

# 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	<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
2	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
3	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	9.8	236
4	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. <i>MSphere</i> , 2019, 4, .	2.9	40
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	Stool-based biomarkers of interstitial cystitis/bladder pain syndrome. <i>Scientific Reports</i> , 2016, 6, 26083.	3.3	53
14	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
15	Specific microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. <i>ISME Journal</i> , 2016, 10, 2958-2972.	9.8	564
16	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
17	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
18	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

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19	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
20	Variable responses of human and non-human primate gut microbiomes to a Western diet. <i>Microbiome</i> , 2015, 3, 53.	11.1	108
21	Individualized medicine and the microbiome in reproductive tract. <i>Frontiers in Physiology</i> , 2015, 6, 97.	2.8	38
22	Draft Genome Sequences of 24 Microbial Strains Assembled from Direct Sequencing from 4 Stool Samples. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
23	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
24	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
25	Functional phylotyping approach for assessing intraspecific diversity of <i>Ruminococcus albus</i> within the rumen microbiome. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-10.	1.8	12
26	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015, 17, 3407-3426.	3.8	104
27	Gut microbiome composition and metabolomic profiles of wild western lowland gorillas ( <i>Gorilla</i> ). <i>Journal of Applied Physiology</i> , 2015, 118, 1059-1066.	3.9	171
28	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
29	Caste-Specific Differences in Hindgut Microbial Communities of Honey Bees ( <i>Apis mellifera</i> ). <i>PLoS ONE</i> , 2015, 10, e0123911.	2.5	108
30	Potential Role of the Bovine Rumen Microbiome in Modulating Milk Composition and Feed Efficiency. <i>PLoS ONE</i> , 2014, 9, e85423.	2.5	417
31	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
32	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
33	Effects of tylosin administration on C-reactive protein concentration and carriage of <i>Salmonella enterica</i> in pigs. <i>American Journal of Veterinary Research</i> , 2014, 75, 460-467.	0.6	6
34	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
35	Primate vaginal microbiomes exhibit species specificity without universal <i>Lactobacillus</i> dominance. <i>ISME Journal</i> , 2014, 8, 2431-2444.	9.8	149
36	The role of gut microbes in satisfying the nutritional demands of adult and juvenile wild, black howler monkeys ( <i>Alouatta pigra</i> ). <i>American Journal of Physical Anthropology</i> , 2014, 155, 652-664.	2.1	103

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37	Gastrointestinal Tract Microbiota and Probiotics in Production Animals. Annual Review of Animal Biosciences, 2014, 2, 469-486.	7.4	158
38	Biomass Utilization by Gut Microbiomes. Annual Review of Microbiology, 2014, 68, 279-296.	7.3	161
39	Molecular Methods To Study Complex Microbial Communities. , 2014, , 323-345.		0
40	Pregnancy's Stronghold on the Vaginal Microbiome. PLoS ONE, 2014, 9, e98514.	2.5	146
41	Atypical Cohesin-Dockerin Complex Responsible for Cell Surface Attachment of Cellulosomal Components. Journal of Biological Chemistry, 2013, 288, 16827-16838.	3.4	38
42	Compression-based distance (CBD): a simple, rapid, and accurate method for microbiota composition comparison. BMC Bioinformatics, 2013, 14, 136.	2.6	5
43	Habitat degradation impacts black howler monkey ( <i>Alouatta pigra</i> ) gastrointestinal microbiomes. ISME Journal, 2013, 7, 1344-1353.	9.8	1,031
44	Modulation of Systemic Immune Responses through Commensal Gastrointestinal Microbiota. PLoS ONE, 2013, 8, e53969.	2.5	42
45	The primate vaginal microbiome: Comparative context and implications for human health and disease. American Journal of Physical Anthropology, 2013, 152, 119-134.	2.1	115
46	A Multi-Omic Systems-Based Approach Reveals Metabolic Markers of Bacterial Vaginosis and Insight into the Disease. PLoS ONE, 2013, 8, e56111.	2.5	122
47	Crystal Structure of an Uncommon Cellulosome-Related Protein Module from <i>Ruminococcus flavefaciens</i> That Resembles Papain-Like Cysteine Peptidases. PLoS ONE, 2013, 8, e56138.	2.5	19
48	Expression of Cellulosome Components and Type IV Pili within the Extracellular Proteome of <i>Ruminococcus flavefaciens</i> 007. PLoS ONE, 2013, 8, e65333.	2.5	25
49	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. PLoS ONE, 2013, 8, e78687.	2.5	117
50	Shifts in the fecal microbial community composition are associated with dietary fiber solubility. FASEB Journal, 2013, 27, 1056.2.	0.5	0
51	Microbial shifts in the swine distal gut in response to the treatment with antimicrobial growth promoter, tylosin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15485-15490.	7.1	231
52	The microbiome of the chicken gastrointestinal tract. Animal Health Research Reviews, 2012, 13, 89-99.	3.1	239
53	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. Journal of Proteome Research, 2012, 11, 5924-5933.	3.7	79
54	Loss of Sex and Age Driven Differences in the Gut Microbiome Characterize Arthritis-Susceptible *0401 Mice but Not Arthritis-Resistant *0402 Mice. PLoS ONE, 2012, 7, e36095.	2.5	195

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55	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
56	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
57	Comparative analysis of the vaginal microbiome in health and disease. <i>Genome Biology</i> , 2011, 12, .	9.6	0
58	The vaginal microbiome in health and disease. <i>Trends in Endocrinology and Metabolism</i> , 2011, 22, 389-393.	7.1	91
59	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
60	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
61	Towards an Evolutionary Model of Animal-Associated Microbiomes. <i>Entropy</i> , 2011, 13, 570-594.	2.2	48
62	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
63	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
64	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
65	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
66	Robust Computational Analysis of rRNA Hypervariable Tag Datasets. <i>PLoS ONE</i> , 2010, 5, e15220.	2.5	15
67	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
68	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
69	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
70	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
71	The use of pyrosequencing to identify diet-induced changes in the canine gut microbiome. <i>FASEB Journal</i> , 2009, 23, 905.4.	0.5	1
72	From cellulosomes to cellulosomics. <i>Chemical Record</i> , 2008, 8, 364-377.	5.8	267

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73	Cellulosome gene cluster analysis for gauging the diversity of the ruminal cellulolytic bacterium <i>Ruminococcus flavefaciens</i> . FEMS Microbiology Letters, 2008, 285, 188-194.	1.8	56
74	Functional metagenomic profiling of nine biomes. Nature, 2008, 452, 629-632.	27.8	842
75	Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. Nature Reviews Microbiology, 2008, 6, 121-131.	28.6	1,407
76	Application of Suppressive Subtractive Hybridization to Uncover the Metagenomic Diversity of Environmental Samples. Methods in Molecular Biology, 2008, 410, 295-334.	0.9	4
77	Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene Transfer Elements in the Chicken Cecum Microbiome. PLoS ONE, 2008, 3, e2945.	2.5	247
78	Testing an ecological model for transmission of <i>Salmonella enterica</i> in swine production ecosystems using genotyping data. Preventive Veterinary Medicine, 2007, 81, 274-289.	1.9	14
79	Conservation and Divergence in Cellulosome Architecture between Two Strains of <i>Ruminococcus flavefaciens</i> . Journal of Bacteriology, 2006, 188, 7971-7976.	2.2	52
80	Suppressive subtractive hybridization as a tool for identifying genetic diversity in an environmental metagenome: the rumen as a model. Environmental Microbiology, 2004, 6, 928-937.	3.8	80
81	Strain-specific genomic regions of <i>Ruminococcus flavefaciens</i> FD-1 as revealed by combinatorial random-phase genome sequencing and suppressive subtractive hybridization. Environmental Microbiology, 2004, 6, 335-346.	3.8	21
82	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> . Veterinary Microbiology, 2004, 100, 205-217.	1.9	72
83	Characterization of the gene encoding glutamate dehydrogenase ( <i>gdhA</i> ) from the ruminal bacterium <i>Ruminococcus flavefaciens</i> FD-1. Archives of Microbiology, 2003, 179, 184-190.	2.2	13
84	Phylogenetic reconstruction of Gram-positive organisms based on comparative sequence analysis of molecular chaperones from the ruminal microorganism <i>Ruminococcus flavefaciens</i> FD-1. FEMS Microbiology Letters, 2003, 227, 1-7.	1.8	4
85	Comparative Microbial Diversity in the Gastrointestinal Tracts of Food Animal Species. Integrative and Comparative Biology, 2002, 42, 327-331.	2.0	13
86	Analysis of the Rumen Bacterial Diversity under two Different Diet Conditions using Denaturing Gradient Gel Electrophoresis, Random Sequencing, and Statistical Ecology Approaches. Anaerobe, 2001, 7, 119-134.	2.1	173
87	Diversity of Extracellular Proteolytic Activities Among <i>Prevotella</i> Species from the Rumen. Current Microbiology, 1999, 39, 187-194.	2.2	60
88	Application of denaturant gradient gel electrophoresis for the analysis of the porcine gastrointestinal microbiota. Journal of Microbiological Methods, 1999, 36, 167-179.	1.6	221
89	Polysaccharide Degradation in the Rumen and Large Intestine. , 1997, , 319-379.		68
90	Genetics of Ruminal Anaerobic Bacteria. , 1997, , 321-370.		4

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91	Complete nucleotide sequence of a cryptic plasmid, pbaw301, from the ruminal anaerobe <i>Ruminococcus flavefaciens</i> R13e2. <i>FEMS Microbiology Letters</i> , 1996, 144, 221-227.	1.8	5
92	An endo- $\beta$ -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
93	Genetic systems development in the clostridia. <i>FEMS Microbiology Reviews</i> , 1995, 17, 349-356.	8.6	8
94	Nucleotide sequence and transcriptional analysis of the <i>celD</i> $\beta$ -glucanase gene from <i>Ruminococcus flavefaciens</i> FD-1. <i>Canadian Journal of Microbiology</i> , 1995, 41, 27-34.	1.7	15
95	DNA sequence and transcriptional characterization of a $\beta$ -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
96	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
97	Inhibition of the exo- $\beta$ -1,4-glucanase from <i>Ruminococcus flavefaciens</i> FD-1 by a specific monoclonal antibody. <i>Enzyme and Microbial Technology</i> , 1994, 16, 2-9.	3.2	5
98	The restriction endonuclease RflFII, 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</i> , 1994, 122, 181-185.	1.8	7
99	Transcriptional analysis of the <i>Clostridium cellulovorans</i> endoglucanase gene, <i>engB</i> . <i>FEMS Microbiology Letters</i> , 1994, 124, 277-284.	1.8	10
100	Partial purification and characterization of Ral8I, a class-III restriction endonuclease from <i>Ruminococcus albus</i> 8 which recognizes 5'-GGATC. <i>Gene</i> , 1992, 111, 105-108.	2.2	16
101	$\beta$ -Glucanase expression by <i>Ruminococcus flavefaciens</i> FD-1. <i>FEMS Microbiology Letters</i> , 1992, 93, 147-153.	1.8	21
102	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
103	Cloning in <i>Escherichia coli</i> of a bifunctional cellulase/xylanase enzyme from <i>Ruminococcus flavefaciens</i> FD-1. <i>Animal Biotechnology</i> , 1990, 1, 95-106.	1.5	11
104	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
105	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
106	Molecular Cloning and Expression of Cellulase Genes from <i>Ruminococcus albus</i> 8 in <i>Escherichia coli</i> Bacteriophage $\lambda$ . <i>Applied and Environmental Microbiology</i> , 1988, 54, 1752-1755.	3.1	52
107	Isolation and structure of the <i>Streptococcus faecalis</i> sex pheromone, cAM373. <i>FEBS Letters</i> , 1986, 206, 69-72.	2.8	44
108	Enzymatic Hydrolysis of Forage Cell Walls. <i>Assa, Cssa and Sssa</i> , 0, , 455-484.	0.6	12