 10, 216-227   | 8.4  | 67   |
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| 571 | Neutrophilic proteolysis in the cystic fibrosis lung correlates with a pathogenic microbiome. <i>Microbiome</i> , <b>2019</b> , 7, 23  | 16.2 | 32   |
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| 566 | Reply to Moossavi and Azad, "Quantifying and Interpreting the Association between Early-Life Gut Microbiota Composition and Childhood Obesity". <i>MBio</i> , <b>2019</b> , 10,                          | 7.6  |      |

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| 563 | Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , <b>2019</b> , 6, 322                                 | 8    | 2   |
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| 560 | Disease-modifying therapies alter gut microbial composition in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , <b>2019</b> , 6, e517                             | 8.9  | 39  |
| 559 | Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. <i>Trends in Microbiology</i> , <b>2019</b> , 27, 105-117                               | 12   | 328 |
| 558 | Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. <i>Journal of Forensic Sciences</i> , <b>2019</b> , 64, 791-798                           | 1.8  | 19  |
| 557 | Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , <b>2019</b> , 17, 218-230          | 6.6  | 104 |
| 556 | GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , <b>2019</b> , 4, 396-403  | 25.8 | 276 |
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| 540 | Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <i>MSystems</i> , <b>2018</b> , 3,                                     | 7.4  | 109 |
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| 216 | Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , <b>2012</b> , 6, 94-103   | 11.6 | 378  |
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| 212 | Defining the human microbiome. <i>Nutrition Reviews</i> , <b>2012</b> , 70 Suppl 1, S38-44  | 6.2  | 442  |
| 211 | Host remodeling of the gut microbiome and metabolic changes during pregnancy. <i>Cell</i> , <b>2012</b> , 150, 470-80   | 4.5  | 1109 |
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| 209 | Microbiota regulate intestinal absorption and metabolism of fatty acids in the zebrafish. <i>Cell Host and Microbe</i> , <b>2012</b> , 12, 277-88                                       | 22.8 | 467  |
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| 202 | Microbiota restoration: natural and supplemented recovery of human microbial communities. <i>Nature Reviews Microbiology</i> , <b>2011</b> , 9, 27-38  | 21.4 | 358  |
| 201 | UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , <b>2011</b> , 5, 169-72  | 11.6 | 1453 |
| 200 | Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , <b>2011</b> , 5, 570-3   | 11.6 | 35   |
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| 198 | Examining the global distribution of dominant archaeal populations in soil. <i>ISME Journal</i> , <b>2011</b> , 5, 908-17  | 11.6 | 816  |
| 197 | The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , <b>2011</b> , 5, 1565-7  | 11.6 | 48   |
| 196 | The under-recognized dominance of Verrucomicrobia in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , <b>2011</b> , 43, 1450-1455  | 7.4  | 437  |
| 195 | Our microbial selves: what ecology can teach us. <i>EMBO Reports</i> , <b>2011</b> , 12, 775-84  | 6.3  | 66   |
| 194 | Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , <b>2011</b> , 8, 761-3  | 11.1 | 748  |
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| 192 | Sources of bacteria in outdoor air across cities in the midwestern United States. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 6350-6   | 4.6  | 190  |
| 191 | Pan-genome of the dominant human gut-associated archaeon, <i>Methanobrevibacter smithii</i> , studied in twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108 Suppl 1, 4599-606 | 11.1 | 163  |
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| 189 | Host-associated and free-living phage communities differ profoundly in phylogenetic composition. <i>PLoS ONE</i> , <b>2011</b> , 6, e16900   | 3.6  | 21   |
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| 186 | TopharyExplorer: visualizing large phylogenetic trees with environmental metadata. <i>Bioinformatics</i> , <b>2011</b> , 27, 3067-9   | 6.8  | 15   |
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| 182 | The Genomic Standards Consortium. <i>PLoS Biology</i> , <b>2011</b> , 9, e1001088   | 9.4  | 141  |
| 181 | PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , <b>2011</b> , 27, 1159-61  | 6.8  | 270  |
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| 177 | Using QIIME to analyze 16S rRNA gene sequences from microbial communities. <i>Current Protocols in Bioinformatics</i> , <b>2011</b> , Chapter 10, Unit 10.7.  | 23.1 | 368  |
| 176 | Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. <i>Science</i> , <b>2011</b> , 332, 970-4   | 32.2 | 1198 |
| 175 | Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108 Suppl 1, 4516-22 | 11.1 | 4626 |
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| 162 | Composition of human skin microbiota affects attractiveness to malaria mosquitoes. <i>PLoS ONE</i> , <b>2011</b> , 6, e28991  | 3.6  | 152  |
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| 160 | Metabolic syndrome and altered gut microbiota in mice lacking Toll-like receptor 5. <i>Science</i> , <b>2010</b> , 328, 228-31  | 32.2 | 1514 |
| 159 | Estimate of the abundance of cardiomyopathic mutations in the $\beta$ -myosin gene. <i>International Journal of Cardiology</i> , <b>2010</b> , 144, 124-6   | 3    | 5    |
| 158 | Changes through time: integrating microorganisms into the study of succession. <i>Research in Microbiology</i> , <b>2010</b> , 161, 635-42  | 3.9  | 228  |
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| 154 | Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. <i>Ecology</i> , <b>2010</b> , 91, 3463-70; discussion 3503-14   | 4.5  | 360  |
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| 150 | Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. <i>BMC Microbiology</i> , <b>2010</b> , 10, 206   | 4.3  | 279   |
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| 148 | Bacterial communities of disease vectors sampled across time, space, and species. <i>ISME Journal</i> , <b>2010</b> , 4, 223-31  | 11.6 | 42    |
| 147 | Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. <i>ISME Journal</i> , <b>2010</b> , 4, 17-27                | 11.6 | 856   |
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| 145 | Postprandial remodeling of the gut microbiota in Burmese pythons. <i>ISME Journal</i> , <b>2010</b> , 4, 1375-85   | 11.6 | 177   |
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| 143 | QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , <b>2010</b> , 7, 335-6   | 21   | 22581 |
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| 134 | Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 3869-79   | 19.4 | 74    |

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| 128 | The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Nature Precedings</i> , <b>2009</b> ,  |      | 2    |
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| 117 | A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , <b>2009</b> , 3, 442-53  | 11.6 | 720  |
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| 114 | The effect of diet on the human gut microbiome: a metagenomic analysis in humanized gnotobiotic mice. <i>Science Translational Medicine</i> , <b>2009</b> , 1, 6ra14   | 16.9 | 1964 |
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| 91 | The convergence of carbohydrate active gene repertoires in human gut microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 15076-81          | 11.1 | 103  |
| 90 | The macaque gut microbiome in health, lentiviral infection, and chronic enterocolitis. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e20  | 7.4  | 329  |
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| 87 | Multiple pattern matching: a Markov chain approach. <i>Journal of Mathematical Biology</i> , <b>2008</b> , 56, 51-92   | 2    | 22   |
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| 85 | Short pyrosequencing reads suffice for accurate microbial community analysis. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, e120   | 19.4 | 505  |
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| 83 | Quantitative and qualitative beta diversity measures lead to different insights into factors that structure microbial communities. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 1576-85 | 4.6  | 1580 |
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| 72 | Natural selection is not required to explain universal compositional patterns in rRNA secondary structure categories. <i>Rna</i> , <b>2006</b> , 12, 1-14  | 5.6  | 52   |
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| 64 | Does protein structure influence trypsin miscleavage? Using structural properties to predict the behavior of related proteins. <i>IEEE Engineering in Medicine and Biology Magazine</i> , <b>2005</b> , 24, 58-66  |      | 9    |
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| 61 | BayesFold: rational 2 degrees folds that combine thermodynamic, covariation, and chemical data for aligned RNA sequences. <i>Rna</i> , <b>2004</b> , 10, 1323-36  | 5.6  | 36  |
| 60 | How biologists conceptualize genes: an empirical study. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , <b>2004</b> , 35, 647-673 | 0.6  | 73  |
| 59 | Finding specific RNA motifs: function in a zeptomole world?. <i>Rna</i> , <b>2003</b> , 9, 218-30   | 5.6  | 44  |
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| 57 | Impacts of the Marine Hatchery Built Environment, Water and Feed on Mucosal Microbiome Colonization Across Ontogeny in Yellowtail Kingfish, <i>Seriola lalandi</i> . <i>Frontiers in Marine Science</i> , 8,            | 4.4  | 1   |
| 56 | Automated, miniaturized, and scalable screening of healthcare workers, first responders, and students for SARS-CoV-2 in San Diego County  |      | 2   |
| 55 | Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment   |      | 2   |
| 54 | Rapid, large-scale wastewater surveillance and automated reporting system enabled early detection of nearly 85% of COVID-19 cases on a University campus  |      | 1   |
| 53 | OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures   |      | 6   |
| 52 | EMP DNA Extraction Protocol v1  |      | 2   |
| 51 | EMP 18S Illumina Amplicon Protocol v1   |      | 3   |
| 50 | Earth Microbiome Project (EMP) high throughput (HTP) DNA extraction protocol v1   |      | 3   |
| 49 | EMP Sample Submission Guide v1  |      | 2   |
| 48 | Reference Data Based Insights Expand Understanding of Human Metabolomes. <i>SSRN Electronic Journal</i> ,   | 1    | 1   |
| 47 | Dramatic differences in gut bacterial densities help to explain the relationship between diet and habitat in rainforest ants  |      | 3   |
| 46 | BugBase predicts organism-level microbiome phenotypes   |      | 77  |
| 45 | Revisiting microbe-metabolite interactions: doing better than random  |      | 1   |
| 44 | Visualizing $\beta$ mic feature rankings and log-ratios using Qurro   |      | 5   |

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| 43 | Taxonomic Signatures of Long-Term Mortality Risk in Human Gut Microbiota  | 16 |
| 42 | Expanding magnetic organelle biogenesis in the domain Bacteria  | 1  |
| 41 | Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree  | 3  |
| 40 | Early prediction of liver disease using conventional risk factors and gut microbiome-augmented gradient boosting          | 10 |
| 39 | Large-scale association analyses identify host factors influencing human gut microbiome composition                       | 9  |
| 38 | Reference data based insights expand understanding of human metabolomes   | 3  |
| 37 | Links between gut microbiome composition and fatty liver disease in a large population sample                             | 2  |
| 36 | Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort     | 4  |
| 35 | EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets                                 | 4  |
| 34 | A scale-free, fully connected global transition network underlies known microbiome diversity                              | 1  |
| 33 | American Gut: an Open Platform for Citizen-Science Microbiome Research  | 11 |
| 32 | Links between environment, diet, and the hunter-gatherer microbiome   | 2  |
| 31 | Evaluating the information content of shallow shotgun metagenomics  | 3  |
| 30 | Age and sex-dependent patterns of gut microbial diversity in human adults   | 1  |
| 29 | Quantifying and understanding well-to-well contamination in microbiome research   | 3  |
| 28 | MASST: A Web-based Basic Mass Spectrometry Search Tool for Molecules to Search Public Data                                | 8  |
| 27 | Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing | 24 |
| 26 | Chemical Impacts of the Microbiome Across Scales Reveal Novel Conjugated Bile Acids                                       | 2  |



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| 25 | Temporal, environmental, and biological drivers of the mucosal microbiome in a wild marine fish, <i>Scomber japonicus</i>               | 5   |
| 24 | Repository-scale Co- and Re-analysis of Tandem Mass Spectrometry Data   | 13  |
| 23 | Structure-Based Protein Function Prediction using Graph Convolutional Networks  | 10  |
| 22 | Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules        | 4   |
| 21 | Database-Driven Grid Computing and Distributed Web Applications: A Comparison 247-266   | 1   |
| 20 | A lightweight, scalable grid computing framework for parallel bioinformatics applications   | 3   |
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| 18 | Context-aware deconvolution of cell-cell communication with Tensor-cell2cell  | 2   |
| 17 | Metabolome-informed microbiome analysis refines metadata classifications and reveals unexpected medication transfer in captive cheetahs | 2   |
| 16 | Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data                                     | 5   |
| 15 | QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science  | 36  |
| 14 | QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science  | 134 |
| 13 | Optimizing taxonomic classification of marker gene amplicon sequences   | 1   |
| 12 | Optimizing taxonomic classification of marker gene amplicon sequences   | 4   |
| 11 | A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments                           | 2   |
| 10 | A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments                           | 2   |
| 9  | A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments                           | 8   |
| 8  | TaskSpaces: A Software Framework for Parallel Bioinformatics on Computational Grids 651-670   |     |

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| 7 | MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides                          | 1 |
| 6 | EMP ITS Illumina Amplicon Protocol v1  | 2 |
| 5 | Species abundance information improves sequence taxonomy classification accuracy   | 2 |
| 4 | Red Sea SAR11 and Prochlorococcus Single-cell Genomes Reflect Globally Distributed Pangenomes  | 1 |
| 3 | Temporal variability is a personalized feature of the human microbiome   | 1 |
| 2 | Mathematical Approaches for Describing Microbial Populations: Practice and Theory for Extrapolation of Rich Environments 85-104                            | 0 |
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