

Phillip B Pope

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

6,725
citations

101543

36
h-index

79698

73
g-index

86
all docs

86
docs citations

86
times ranked

7969
citing authors

#	ARTICLE	IF	CITATIONS
1	Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. <i>Scientific Reports</i> , 2015, 5, 14567.	3.3	1,172
2	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
3	DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020, 48, 8883-8900.	14.5	410
4	Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , 2018, 3, 870-880.	13.3	372
5	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14793-14798.	7.1	234
6	The human gut Firmicute <i>Roseburia intestinalis</i> is a primary degrader of dietary β -mannans. <i>Nature Communications</i> , 2019, 10, 905.	12.8	202
7	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011, 8, 191-192.	19.0	198
8	Characterization of microbial community structure during continuous anaerobic digestion of straw and cow manure. <i>Microbial Biotechnology</i> , 2015, 8, 815-827.	4.2	197
9	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. <i>PLoS ONE</i> , 2012, 7, e38571.	2.5	190
10	Isolation of <i>Succinivibrionaceae</i> Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	12.6	179
11	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
12	Do Rumen <i>Bacteroidetes</i> Utilize an Alternative Mechanism for Cellulose Degradation?. <i>MBio</i> , 2014, 5, e01401-14.	4.1	150
13	Major faecal microbiota shifts in composition and diversity with age in a geographically restricted cohort of mothers and their children. <i>FEMS Microbiology Ecology</i> , 2014, 87, 280-290.	2.7	144
14	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , 2018, 3, 1274-1284.	13.3	144
15	Improved metagenome assemblies and taxonomic binning using long-read circular consensus sequence data. <i>Scientific Reports</i> , 2016, 6, 25373.	3.3	139
16	Resistant starch diet induces change in the swine microbiome and a predominance of beneficial bacterial populations. <i>Microbiome</i> , 2015, 3, 16.	11.1	132
17	Polysaccharide degradation by the <i>Bacteroidetes</i> : mechanisms and nomenclature. <i>Environmental Microbiology Reports</i> , 2021, 13, 559-581.	2.4	119
18	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2021, 9, 137.	11.1	110

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19	Plant biomass degradation by gut microbiomes: more of the same or something new?. <i>Current Opinion in Biotechnology</i> , 2009, 20, 358-363.	6.6	102
20	The Potential of Class II Bacteriocins to Modify Gut Microbiota to Improve Host Health. <i>PLoS ONE</i> , 2016, 11, e0164036.	2.5	102
21	From Genomes to Phenotypes: Traitair, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	3.8	102
22	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.	9.8	93
23	Stable Core Gut Microbiota across the Freshwater-to-Saltwater Transition for Farmed Atlantic Salmon. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	90
24	The Skin-Mucus Microbial Community of Farmed Atlantic Salmon (<i>Salmo salar</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 2043.	3.5	72
25	A polysaccharide utilization locus from <i>Flavobacterium johnsoniae</i> enables conversion of recalcitrant chitin. <i>Biotechnology for Biofuels</i> , 2016, 9, 260.	6.2	70
26	Quantitative Metaproteomics Highlight the Metabolic Contributions of Uncultured Phylotypes in a Thermophilic Anaerobic Digester. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	67
27	Metagenomic analysis of a freshwater toxic cyanobacteria bloom. <i>FEMS Microbiology Ecology</i> , 2008, 64, 9-27.	2.7	64
28	Microbial community structure and dynamics during co-digestion of whey permeate and cow manure in continuous stirred tank reactor systems. <i>Bioresource Technology</i> , 2014, 171, 350-359.	9.6	56
29	Outer membrane vesicles from <i>Fibrobacter succinogenes</i> S85 contain an array of carbohydrate-active enzymes with versatile polysaccharide-degrading capacity. <i>Environmental Microbiology</i> , 2017, 19, 2701-2714.	3.8	55
30	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020, 11, 5773.	12.8	55
31	Wood-Derived Dietary Fibers Promote Beneficial Human Gut Microbiota. <i>MSphere</i> , 2019, 4, .	2.9	48
32	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	9.8	46
33	A Polysaccharide Utilization Locus from an Uncultured Bacteroidetes Phylotype Suggests Ecological Adaptation and Substrate Versatility. <i>Applied and Environmental Microbiology</i> , 2015, 81, 187-195.	3.1	45
34	Rumen and Cecum Microbiomes in Reindeer (<i>Rangifer tarandus tarandus</i>) Are Changed in Response to a Lichen Diet and May Affect Enteric Methane Emissions. <i>PLoS ONE</i> , 2016, 11, e0155213.	2.5	42
35	Analysis of the bovine rumen microbiome reveals a diversity of Sus-like polysaccharide utilization loci from the bacterial phylum <i>Bacteroidetes</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 601-606.	3.0	41
36	Omics-based interpretation of synergism in a soil-derived cellulose-degrading microbial community. <i>Scientific Reports</i> , 2014, 4, 5288.	3.3	39

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37	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
38	Proteomic insights into mannan degradation and protein secretion by the forest floor bacterium <i>Chitinophaga pinensis</i> . <i>Journal of Proteomics</i> , 2017, 156, 63-74.	2.4	34
39	High-Yield and Phylogenetically Robust Methods of DNA Recovery for Analysis of Microbial Biofilms Adherent to Plant Biomass in the Herbivore Gut. <i>Microbial Ecology</i> , 2011, 61, 448-454.	2.8	33
40	Two SusD-Like Proteins Encoded within a Polysaccharide Utilization Locus of an Uncultured Ruminant Bacteroidetes Phylotype Bind Strongly to Cellulose. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5935-5937.	3.1	33
41	“ <i>Candidatus Paraporphyromonas polyenzymogenes</i> ” encodes multi-modular cellulases linked to the type IX secretion system. <i>Microbiome</i> , 2018, 6, 44.	11.1	32
42	Human Gut <i>Faecalibacterium prausnitzii</i> Deploys a Highly Efficient Conserved System To Cross-Feed on β -Mannan-Derived Oligosaccharides. <i>MBio</i> , 2021, 12, e0362820.	4.1	31
43	Novel Syntrophic Populations Dominate an Ammonia-Tolerant Methanogenic Microbiome. <i>MSystems</i> , 2016, 1, .	3.8	30
44	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i> . <i>ISME Journal</i> , 2019, 13, 603-617.	9.8	30
45	Proteomic Dissection of the Cellulolytic Machineries Used by Soil-Dwelling <i>Bacteroidetes</i> . <i>MSystems</i> , 2018, 3, .	3.8	29
46	Microbial community structure in a biogas digester utilizing the marine energy crop <i>Saccharina latissima</i> . <i>3 Biotech</i> , 2013, 3, 407-414.	2.2	28
47	Integration of absolute multi-omics reveals dynamic protein-to-RNA ratios and metabolic interplay within mixed-domain microbiomes. <i>Nature Communications</i> , 2020, 11, 4708.	12.8	28
48	The effect of storage conditions on microbial community composition and biomethane potential in a biogas starter culture. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5749-5761.	3.6	27
49	Glycan processing in gut microbiomes. <i>Current Opinion in Microbiology</i> , 2022, 67, 102143.	5.1	27
50	The Farmed Atlantic Salmon (<i>Salmo salar</i>) Skin “Mucus Proteome and Its Nutrient Potential for the Resident Bacterial Community. <i>Genes</i> , 2019, 10, 515.	2.4	26
51	Succession of <i>Bifidobacterium longum</i> Strains in Response to a Changing Early Life Nutritional Environment Reveals Dietary Substrate Adaptations. <i>IScience</i> , 2020, 23, 101368.	4.1	26
52	Structural Features of a <i>Bacteroidetes</i> -Affiliated Cellulase Linked with a Polysaccharide Utilization Locus. <i>Scientific Reports</i> , 2015, 5, 11666.	3.3	24
53	Potential applications of gut microbiota to control human physiology. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 609-618.	1.7	23
54	Discovery and characterization of a thermostable two-domain GH6 endoglucanase from a compost metagenome. <i>PLoS ONE</i> , 2018, 13, e0197862.	2.5	23

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55	Rumen Virus Populations: Technological Advances Enhancing Current Understanding. <i>Frontiers in Microbiology</i> , 2020, 11, 450.	3.5	22
56	Draft Genome Sequence of the Methane-Oxidizing Bacterium <i>Methylococcus capsulatus</i> (Texas). <i>Journal of Bacteriology</i> , 2012, 194, 6626-6626.	2.2	21
57	Rumen metaproteomics: Closer to linking rumen microbial function to animal productivity traits. <i>Methods</i> , 2021, 186, 42-51.	3.8	21
58	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. <i>Nature Microbiology</i> , 2022, 7, 556-569.	13.3	21
59	Inference of phenotype-defining functional modules of protein families for microbial plant biomass degraders. <i>Biotechnology for Biofuels</i> , 2014, 7, 124.	6.2	19
60	Metagenomics and CAZyme Discovery. <i>Methods in Molecular Biology</i> , 2017, 1588, 255-277.	0.9	19
61	De novo prediction of the genomic components and capabilities for microbial plant biomass degradation from (meta-)genomes. <i>Biotechnology for Biofuels</i> , 2013, 6, 24.	6.2	18
62	Characterization of the cecum microbiome from wild and captive rock ptarmigans indigenous to Arctic Norway. <i>PLoS ONE</i> , 2019, 14, e0213503.	2.5	18
63	First insight into the faecal microbiota of the high Arctic muskoxen (<i>Ovibos moschatus</i>). <i>Microbial Genomics</i> , 2016, 2, e000066.	2.0	18
64	Nitrous oxide respiring bacteria in biogas digestates for reduced agricultural emissions. <i>ISME Journal</i> , 2022, 16, 580-590.	9.8	16
65	Concepts and Consequences of a Core Gut Microbiota for Animal Growth and Development. <i>Annual Review of Animal Biosciences</i> , 2022, 10, 177-201.	7.4	16
66	Probiotic Dosing of <i>Ruminococcus flavefaciens</i> Affects Rumen Microbiome Structure and Function in Reindeer. <i>Microbial Ecology</i> , 2013, 66, 840-849.	2.8	15
67	Biochemical characterization of two cellobiose 2-epimerases and application for efficient production of lactulose and epilactose. <i>Current Research in Biotechnology</i> , 2021, 3, 57-64.	3.7	10
68	Muramidases found in the foregut microbiome of the Tammar wallaby can direct cell aggregation and biofilm formation. <i>ISME Journal</i> , 2011, 5, 341-350.	9.8	9
69	Structural insights of the enzymes from the chitin utilization locus of <i>Flavobacterium johnsoniae</i> . <i>Scientific Reports</i> , 2020, 10, 13775.	3.3	9
70	Proteomic data on enzyme secretion and activity in the bacterium <i>Chitinophaga pinensis</i> . <i>Data in Brief</i> , 2017, 11, 484-490.	1.0	8
71	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	8
72	Transkingdom network analysis provides insight into host-microbiome interactions in Atlantic salmon. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1028-1034.	4.1	4

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73	The Reindeer Rumen Microbiome. , 2013, , 1-12.		3
74	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	1
75	The Reindeer Rumen Microbiome. , 2015, , 722-732.		1