

Phillip B Pope

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3385537/publications.pdf>

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	Nitrous oxide respiring bacteria in biogas digestates for reduced agricultural emissions. ISME Journal, 2022, 16, 580-590.	9.8	16
2	Concepts and Consequences of a Core Gut Microbiota for Animal Growth and Development. Annual Review of Animal Biosciences, 2022, 10, 177-201.	7.4	16
3	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. Nature Microbiology, 2022, 7, 556-569.	13.3	21
4	Glycan processing in gut microbiomes. Current Opinion in Microbiology, 2022, 67, 102143.	5.1	27
5	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
6	Rumen metaproteomics: Closer to linking rumen microbial function to animal productivity traits. Methods, 2021, 186, 42-51.	3.8	21
7	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. ISME Journal, 2021, 15, 421-434.	9.8	46
8	Transkingdom network analysis provides insight into host-microbiome interactions in Atlantic salmon. Computational and Structural Biotechnology Journal, 2021, 19, 1028-1034.	4.1	4
9	Biochemical characterization of two cellobiose 2-epimerases and application for efficient production of lactulose and epilactose. Current Research in Biotechnology, 2021, 3, 57-64.	3.7	10
10	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	1
11	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	8
12	Human Gut Faecalibacterium prausnitzii Deploys a Highly Efficient Conserved System To Cross-Feed on Î²-Mannan-Derived Oligosaccharides. MBio, 2021, 12, e0362820.	4.1	31
13	Polysaccharide degradation by the Bacteroidetes: mechanisms and nomenclature. Environmental Microbiology Reports, 2021, 13, 559-581.	2.4	119
14	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. Microbiome, 2021, 9, 137.	11.1	110
15	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. Microbiome, 2021, 9, 243.	11.1	36
16	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. Nature Communications, 2020, 11, 5773.	12.8	55
17	DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Research, 2020, 48, 8883-8900.	14.5	410
18	Succession of Bifidobacterium longum Strains in Response to a Changing Early Life Nutritional Environment Reveals Dietary Substrate Adaptations. IScience, 2020, 23, 101368.	4.1	26

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Rumen Virus Populations: Technological Advances Enhancing Current Understanding. <i>Frontiers in Microbiology</i> , 2020, 11, 450.	3.5	22
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	The Farmed Atlantic Salmon (<i>Salmo salar</i>) Skinâ€™Mucus Proteome and Its Nutrient Potential for the Resident Bacterial Community. <i>Genes</i> , 2019, 10, 515.	2.4	26
24	Wood-Derived Dietary Fibers Promote Beneficial Human Gut Microbiota. <i>MSphere</i> , 2019, 4, .	2.9	48
25	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
26	The human gut Firmicute <i>Roseburia intestinalis</i> is a primary degrader of dietary Î²-mannans. <i>Nature Communications</i> , 2019, 10, 905.	12.8	202
27	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i> . <i>ISME Journal</i> , 2019, 13, 603-617.	9.8	30
28	â€™Candidatus <i>Paraporphyromonas polyenzymogenes</i> â€™ encodes multi-modular cellulases linked to the type IX secretion system. <i>Microbiome</i> , 2018, 6, 44.	11.1	32
29	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
30	Proteomic Dissection of the Cellulolytic Machineries Used by Soil-Dwelling <i>Bacteroidetes</i> . <i>MSystems</i> , 2018, 3, .	3.8	29
31	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , 2018, 3, 1274-1284.	13.3	144
32	Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , 2018, 3, 870-880.	13.3	372
33	Discovery and characterization of a thermostable two-domain GH6 endoglucanase from a compost metagenome. <i>PLoS ONE</i> , 2018, 13, e0197862.	2.5	23
34	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
35	Metagenomics and CAZyme Discovery. <i>Methods in Molecular Biology</i> , 2017, 1588, 255-277.	0.9	19
36	Outer membrane vesicles from <i>Fibrobacter succinogenes</i> S85 contain an array of carbohydrateâ€™active enzymes with versatile polysaccharideâ€™degrading capacity. <i>Environmental Microbiology</i> , 2017, 19, 2701-2714.	3.8	55

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	The Skin-Mucus Microbial Community of Farmed Atlantic Salmon (<i>Salmo salar</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 2043.	3.5	72
40	The Potential of Class II Bacteriocins to Modify Gut Microbiota to Improve Host Health. <i>PLoS ONE</i> , 2016, 11, e0164036.	2.5	102
41	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
42	From Genomes to Phenotypes: TraitAr, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	3.8	102
43	Novel Syntrophic Populations Dominate an Ammonia-Tolerant Methanogenic Microbiome. <i>MSystems</i> , 2016, 1, .	3.8	30
44	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
45	Improved metagenome assemblies and taxonomic binning using long-read circular consensus sequence data. <i>Scientific Reports</i> , 2016, 6, 25373.	3.3	139
46	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
47	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
48	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
49	Structural Features of a Bacteroidetes-Affiliated Cellulase Linked with a Polysaccharide Utilization Locus. <i>Scientific Reports</i> , 2015, 5, 11666.	3.3	24
50	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
51	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
52	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
53	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
54	The Reindeer Rumen Microbiome. , 2015, , 722-732.		1

#	ARTICLE	IF	CITATIONS
55	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
56	Do Rumen <i>Bacteroidetes</i> Utilize an Alternative Mechanism for Cellulose Degradation?. <i>MBio</i> , 2014, 5, e01401-14.	4.1	150
57	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
58	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
59	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
60	Omics-based interpretation of synergism in a soil-derived cellulose-degrading microbial community. <i>Scientific Reports</i> , 2014, 4, 5288.	3.3	39
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	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
63	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
64	Potential applications of gut microbiota to control human physiology. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 609-618.	1.7	23
65	The Reindeer Rumen Microbiome. , 2013, , 1-12.		3
66	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
67	Two SusD-Like Proteins Encoded within a Polysaccharide Utilization Locus of an Uncultured Ruminant <i>Bacteroidetes</i> Phylotype Bind Strongly to Cellulose. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5935-5937.	3.1	33
68	Metagenomics of the Svalbard Reindeer Rumen Microbiome Reveals Abundance of Polysaccharide Utilization Loci. <i>PLoS ONE</i> , 2012, 7, e38571.	2.5	190
69	Isolation of <i>Succinivibrionaceae</i> Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	12.6	179
70	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011, 8, 191-192.	19.0	198
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	Adaptation to herbivory by the Tamar 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
74	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
75	Metagenomic analysis of a freshwater toxic cyanobacteria bloom. <i>FEMS Microbiology Ecology</i> , 2008, 64, 9-27.	2.7	64