

# Assembly of 913 microbial genomes from metagenomic

Nature Communications

9, 870

DOI: [10.1038/s41467-018-03317-6](https://doi.org/10.1038/s41467-018-03317-6)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Prediction of functional metagenomic composition using archived 16S rDNA sequence data from the gut microbiota of livestock. <i>Livestock Science</i> , 2018, 213, 28-34.	0.6	6
2	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	5.8	51
3	Comparison of Mothur and QIIME for the Analysis of Rumen Microbiota Composition Based on 16S rRNA Amplicon Sequences. <i>Frontiers in Microbiology</i> , 2018, 9, 3010.	1.5	67
4	The human archaeome: methodological pitfalls and knowledge gaps. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 469-482.	1.1	31
5	Understanding the microbial basis of body odor in pre-pubescent children and teenagers. <i>Microbiome</i> , 2018, 6, 213.	4.9	47
6	Characterization of novel glycosyl hydrolases discovered by cell wall glycan directed monoclonal antibody screening and metagenome analysis of maize aerial root mucilage. <i>PLoS ONE</i> , 2018, 13, e0204525.	1.1	34
7	Review: The application of omics to rumen microbiota function. <i>Animal</i> , 2018, 12, s233-s245.	1.3	31
8	Genomes from uncultivated prokaryotes: a comparison of metagenome-assembled and single-amplified genomes. <i>Microbiome</i> , 2018, 6, 173.	4.9	86
9	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , 2018, 3, 1274-1284.	5.9	144
10	The Planktonic Core Microbiome and Core Functions in the Cattle Rumen by Next Generation Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2285.	1.5	62
11	Effect of slow-release urea on the composition of ruminal bacteria and fungi communities in yak. <i>Animal Feed Science and Technology</i> , 2018, 244, 18-27.	1.1	20
12	A metagenomic analysis of the camel rumen's microbiome identifies the major microbes responsible for lignocellulose degradation and fermentation. <i>Biotechnology for Biofuels</i> , 2018, 11, 216.	6.2	96
13	Evaluating Established Methods for Rumen 16S rRNA Amplicon Sequencing With Mock Microbial Populations. <i>Frontiers in Microbiology</i> , 2018, 9, 1365.	1.5	44
14	The Present and Future of Whole Genome Sequencing (WGS) and Whole Metagenome Sequencing (WMS) for Surveillance of Antimicrobial Resistant Microorganisms and Antimicrobial Resistance Genes across the Food Chain. <i>Genes</i> , 2018, 9, 268.	1.0	99
15	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	1.5	255
16	Analysis of sequencing strategies and tools for taxonomic annotation: Defining standards for progressive metagenomics. <i>Scientific Reports</i> , 2018, 8, 12034.	1.6	93
17	Functional metagenomics reveals abundant polysaccharide-degrading gene clusters and cellobiose utilization pathways within gut microbiota of a wood-feeding higher termite. <i>ISME Journal</i> , 2019, 13, 104-117.	4.4	93
18	MetaTOR: A Computational Pipeline to Recover High-Quality Metagenomic Bins From Mammalian Gut Proximity-Ligation (meta3C) Libraries. <i>Frontiers in Genetics</i> , 2019, 10, 753.	1.1	22

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19	Applications of the Soil, Plant and Rumen Microbiomes in Pastoral Agriculture. <i>Frontiers in Nutrition</i> , 2019, 6, 107.	1.6	30
20	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. <i>Nature Biotechnology</i> , 2019, 37, 953-961.	9.4	353
21	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	3.8	66
22	On the Role of Bioinformatics and Data Science in Industrial Microbiome Applications. <i>Frontiers in Genetics</i> , 2019, 10, 721.	1.1	11
23	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	4.4	132
24	BOARD INVITED REVIEW: The pig microbiota and the potential for harnessing the power of the microbiome to improve growth and health <sup>1</sup> . <i>Journal of Animal Science</i> , 2019, 97, 3741-3757.	0.2	39
25	Current Status and Potential Applications of Underexplored Prokaryotes. <i>Microorganisms</i> , 2019, 7, 468.	1.6	17
26	Metagenomic Analyses of Microbial and Carbohydrate-Active Enzymes in the Rumen of Holstein Cows Fed Different Forage-to-Concentrate Ratios. <i>Frontiers in Microbiology</i> , 2019, 10, 649.	1.5	90
27	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. <i>Genome Biology</i> , 2019, 20, 217.	3.8	269
28	Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 701.	1.1	43
29	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	4.9	65
30	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. <i>Genome Biology and Evolution</i> , 2019, 11, 2750-2766.	1.1	70
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33	Meta-omics based analyses of microbiome involved in biomethanation of rice straw in a thermophilic anaerobic bioreactor under optimized conditions. <i>Bioresource Technology</i> , 2019, 279, 25-33.	4.8	17
34	Horizontal Gene Transfer as an Indispensable Driver for Evolution of Neocallimastigomycota into a Distinct Gut-Dwelling Fungal Lineage. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	61
35	Metatranscriptomics of the Hu sheep rumen microbiome reveals novel cellulases. <i>Biotechnology for Biofuels</i> , 2019, 12, 153.	6.2	42
36	Long-read based de novo assembly of low-complexity metagenome samples results in finished genomes and reveals insights into strain diversity and an active phage system. <i>BMC Microbiology</i> , 2019, 19, 143.	1.3	104

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37	Carbohydrate Hydrolytic Potential and Redundancy of an Anaerobic Digestion Microbiome Exposed to Acidosis, as Uncovered by Metagenomics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
38	Fibre digestion by rumen microbiota " a review of recent metagenomic and metatranscriptomic studies. <i>Canadian Journal of Animal Science</i> , 2019, 99, 678-692.	0.7	38
39	Linking the resistome and plasmidome to the microbiome. <i>ISME Journal</i> , 2019, 13, 2437-2446.	4.4	183
40	Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. <i>Microbiome</i> , 2019, 7, 92.	4.9	230
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42	A metagenomic analysis of the relationship between microorganisms and flavor development in Shaoxing mechanized huangjiu fermentation mashes. <i>International Journal of Food Microbiology</i> , 2019, 303, 9-18.	2.1	116
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48	De novo Assembly Vastly Expands the Known Microbial Universe. <i>Trends in Microbiology</i> , 2019, 27, 385-386.	3.5	0
49	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	13.7	505
50	Metagenomics of the Viral Community in Three Cattle Slurry Samples. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
51	Mining of camel rumen metagenome to identify novel alkali-thermostable xylanase capable of enhancing the recalcitrant lignocellulosic biomass conversion. <i>Bioresource Technology</i> , 2019, 281, 343-350.	4.8	42
52	Molecular Dating of the Emergence of Anaerobic Rumen Fungi and the Impact of Laterally Acquired Genes. <i>MSystems</i> , 2019, 4, .	1.7	28
53	A Cautionary Report for Pathogen Identification Using Shotgun Metagenomics; A Comparison to Aerobic Culture and Polymerase Chain Reaction for <i>Salmonella enterica</i> Identification. <i>Frontiers in Microbiology</i> , 2019, 10, 2499.	1.5	27
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56	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. <i>Animal Microbiome</i> , 2019, 1, 15.	1.5	27
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59	Recovering microbial genomes from metagenomes in hypersaline environments: The Good, the Bad and the Ugly. <i>Systematic and Applied Microbiology</i> , 2019, 42, 30-40.	1.2	29
60	MAGpy: a reproducible pipeline for the downstream analysis of metagenome-assembled genomes (MAGs). <i>Bioinformatics</i> , 2019, 35, 2150-2152.	1.8	33
61	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. <i>Microbiome</i> , 2019, 7, 6.	4.9	150
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65	Nature's recyclers: anaerobic microbial communities drive crude biomass deconstruction. <i>Current Opinion in Biotechnology</i> , 2020, 62, 38-47.	3.3	35
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68	CAMITAX: Taxon labels for microbial genomes. <i>GigaScience</i> , 2020, 9, .	3.3	6
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70	Manipulating the rumen microbiome to address challenges facing Australasian dairy farming. <i>Animal Production Science</i> , 2020, 60, 36.	0.6	4
71	Microbiome Diagnostics. <i>Clinical Chemistry</i> , 2020, 66, 68-76.	1.5	27
72	Biotechnological utilization of animal gut microbiota for valorization of lignocellulosic biomass. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 489-508.	1.7	39

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74	Discovery of an Abundance of Biosynthetic Gene Clusters in Shark Bay Microbial Mats. <i>Frontiers in Microbiology</i> , 2020, 11, 1950.	1.5	39
75	Metagenomic insights into the diversity of carbohydrate-degrading enzymes in the yak fecal microbial community. <i>BMC Microbiology</i> , 2020, 20, 302.	1.3	24
76	Experimental approaches to tracking mobile genetic elements in microbial communities. <i>FEMS Microbiology Reviews</i> , 2020, 44, 606-630.	3.9	23
77	Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	20
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80	Altitude influences microbial diversity and herbage fermentation in the rumen of yaks. <i>BMC Microbiology</i> , 2020, 20, 370.	1.3	57
81	Inclusion of Oxford Nanopore long reads improves all microbial and viral metagenome-assembled genomes from a complex aquifer system. <i>Environmental Microbiology</i> , 2020, 22, 4000-4013.	1.8	42
82	Widespread transfer of mobile antibiotic resistance genes within individual gut microbiomes revealed through bacterial Hi-C. <i>Nature Communications</i> , 2020, 11, 4379.	5.8	116
83	1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. <i>Genome Biology</i> , 2020, 21, 229.	3.8	38
84	Microbial dark matter filling the niche in hypersaline microbial mats. <i>Microbiome</i> , 2020, 8, 135.	4.9	35
85	Meta-analysis of cheese microbiomes highlights contributions to multiple aspects of quality. <i>Nature Food</i> , 2020, 1, 500-510.	6.2	60
86	Dietary Supplementation with Sugar Beet Fructooligosaccharides and Garlic Residues Promotes Growth of Beneficial Bacteria and Increases Weight Gain in Neonatal Lambs. <i>Biomolecules</i> , 2020, 10, 1179.	1.8	4
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88	A rather dry subject; investigating the study of arid-associated microbial communities. <i>Environmental Microbiomes</i> , 2020, 15, 20.	2.2	15
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92	In silico Prediction of Virus-Host Interactions for Marine Bacteroidetes With the Use of Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 738.	1.5	20
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94	Metagenomic Analyses of Microbial and Carbohydrate-Active Enzymes in the Rumen of Dairy Goats Fed Different Rumen Degradable Starch. <i>Frontiers in Microbiology</i> , 2020, 11, 1003.	1.5	47
95	An Overview of the Elusive Passenger in the Gastrointestinal Tract of Cattle: The Shiga Toxin Producing <i>Escherichia coli</i> . <i>Microorganisms</i> , 2020, 8, 877.	1.6	31
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100	A novel thermostable cellulase cocktail enhances lignocellulosic bioconversion and biorefining in a broad range of pH. <i>International Journal of Biological Macromolecules</i> , 2020, 154, 349-360.	3.6	47
101	Characteristics and Functions of the Rumen Microbial Community of Cattle-Yak at Different Ages. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	24
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105	Effects of Exogenous Glucoamylase Enzymes Alone or in Combination with a Neutral Protease on Apparent Total Tract Digestibility and Feces D-Lactate in Crossbred Angus Bulls Fed a Ration Rich in Rolled Corn. <i>Animals</i> , 2020, 10, 1077.	1.0	3
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107	Identification of Microbial Genetic Capacities and Potential Mechanisms Within the Rumen Microbiome Explaining Differences in Beef Cattle Feed Efficiency. <i>Frontiers in Microbiology</i> , 2020, 11, 1229.	1.5	28
108	Review: Ruminal microbiome and microbial metabolome: effects of diet and ruminant host. <i>Animal</i> , 2020, 14, s78-s86.	1.3	93

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110	Metagenomic Insights of the Root Colonizing Microbiome Associated with Symptomatic and Non-Symptomatic Bananas in Fusarium Wilt Infected Fields. <i>Plants</i> , 2020, 9, 263.	1.6	30
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112	Effects of oregano essential oil on in vitro ruminal fermentation, methane production, and ruminal microbial community. <i>Journal of Dairy Science</i> , 2020, 103, 2303-2314.	1.4	59
113	A Comparison between Hi-C and 10X Genomics Linked Read Sequencing for Whole Genome Phasing in Hanwoo Cattle. <i>Genes</i> , 2020, 11, 332.	1.0	2
114	Identification of Complex Rumen Microbiome Interaction Within Diverse Functional Niches as Mechanisms Affecting the Variation of Methane Emissions in Bovine. <i>Frontiers in Microbiology</i> , 2020, 11, 659.	1.5	51
115	Association between Rumen Microbiota and Marbling Score in Korean Native Beef Cattle. <i>Animals</i> , 2020, 10, 712.	1.0	16
116	A practical guide to amplicon and metagenomic analysis of microbiome data. <i>Protein and Cell</i> , 2021, 12, 315-330.	4.8	376
117	Probing the Mobilome: Discoveries in the Dynamic Microbiome. <i>Trends in Microbiology</i> , 2021, 29, 158-170.	3.5	41
118	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0
119	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
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121	Metagenomic analysis reveals a dynamic microbiome with diversified adaptive functions to utilize high lignocellulosic forages in the cattle rumen. <i>ISME Journal</i> , 2021, 15, 1108-1120.	4.4	87
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123	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	4.4	46
124	Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. <i>Scientific Reports</i> , 2021, 11, 1990.	1.6	32
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126	Quantifying fluorescent glycan uptake to elucidate strain-level variability in foraging behaviors of rumen bacteria. <i>Microbiome</i> , 2021, 9, 23.	4.9	16



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128	Potentilla anserina L. developmental changes affect the rhizosphere prokaryotic community. Scientific Reports, 2021, 11, 2838.	1.6	4
130	Tracking Reservoirs of Antimicrobial Resistance Genes in a Complex Microbial Community Using Metagenomic Hi-C: The Case of Bovine Digital Dermatitis. Antibiotics, 2021, 10, 221.	1.5	6
131	A homodimeric bacterial exo- $\beta$ -1,3-glucanase derived from moose rumen microbiome shows a structural framework similar to yeast exo- $\beta$ -1,3-glucanases. Enzyme and Microbial Technology, 2021, 143, 109723.	1.6	7
132	Approaches for characterizing and tracking hospital-associated multidrug-resistant bacteria. Cellular and Molecular Life Sciences, 2021, 78, 2585-2606.	2.4	21
133	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	5.9	116
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137	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. Npj Biofilms and Microbiomes, 2021, 7, 23.	2.9	29
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140	Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. Nature Protocols, 2021, 16, 2520-2541.	5.5	25
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144	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. PeerJ, 2021, 9, e10941.	0.9	79
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150	Diversity and genomic determinants of the microbiomes associated with COVID-19 and non-COVID respiratory diseases. Gene Reports, 2021, 23, 101200.	0.4	25

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152	Insights into rumen microbial biosynthetic gene cluster diversity through genome-resolved metagenomics. <i>Communications Biology</i> , 2021, 4, 818.	2.0	20
153	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2021, 9, 137.	4.9	110
154	Recovery of human gut microbiota genomes with third-generation sequencing. <i>Cell Death and Disease</i> , 2021, 12, 569.	2.7	10
155	Disentangling the syntrophic electron transfer mechanisms of <i>Candidatus geobacter eutrophica</i> through electrochemical stimulation and machine learning. <i>Scientific Reports</i> , 2021, 11, 15140.	1.6	8
156	Hi-C deconvolution of a textile dye-related microbiome reveals novel taxonomic landscapes and links phenotypic potential to individual genomes. <i>International Microbiology</i> , 2022, 25, 99-110.	1.1	4
157	Assessing Dietary Effects on the Rumen Microbiome: Different Sequencing Methods Tell Different Stories. <i>Veterinary Sciences</i> , 2021, 8, 138.	0.6	3
158	Metagenome-Assembled Genomes Contribute to Unraveling of the Microbiome of Cocoa Fermentation. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0058421.	1.4	11
160	Disproportionate microbial responses to decadal drainage on a Siberian floodplain. <i>Global Change Biology</i> , 2021, 27, 5124-5140.	4.2	8
161	Effects of rumen-protected methionine and lysine supplementation on milk yields and components, rumen fermentation, and the rumen microbiome in lactating yaks ( <i>Bos grunniens</i> ). <i>Animal Feed Science and Technology</i> , 2021, 277, 114972.	1.1	15
162	Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with <i>Salmonella enterica</i> Serovar Heidelberg. <i>MSystems</i> , 2021, 6, e0072921.	1.7	8
163	Effects of Age, Diet CP, NDF, EE, and Starch on the Rumen Bacteria Community and Function in Dairy Cattle. <i>Microorganisms</i> , 2021, 9, 1788.	1.6	9
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