

Bryan A White

List of Publications by Year in descending order

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108
papers

13,662
citations

28274

55
h-index

30087

103
g-index

113
all docs

113
docs citations

113
times ranked

15339
citing authors

#	ARTICLE	IF	CITATIONS
1	Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. <i>Nature Reviews Microbiology</i> , 2008, 6, 121-131.	28.6	1,407
2	Habitat degradation impacts black howler monkey (<i>Alouatta pigra</i>) gastrointestinal microbiomes. <i>ISME Journal</i> , 2013, 7, 1344-1353.	9.8	1,031
3	Functional metagenomic profiling of nine biomes. <i>Nature</i> , 2008, 452, 629-632.	27.8	842
4	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1948-1953.	7.1	669
5	Specific microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. <i>ISME Journal</i> , 2016, 10, 2958-2972.	9.8	564
6	Potential Role of the Bovine Rumen Microbiome in Modulating Milk Composition and Feed Efficiency. <i>PLoS ONE</i> , 2014, 9, e85423.	2.5	417
7	Comparative Genome Analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : Insights into Their Environmental Niche. <i>Microbial Ecology</i> , 2010, 60, 721-729.	2.8	293
8	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. <i>ISME Journal</i> , 2011, 5, 639-649.	9.8	292
9	Longitudinal investigation of the age-related bacterial diversity in the feces of commercial pigs. <i>Veterinary Microbiology</i> , 2011, 153, 124-133.	1.9	274
10	From cellulosomes to cellulosomics. <i>Chemical Record</i> , 2008, 8, 364-377.	5.8	267
11	The Gut Microbiota Appears to Compensate for Seasonal Diet Variation in the Wild Black Howler Monkey (<i>Alouatta pigra</i>). <i>Microbial Ecology</i> , 2015, 69, 434-443.	2.8	254
12	Diet and exercise orthogonally alter the gut microbiome and reveal independent associations with anxiety and cognition. <i>Molecular Neurodegeneration</i> , 2014, 9, 36.	10.8	250
13	Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene Transfer Elements in the Chicken Cecum Microbiome. <i>PLoS ONE</i> , 2008, 3, e2945.	2.5	247
14	The microbiome of the chicken gastrointestinal tract. <i>Animal Health Research Reviews</i> , 2012, 13, 89-99.	3.1	239
15	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	9.8	236
16	Microbial shifts in the swine distal gut in response to the treatment with antimicrobial growth promoter, tylosin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15485-15490.	7.1	231
17	Gut Microbiome of Coexisting BaAka Pygmies and Bantu Reflects Gradients of Traditional Subsistence Patterns. <i>Cell Reports</i> , 2016, 14, 2142-2153.	6.4	231
18	Characterization of the Fecal Microbiome from Non-Human Wild Primates Reveals Species Specific Microbial Communities. <i>PLoS ONE</i> , 2010, 5, e13963.	2.5	225

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19	Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e9768.	2.5	223
20	Application of denaturant gradient gel electrophoresis for the analysis of the porcine gastrointestinal microbiota. <i>Journal of Microbiological Methods</i> , 1999, 36, 167-179.	1.6	221
21	Voluntary and forced exercise differentially alters the gut microbiome in C57BL/6J mice. <i>Journal of Applied Physiology</i> , 2015, 118, 1059-1066.	2.5	212
22	Loss of Sex and Age Driven Differences in the Gut Microbiome Characterize Arthritis-Susceptible *0401 Mice but Not Arthritis-Resistant *0402 Mice. <i>PLoS ONE</i> , 2012, 7, e36095.	2.5	195
23	Analysis of the Rumen Bacterial Diversity under two Different Diet Conditions using Denaturing Gradient Gel Electrophoresis, Random Sequencing, and Statistical Ecology Approaches. <i>Anaerobe</i> , 2001, 7, 119-134.	2.1	173
24	Gut microbiome composition and metabolomic profiles of wild western lowland gorillas (<i>Gorilla</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.9	171
25	Biomass Utilization by Gut Microbiomes. <i>Annual Review of Microbiology</i> , 2014, 68, 279-296.	7.3	161
26	Gastrointestinal Tract Microbiota and Probiotics in Production Animals. <i>Annual Review of Animal Biosciences</i> , 2014, 2, 469-486.	7.4	158
27	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. <i>ISME Journal</i> , 2014, 8, 2431-2444.	9.8	149
28	Pregnancy's Stronghold on the Vaginal Microbiome. <i>PLoS ONE</i> , 2014, 9, e98514.	2.5	146
29	Quantification of the relative roles of niche and neutral processes in structuring gastrointestinal microbiomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9692-9698.	7.1	133
30	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 207-227.	3.8	128
31	Diversity and Strain Specificity of Plant Cell Wall Degrading Enzymes Revealed by the Draft Genome of <i>Ruminococcus flavefaciens</i> FD-1. <i>PLoS ONE</i> , 2009, 4, e6650.	2.5	124
32	Comparative Genomics of <i>Gardnerella vaginalis</i> Strains Reveals Substantial Differences in Metabolic and Virulence Potential. <i>PLoS ONE</i> , 2010, 5, e12411.	2.5	124
33	A Multi-Omic Systems-Based Approach Reveals Metabolic Markers of Bacterial Vaginosis and Insight into the Disease. <i>PLoS ONE</i> , 2013, 8, e56111.	2.5	122
34	Low Incidence of Spontaneous Type 1 Diabetes in Non-Obese Diabetic Mice Raised on Gluten-Free Diets Is Associated with Changes in the Intestinal Microbiome. <i>PLoS ONE</i> , 2013, 8, e78687.	2.5	117
35	The primate vaginal microbiome: Comparative context and implications for human health and disease. <i>American Journal of Physical Anthropology</i> , 2013, 152, 119-134.	2.1	115
36	Heritable Bovine Rumen Bacteria Are Phylogenetically Related and Correlated with the Cow's Capacity To Harvest Energy from Its Feed. <i>MBio</i> , 2017, 8, .	4.1	110

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37	Variable responses of human and non-human primate gut microbiomes to a Western diet. <i>Microbiome</i> , 2015, 3, 53.	11.1	108
38	Caste-Specific Differences in Hindgut Microbial Communities of Honey Bees (<i>Apis mellifera</i>). <i>PLoS ONE</i> , 2015, 10, e0123911.	2.5	108
39	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. <i>Genome Medicine</i> , 2018, 10, 78.	8.2	107
40	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015, 17, 3407-3426.	3.8	104
41	The role of gut microbes in satisfying the nutritional demands of adult and juvenile wild, black howler monkeys (<i>A. a. louatta pigra</i>). <i>American Journal of Physical Anthropology</i> , 2014, 155, 652-664.	2.1	103
42	Fecal Metabolomic Signatures in Colorectal Adenoma Patients Are Associated with Gut Microbiota and Early Events of Colorectal Cancer Pathogenesis. <i>MBio</i> , 2020, 11, .	4.1	101
43	Exercise and gut immune function: evidence of alterations in colon immune cell homeostasis and microbiome characteristics with exercise training. <i>Immunology and Cell Biology</i> , 2016, 94, 158-163.	2.3	97
44	Recent Advances in Rumen Microbial Ecology and Metabolism: Potential Impact on Nutrient Output. <i>Journal of Dairy Science</i> , 1990, 73, 2971-2995.	3.4	93
45	Detection of glycoproteins separated by nondenaturing polyacrylamide gel electrophoresis using the periodic acid-Schiff stain. <i>Analytical Biochemistry</i> , 1990, 187, 147-150.	2.4	91
46	The vaginal microbiome in health and disease. <i>Trends in Endocrinology and Metabolism</i> , 2011, 22, 389-393.	7.1	91
47	Temporal variation selects for diet-specific microbe co-metabolic traits in the gut of <i>Gorilla</i> spp. <i>ISME Journal</i> , 2016, 10, 514-526.	9.8	84
48	Xylan degradation by the human gut <i>Bacteroides xylanisolvens</i> XB1AT involves two distinct gene clusters that are linked at the transcriptional level. <i>BMC Genomics</i> , 2016, 17, 326.	2.8	81
49	Suppressive subtractive hybridization as a tool for identifying genetic diversity in an environmental metagenome: the rumen as a model. <i>Environmental Microbiology</i> , 2004, 6, 928-937.	3.8	80
50	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. <i>Journal of Proteome Research</i> , 2012, 11, 5924-5933.	3.7	79
51	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. <i>PLoS ONE</i> , 2014, 9, e99221.	2.5	73
52	Comparison of pulsed field gel electrophoresis and repetitive sequence polymerase chain reaction as genotyping methods for detection of genetic diversity and inferring transmission of <i>Salmonella</i> . <i>Veterinary Microbiology</i> , 2004, 100, 205-217.	1.9	72
53	Fecal microbiomes of non-human primates in Western Uganda reveal species-specific communities largely resistant to habitat perturbation. <i>American Journal of Primatology</i> , 2014, 76, 347-354.	1.7	72
54	Polysaccharide Degradation in the Rumen and Large Intestine. , 1997, , 319-379.		68

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55	Abundance and Diversity of Dockerin-Containing Proteins in the Fiber-Degrading Rumen Bacterium, <i>Ruminococcus flavefaciens</i> FD-1. <i>PLoS ONE</i> , 2010, 5, e12476.	2.5	65
56	Synthesis of multi-omic data and community metabolic models reveals insights into the role of hydrogen sulfide in colon cancer. <i>Methods</i> , 2018, 149, 59-68.	3.8	63
57	Diversity of Extracellular Proteolytic Activities Among <i>Prevotella</i> Species from the Rumen. <i>Current Microbiology</i> , 1999, 39, 187-194.	2.2	60
58	Cellulosome gene cluster analysis for gauging the diversity of the ruminal cellulolytic bacterium <i>Ruminococcus flavefaciens</i> . <i>FEMS Microbiology Letters</i> , 2008, 285, 188-194.	1.8	56
59	Stool-based biomarkers of interstitial cystitis/bladder pain syndrome. <i>Scientific Reports</i> , 2016, 6, 26083.	3.3	53
60	Conservation and Divergence in Cellulosome Architecture between Two Strains of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7971-7976.	2.2	52
61	Molecular Cloning and Expression of Cellulase Genes from <i>Ruminococcus albus</i> 8 in <i>Escherichia coli</i> Bacteriophage ϕ . <i>Applied and Environmental Microbiology</i> , 1988, 54, 1752-1755.	3.1	52
62	Towards an Evolutionary Model of Animal-Associated Microbiomes. <i>Entropy</i> , 2011, 13, 570-594.	2.2	48
63	The Intestinal Microbiota Influences <i>Campylobacter jejuni</i> Colonization and Extraintestinal Dissemination in Mice. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4642-4650.	3.1	45
64	Isolation and structure of the <i>Streptococcus faecalis</i> sex pheromone, cAM373. <i>FEBS Letters</i> , 1986, 206, 69-72.	2.8	44
65	Modulation of Systemic Immune Responses through Commensal Gastrointestinal Microbiota. <i>PLoS ONE</i> , 2013, 8, e53969.	2.5	42
66	Analysis of antibiotic susceptibility and extrachromosomal DNA content of <i>Ruminococcus albus</i> and <i>Ruminococcus flavefaciens</i> . <i>Canadian Journal of Microbiology</i> , 1988, 34, 1109-1115.	1.7	40
67	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. <i>MSphere</i> , 2019, 4, .	2.9	40
68	Atypical Cohesin-Dockerin Complex Responsible for Cell Surface Attachment of Cellulosomal Components. <i>Journal of Biological Chemistry</i> , 2013, 288, 16827-16838.	3.4	38
69	Individualized medicine and the microbiome in reproductive tract. <i>Frontiers in Physiology</i> , 2015, 6, 97.	2.8	38
70	Complexity of the <i>Ruminococcus flavefaciens</i> FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. <i>Scientific Reports</i> , 2017, 7, 42355.	3.3	31
71	Effect of weaning diet on the ecology of adherent lactobacilli in the gastrointestinal tract of the pig. <i>Journal of Animal Science</i> , 1995, 73, 2347-2354.	0.5	30
72	Impact of stress on the gut microbiome of free-ranging western lowland gorillas. <i>Microbiology (United Kingdom)</i> , 2018, 164, 40-44.	1.8	29

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73	Cellulosomics, a Gene-Centric Approach to Investigating the Intraspecific Diversity and Adaptation of <i>Ruminococcus flavefaciens</i> within the Rumen. <i>PLoS ONE</i> , 2011, 6, e25329.	2.5	28
74	<i>In Vivo</i> Competitions between <i>Fibrobacter succinogenes</i> , <i>Ruminococcus flavefaciens</i> , and <i>Ruminococcus albus</i> in a Gnotobiotic Sheep Model Revealed by Multi-Omic Analyses. <i>MBio</i> , 2021, 12, .	4.1	26
75	Expression of Cellulosome Components and Type IV Pili within the Extracellular Proteome of <i>Ruminococcus flavefaciens</i> 007. <i>PLoS ONE</i> , 2013, 8, e65333.	2.5	25
76	Capturing One of the Human Gut Microbiome's Most Wanted: Reconstructing the Genome of a Novel Butyrate-Producing, Clostridial Scavenger from Metagenomic Sequence Data. <i>Frontiers in Microbiology</i> , 2016, 7, 783.	3.5	24
77	α-Glucanase expression by <i>Ruminococcus flavefaciens</i> FD-1. <i>FEMS Microbiology Letters</i> , 1992, 93, 147-153.	1.8	21
78	Strain-specific genomic regions of <i>Ruminococcus flavefaciens</i> FD-1 as revealed by combinatorial random-phase genome sequencing and suppressive subtractive hybridization. <i>Environmental Microbiology</i> , 2004, 6, 335-346.	3.8	21
79	Relationships Between Gastrointestinal Parasite Infections and the Fecal Microbiome in Free-Ranging Western Lowland Gorillas. <i>Frontiers in Microbiology</i> , 2018, 9, 1202.	3.5	21
80	DNA sequence and transcriptional characterization of a β -glucanase gene (<i>celB</i>) from <i>Ruminococcus flavefaciens</i> FD-1. <i>Canadian Journal of Microbiology</i> , 1995, 41, 869-876.	1.7	20
81	Crystal Structure of an Uncommon Cellulosome-Related Protein Module from <i>Ruminococcus flavefaciens</i> That Resembles Papain-Like Cysteine Peptidases. <i>PLoS ONE</i> , 2013, 8, e56138.	2.5	19
82	Effect of Antibiotic Treatment on the Gastrointestinal Microbiome of Free-Ranging Western Lowland Gorillas (<i>Gorilla g. gorilla</i>). <i>Microbial Ecology</i> , 2016, 72, 943-954.	2.8	19
83	Partial purification and characterization of Ral8I, a class-IIS restriction endonuclease from <i>Ruminococcus albus</i> 8 which recognizes 5'-GGATC. <i>Gene</i> , 1992, 111, 105-108.	2.2	16
84	Nucleotide sequence and transcriptional analysis of the <i>celD</i> β -glucanase gene from <i>Ruminococcus flavefaciens</i> FD-1. <i>Canadian Journal of Microbiology</i> , 1995, 41, 27-34.	1.7	15
85	Robust Computational Analysis of rRNA Hypervariable Tag Datasets. <i>PLoS ONE</i> , 2010, 5, e15220.	2.5	15
86	Gut microbiome composition of wild western lowland gorillas is associated with individual age and sex factors. <i>American Journal of Physical Anthropology</i> , 2019, 169, 575-585.	2.1	15
87	Testing an ecological model for transmission of <i>Salmonella enterica</i> in swine production ecosystems using genotyping data. <i>Preventive Veterinary Medicine</i> , 2007, 81, 274-289.	1.9	14
88	An endo- β -1,4-glucanase gene (<i>celA</i>) from the rumen anaerobe <i>Ruminococcus albus</i> 8: cloning, sequencing, and transcriptional analysis. <i>Canadian Journal of Microbiology</i> , 1996, 42, 267-278.	1.7	13
89	Comparative Microbial Diversity in the Gastrointestinal Tracts of Food Animal Species. <i>Integrative and Comparative Biology</i> , 2002, 42, 327-331.	2.0	13
90	Characterization of the gene encoding glutamate dehydrogenase (<i>gdhA</i>) from the ruminal bacterium <i>Ruminococcus flavefaciens</i> FD-1. <i>Archives of Microbiology</i> , 2003, 179, 184-190.	2.2	13

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91	Enzymatic Hydrolysis of Forage Cell Walls. <i>Assa, Cssa and Sssa, 0, , 455-484.</i>	0.6	12
92	Functional phylotyping approach for assessing intraspecific diversity of <i>Ruminococcus albus</i> within the rumen microbiome. <i>FEMS Microbiology Letters, 2015, 362, 1-10.</i>	1.8	12
93	Cloning in <i>Escherichia coli</i> of a bifunctional cellulase/xylanase enzyme from <i>Ruminococcus flavefaciens</i> FD-1. <i>Animal Biotechnology, 1990, 1, 95-106.</i>	1.5	11
94	Transcriptional analysis of the <i>Clostridium cellulovorans</i> endoglucanase gene, <i>engB</i> . <i>FEMS Microbiology Letters, 1994, 124, 277-284.</i>	1.8	10
95	Genetic systems development in the clostridia. <i>FEMS Microbiology Reviews, 1995, 17, 349-356.</i>	8.6	8
96	The restriction endonuclease <i>RflFI</i> , isolated from <i>Ruminococcus flavefaciens</i> FD-1, recognizes the sequence 5'-AGTACT-3', and is inhibited by site-specific adenine methylation. <i>FEMS Microbiology Letters, 1994, 122, 181-185.</i>	1.8	7
97	Effects of tylosin administration on C-reactive protein concentration and carriage of <i>Salmonella enterica</i> in pigs. <i>American Journal of Veterinary Research, 2014, 75, 460-467.</i>	0.6	6
98	Inhibition of the exo-1,4-glucanase from <i>Ruminococcus flavefaciens</i> FD-1 by a specific monoclonal antibody. <i>Enzyme and Microbial Technology, 1994, 16, 2-9.</i>	3.2	5
99	Complete nucleotide sequence of a cryptic plasmid, <i>pbaw301</i> , from the ruminal anaerobe <i>Ruminococcus flavefaciens</i> R13e2. <i>FEMS Microbiology Letters, 1996, 144, 221-227.</i>	1.8	5
100	Compression-based distance (CBD): a simple, rapid, and accurate method for microbiota composition comparison. <i>BMC Bioinformatics, 2013, 14, 136.</i>	2.6	5
101	Draft Genome Sequences of 24 Microbial Strains Assembled from Direct Sequencing from 4 Stool Samples. <i>Genome Announcements, 2015, 3, .</i>	0.8	5
102	Phylogenetic reconstruction of Gram-positive organisms based on comparative sequence analysis of molecular chaperones from the ruminal microorganism <i>Ruminococcus flavefaciens</i> FD-1. <i>FEMS Microbiology Letters, 2003, 227, 1-7.</i>	1.8	4
103	Genetics of Ruminal Anaerobic Bacteria. , 1997, , 321-370.		4
104	Application of Suppressive Subtractive Hybridization to Uncover the Metagenomic Diversity of Environmental Samples. <i>Methods in Molecular Biology, 2008, 410, 295-334.</i>	0.9	4
105	The use of pyrosequencing to identify diet-induced changes in the canine gut microbiome. <i>FASEB Journal, 2009, 23, 905.4.</i>	0.5	1
106	Comparative analysis of the vaginal microbiome in health and disease. <i>Genome Biology, 2011, 12, .</i>	9.6	0
107	Molecular Methods To Study Complex Microbial Communities. , 2014, , 323-345.		0
108	Shifts in the fecal microbial community composition are associated with dietary fiber solubility. <i>FASEB Journal, 2013, 27, 1056.2.</i>	0.5	0