

Mark Morrison

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212
papers

12,039
citations

55
h-index

105
g-index

229
ext. papers

15,210
ext. citations

5.3
avg, IF

6.58
L-index

#	Paper	IF	Citations
212	Improved extraction of PCR-quality community DNA from digesta and fecal samples. <i>BioTechniques</i> , 2004 , 36, 808-12	2.5	990
211	Emerging pathogenic links between microbiota and the gut-lung axis. <i>Nature Reviews Microbiology</i> , 2017 , 15, 55-63	22.2	579
210	Comparisons of different hypervariable regions of rrs genes for use in fingerprinting of microbial communities by PCR-denaturing gradient gel electrophoresis. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 4800-6	4.8	387
209	A meta-analysis of the microbial diversity observed in anaerobic digesters. <i>Bioresource Technology</i> , 2011 , 102, 3730-9	11	328
208	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016 , 4, 36	16.6	322
207	Opportunities to improve fiber degradation in the rumen: microbiology, ecology, and genomics. <i>FEMS Microbiology Reviews</i> , 2003 , 27, 663-93	15.1	284
206	Inflammasome signaling affects anxiety- and depressive-like behavior and gut microbiome composition. <i>Molecular Psychiatry</i> , 2016 , 21, 797-805	15.1	268
205	Dysbiosis of fecal microbiota in Crohn's disease patients as revealed by a custom phylogenetic microarray. <i>Inflammatory Bowel Diseases</i> , 2010 , 16, 2034-42	4.5	250
204	Bacterial census of poultry intestinal microbiome. <i>Poultry Science</i> , 2013 , 92, 671-83	3.9	245
203	Development of an assay to quantify rumen ciliate protozoal biomass in cows using real-time PCR. <i>Journal of Nutrition</i> , 2004 , 134, 3378-84	4.1	245
202	Dietary fiber intervention on gut microbiota composition in healthy adults: a systematic review and meta-analysis. <i>American Journal of Clinical Nutrition</i> , 2018 , 107, 965-983	7	228
201	Status of the phylogenetic diversity census of ruminal microbiomes. <i>FEMS Microbiology Ecology</i> , 2011 , 76, 49-63	4.3	226
200	Evaluation of different partial 16S rRNA gene sequence regions for phylogenetic analysis of microbiomes. <i>Journal of Microbiological Methods</i> , 2011 , 84, 81-7	2.8	224
199	Synbiotics Easing Renal Failure by Improving Gut Microbiology (SYNERGY): A Randomized Trial. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2016 , 11, 223-31	6.9	194
198	Comparative genome analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : insights into their environmental niche. <i>Microbial Ecology</i> , 2010 , 60, 721-9	4.4	192
197	Development and application of real-time PCR assays for quantification of erm genes conferring resistance to macrolides-lincosamides-streptogramin B in livestock manure and manure management systems. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4407-16	4.8	192
196	Highlighting new phylogenetic specificities of Crohn's disease microbiota. <i>Inflammatory Bowel Diseases</i> , 2011 , 17, 185-92	4.5	191

195	Invited review: adhesion mechanisms of rumen cellulolytic bacteria. <i>Journal of Dairy Science</i> , 2001 , 84, 1294-309	4	190
194	Electricity generation from cellulose by rumen microorganisms in microbial fuel cells. <i>Biotechnology and Bioengineering</i> , 2007 , 97, 1398-407	4.9	188
193	Increased Systolic and Diastolic Blood Pressure Is Associated With Altered Gut Microbiota Composition and Butyrate Production in Early Pregnancy. <i>Hypertension</i> , 2016 , 68, 974-81	8.5	183
192	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, 14793-8	11.5	163
191	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011 , 8, 191-2	21.6	161
190	Connections Between the Gut Microbiome and Metabolic Hormones in Early Pregnancy in Overweight and Obese Women. <i>Diabetes</i> , 2016 , 65, 2214-23	0.9	153
189	Ruminal nitrogen metabolism: perspectives for integration of microbiology and nutrition for dairy. <i>Journal of Dairy Science</i> , 2007 , 90 Suppl 1, E1-16	4	152
188	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
187	Novel microbial diversity adherent to plant biomass in the herbivore gastrointestinal tract, as revealed by ribosomal intergenic spacer analysis and rrs gene sequencing. <i>Environmental Microbiology</i> , 2005 , 7, 530-43	5.2	141
186	Development and application of real-time PCR assays for quantification of genes encoding tetracycline resistance. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6926-33	4.8	140
185	Metagenomics of the Svalbard reindeer rumen microbiome reveals abundance of polysaccharide utilization loci. <i>PLoS ONE</i> , 2012 , 7, e38571	3.7	130
184	Evaluations of different hypervariable regions of archaeal 16S rRNA genes in profiling of methanogens by Archaea-specific PCR and denaturing gradient gel electrophoresis. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 889-93	4.8	125
183	Isolation of Succinivibrionaceae implicated in low methane emissions from Tammar wallabies. <i>Science</i> , 2011 , 333, 646-8	33.3	119
182	ZAP-70 genotype disrupts the relationship between microbiota and host, leading to spondyloarthritis and ileitis in SKG mice. <i>Arthritis and Rheumatology</i> , 2014 , 66, 2780-92	9.5	115
181	Low dietary fiber intake increases Collinsella abundance in the gut microbiota of overweight and obese pregnant women. <i>Gut Microbes</i> , 2018 , 9, 189-201	8.8	113
180	Association between specific mucosa-associated microbiota in Crohn's disease at the time of resection and subsequent disease recurrence: a pilot study. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2015 , 30, 268-78	4	103
179	Dyspepsia and the microbiome: time to focus on the small intestine. <i>Gut</i> , 2017 , 66, 1168-1169	19.2	100
178	Plant biomass degradation by gut microbiomes: more of the same or something new?. <i>Current Opinion in Biotechnology</i> , 2009 , 20, 358-63	11.4	90

177	Functional gene analysis suggests different acetogen populations in the bovine rumen and tammar wallaby forestomach. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 7785-95	4.8	89
176	Contributions of the maternal oral and gut microbiome to placental microbial colonization in overweight and obese pregnant women. <i>Scientific Reports</i> , 2017 , 7, 2860	4.9	82
175	Adhesion to cellulose by <i>Ruminococcus albus</i> : a combination of cellulosomes and Pil-proteins?. <i>FEMS Microbiology Letters</i> , 2000 , 185, 109-15	2.9	82
174	Evaluation of subsampling-based normalization strategies for tagged high-throughput sequencing data sets from gut microbiomes. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 8795-8	4.8	80
173	Characterization of the gastrointestinal microbiota in health and inflammatory bowel disease. <i>Inflammatory Bowel Diseases</i> , 2012 , 18, 372-90	4.5	79
172	<i>Ruminococcus albus</i> 8 mutants defective in cellulose degradation are deficient in two processive endocellulases, Cel48A and Cel9B, both of which possess a novel modular architecture. <i>Journal of Bacteriology</i> , 2004 , 186, 136-45	3.5	74
171	Food Starch Structure Impacts Gut Microbiome Composition. <i>MSphere</i> , 2018 , 3,	5	72
170	Probiotics for the Prevention of Gestational Diabetes Mellitus in Overweight and Obese Women: Findings From the SPRING Double-Blind Randomized Controlled Trial. <i>Diabetes Care</i> , 2019 , 42, 364-371	14.6	69
169	Pathophysiology of Functional Gastrointestinal Disorders: A Holistic Overview. <i>Digestive Diseases</i> , 2017 , 35 Suppl 1, 5-13	3.2	69
168	Vitamin D and the gut microbiome: a systematic review of in vivo studies. <i>European Journal of Nutrition</i> , 2019 , 58, 2895-2910	5.2	69
167	Metagenomic insights into the carbohydrate-active enzymes carried by the microorganisms adhering to solid digesta in the rumen of cows. <i>PLoS ONE</i> , 2013 , 8, e78507	3.7	68
166	Occurrence and persistence of erythromycin resistance genes (<i>erm</i>) and tetracycline resistance genes (<i>tet</i>) in waste treatment systems on swine farms. <i>Microbial Ecology</i> , 2010 , 60, 479-86	4.4	68
165	Review article: Associations between <i>Helicobacter pylori</i> and obesity--an ecological study. <i>Alimentary Pharmacology and Therapeutics</i> , 2014 , 40, 24-31	6.1	65
164	Numerical ecology validates a biogeographical distribution and gender-based effect on mucosa-associated bacteria along the human colon. <i>ISME Journal</i> , 2011 , 5, 801-9	11.9	63
163	The saliva microbiome profiles are minimally affected by collection method or DNA extraction protocols. <i>Scientific Reports</i> , 2017 , 7, 8523	4.9	62
162	Persistence of resistance to erythromycin and tetracycline in swine manure during simulated composting and lagoon treatments. <i>Microbial Ecology</i> , 2012 , 63, 32-40	4.4	60
161	Oral Microbiome: A New Biomarker Reservoir for Oral and Oropharyngeal Cancers. <i>Theranostics</i> , 2017 , 7, 4313-4321	12.1	60
160	Selected antimicrobial resistance during composting of manure from cattle administered sub-therapeutic antimicrobials. <i>Journal of Environmental Quality</i> , 2009 , 38, 567-75	3.4	60

159	Impact of ethnicity, geography, and disease on the microbiota in health and inflammatory bowel disease. <i>Inflammatory Bowel Diseases</i> , 2013 , 19, 2906-18	4.5	59
158	Rumen cellulosomes: divergent fiber-degrading strategies revealed by comparative genome-wide analysis of six ruminococcal strains. <i>PLoS ONE</i> , 2014 , 9, e99221	3.7	55
157	The Performance of an Oral Microbiome Biomarker Panel in Predicting Oral Cavity and Oropharyngeal Cancers. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 267	5.9	54
156	Adherence of the gram-positive bacterium <i>Ruminococcus albus</i> to cellulose and identification of a novel form of cellulose-binding protein which belongs to the Pil family of proteins. <i>Journal of Bacteriology</i> , 1998 , 180, 5921-7	3.5	53
155	Antibiotic treatment at delivery shapes the initial oral microbiome in neonates. <i>Scientific Reports</i> , 2017 , 7, 43481	4.9	52
154	Small Intestinal Bacterial Overgrowth in Irritable Bowel Syndrome: A Systematic Review and Meta-Analysis of Case-Control Studies. <i>American Journal of Gastroenterology</i> , 2020 , 115, 190-201	0.7	51
153	<i>Proteus</i> spp. as Putative Gastrointestinal Pathogens. <i>Clinical Microbiology Reviews</i> , 2018 , 31,	34	51
152	Community composition and density of methanogens in the foregut of the Tammar wallaby (<i>Macropus eugenii</i>). <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2598-602	4.8	51
151	A Vegetarian Diet Is a Major Determinant of Gut Microbiota Composition in Early Pregnancy. <i>Nutrients</i> , 2018 , 10,	6.7	50
150	Characterisation of the gastrointestinal mucosa-associated microbiota: a novel technique to prevent cross-contamination during endoscopic procedures. <i>Alimentary Pharmacology and Therapeutics</i> , 2016 , 43, 1186-96	6.1	48
149	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. <i>Frontiers in Microbiology</i> , 2015 , 6, 1469	5.7	48
148	The effects from DNA extraction methods on the evaluation of microbial diversity associated with human colonic tissue. <i>Microbial Ecology</i> , 2011 , 61, 353-62	4.4	47
147	Shotgun metagenomics reveals an enrichment of potentially cross-reactive bacterial epitopes in ankylosing spondylitis patients, as well as the effects of TNFi therapy upon microbiome composition. <i>Annals of the Rheumatic Diseases</i> , 2020 , 79, 132-140	2.4	47
146	Mothers Secretor Status Affects Development of Childrens Microbiota Composition and Function: A Pilot Study. <i>PLoS ONE</i> , 2016 , 11, e0161211	3.7	47
145	Plasmacytoid dendritic cells protect from viral bronchiolitis and asthma through semaphorin 4a-mediated T reg expansion. <i>Journal of Experimental Medicine</i> , 2018 , 215, 537-557	16.6	45
144	A novel family of carbohydrate-binding modules identified with <i>Ruminococcus albus</i> proteins. <i>FEBS Letters</i> , 2004 , 566, 11-6	3.8	44
143	Draft genome sequence of <i>Turicibacter sanguinis</i> PC909, isolated from human feces. <i>Journal of Bacteriology</i> , 2011 , 193, 1288-9	3.5	43
142	Populations of select cultured and uncultured bacteria in the rumen of sheep and the effect of diets and ruminal fractions. <i>International Journal of Microbiology</i> , 2011 , 2011, 750613	3.6	43

141	Technical note: Specific PCR amplification of protozoal 18S rDNA sequences from DNA extracted from ruminal samples of cows. <i>Journal of Animal Science</i> , 2003 , 81, 812-5	0.7	43
140	Novel molecular features of the fibrolytic intestinal bacterium <i>Fibrobacter intestinalis</i> not shared with <i>Fibrobacter succinogenes</i> as determined by suppressive subtractive hybridization. <i>Journal of Bacteriology</i> , 2005 , 187, 3739-51	3.5	43
139	Biochemical characterization and relative expression levels of multiple carbohydrate esterases of the xylanolytic rumen bacterium <i>Prevotella ruminicola</i> 23 grown on an ester-enriched substrate. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 5671-81	4.8	42
138	The functional repertoire of prokaryote cellulosomes includes the serpin superfamily of serine proteinase inhibitors. <i>Molecular Microbiology</i> , 2006 , 60, 1344-54	4.1	42
137	Dairy and plant based food intakes are associated with altered faecal microbiota in 2 to 3 year old Australian children. <i>Scientific Reports</i> , 2016 , 6, 32385	4.9	41
136	Cell surface enzyme attachment is mediated by family 37 carbohydrate-binding modules, unique to <i>Ruminococcus albus</i> . <i>Journal of Bacteriology</i> , 2008 , 190, 8220-2	3.5	41
135	The gut bacterium and pathobiont <i>Bacteroides vulgatus</i> activates NF- κ B in a human gut epithelial cell line in a strain and growth phase dependent manner. <i>Anaerobe</i> , 2017 , 47, 209-217	2.8	40
134	Shifts in microbial community structure of granular and liquid biomass in response to changes to infeed and digester design in anaerobic digesters receiving food-processing wastes. <i>Bioresource Technology</i> , 2012 , 107, 135-43	11	40
133	Systematic review with meta-analysis: the prevalence of small intestinal bacterial overgrowth in inflammatory bowel disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2019 , 49, 624-635	6.1	39
132	Improved serial analysis of V1 ribosomal sequence tags (SARST-V1) provides a rapid, comprehensive, sequence-based characterization of bacterial diversity and community composition. <i>Environmental Microbiology</i> , 2006 , 8, 603-11	5.2	39
131	The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers. <i>Nutrients</i> , 2019 , 11,	6.7	37
130	An efficient RNA extraction method for estimating gut microbial diversity by polymerase chain reaction. <i>Current Microbiology</i> , 2009 , 58, 464-71	2.4	37
129	Rumen ciliated protozoa decrease generation time and adjust 18S ribosomal DNA copies to adapt to decreased transfer interval, starvation, and monensin. <i>Journal of Dairy Science</i> , 2009 , 92, 256-69	4	37
128	Influence of cigarette smoking on the human duodenal mucosa-associated microbiota. <i>Microbiome</i> , 2018 , 6, 150	16.6	37
127	Analysis of the Effects of Dietary Pattern on the Oral Microbiome of Elite Endurance Athletes. <i>Nutrients</i> , 2019 , 11,	6.7	35
126	Nitrogen metabolism by ruminal microorganisms: current understanding and future perspectives. <i>Australian Journal of Agricultural Research</i> , 1996 , 47, 227		35
125	SYNbiotics Easing Renal failure by improving Gut microbiology (SYNERGY): a protocol of placebo-controlled randomised cross-over trial. <i>BMC Nephrology</i> , 2014 , 15, 106	2.7	34
124	Systematic Review and Meta-Analysis: Prevalence of Small Intestinal Bacterial Overgrowth in Chronic Liver Disease. <i>Seminars in Liver Disease</i> , 2017 , 37, 388-400	7.3	34

123	The <i>Ruminococcus albus</i> pilA1-pilA2 locus: expression and putative role of two adjacent pil genes in pilus formation and bacterial adhesion to cellulose. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 1291-9	2.9	32
122	Identification of metabolically active proteobacterial and archaeal communities in the rumen by DNA- and RNA-derived 16S rRNA gene. <i>Journal of Applied Microbiology</i> , 2013 , 115, 644-53	4.7	31
121	Exploring rumen methanogen genomes to identify targets for methane mitigation strategies. <i>Animal Feed Science and Technology</i> , 2011 , 166-167, 65-75	3	31
120	New Insights into the Diversity of the Genus. <i>Frontiers in Microbiology</i> , 2017 , 8, 1790	5.7	30
119	Overestimation of the abundance of sulfate-reducing bacteria in human feces by quantitative PCR targeting the <i>Desulfovibrio</i> 16S rRNA gene. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3544-6	4.8	30
118	Phylogenetic diversity of bacterial communities in bovine rumen as affected by diets and microenvironments. <i>Folia Microbiologica</i> , 2011 , 56, 453-8	2.8	29
117	Displacement of <i>Escherichia coli</i> O157:H7 from rumen medium containing prebiotic sugars. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 519-24	4.8	29
116	3-Phenylpropanoic Acid Improves the Affinity of <i>Ruminococcus albus</i> for Cellulose in Continuous Culture. <i>Applied and Environmental Microbiology</i> , 1990 , 56, 3220-2	4.8	27
115	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, 5935-7	4.8	26
114	Technical note: Occurrence in fecal microbiota of genes conferring resistance to both macrolide-lincosamide-streptogramin B and tetracyclines concomitant with feeding of beef cattle with tylosin. <i>Journal of Animal Science</i> , 2008 , 86, 2385-91	0.7	26
113	Targeting the Gut Microbiome as a Treatment for Primary Sclerosing Cholangitis: A Conceptual Framework. <i>American Journal of Gastroenterology</i> , 2020 , 115, 814-822	0.7	25
112	Ascites bacterial burden and immune cell profile are associated with poor clinical outcomes in the absence of overt infection. <i>PLoS ONE</i> , 2015 , 10, e0120642	3.7	25
111	Analysis of the bovine rumen microbiome reveals a diversity of Sus-like polysaccharide utilization loci from the bacterial phylum Bacteroidetes. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014 , 41, 601-6	4.2	23
110	Investigation of a new acetogen isolated from an enrichment of the tammar wallaby forestomach. <i>BMC Microbiology</i> , 2014 , 14, 314	4.5	22
109	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, 448-54	4.4	22
108	Nutrient metabolism and rumen micro-organisms in sheep fed a poor-quality tropical grass hay supplemented with sulphate. <i>Journal of Agricultural Science</i> , 1990 , 115, 269-275	1	22
107	Effects of Antibiotic Therapy in Primary Sclerosing Cholangitis with and without Inflammatory Bowel Disease: A Systematic Review and Meta-Analysis. <i>Seminars in Liver Disease</i> , 2019 , 39, 432-441	7.3	20
106	Molecular investigation of bacterial communities on intravascular catheters: no longer just <i>Staphylococcus</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2014 , 33, 1189-98	5.3	20

105	Do ruminal bacteria exchange genetic material?. <i>Journal of Dairy Science</i> , 1996 , 79, 1476-86	4	20
104	Differences down-under: alcohol-fueled methanogenesis by archaea present in Australian macropodids. <i>ISME Journal</i> , 2016 , 10, 2376-88	11.9	20
103	High amylose wheat starch structures display unique fermentability characteristics, microbial community shifts and enzyme degradation profiles. <i>Food and Function</i> , 2020 , 11, 5635-5646	6.1	19
102	Bile acids associate with specific gut microbiota, low-level alcohol consumption and liver fibrosis in patients with non-alcoholic fatty liver disease. <i>Liver International</i> , 2020 , 40, 1356-1365	7.9	19
101	Strategy for modular tagged high-throughput amplicon sequencing. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6310-2	4.8	19
100	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, 335-46	5.2	19
99	The impact of feeding condensed distillers byproducts on rumen microbiology and metabolism. <i>Animal Feed Science and Technology</i> , 1996 , 61, 235-245	3	19
98	The NAD(P)H-dependent glutamate dehydrogenase activities of <i>Prevotella ruminicola</i> B(1)4 can be attributed to one enzyme (GdhA), and <i>gdhA</i> expression is regulated in response to the nitrogen source available for growth. <i>Applied and Environmental Microbiology</i> , 1996 , 62, 3826-33	4.8	19
97	Diet and the Microbiome. <i>Gastroenterology Clinics of North America</i> , 2017 , 46, 49-60	4.4	18
96	Draft genome sequence of <i>Treponema</i> sp. strain JC4, a novel spirochete isolated from the bovine rumen. <i>Journal of Bacteriology</i> , 2012 , 194, 4130	3.5	18
95	Quantitative analysis of intestinal bacterial populations from term infants fed formula supplemented with fructo-oligosaccharides. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2012 , 55, 314-20	2.8	18
94	Effect of soybean hulls, soy lecithin, and soapstock mixtures on ruminal fermentation and milk composition in dairy cows. <i>Journal of Dairy Science</i> , 1998 , 81, 462-70	4	18
93	Dietary intake influences gut microbiota development of healthy Australian children from the age of one to two years. <i>Scientific Reports</i> , 2019 , 9, 12476	4.9	17
92	Elucidation of <i>Proteus mirabilis</i> as a Key Bacterium in Crohn's Disease Inflammation. <i>Gastroenterology</i> , 2021 , 160, 317-330.e11	13.3	17
91	Molecular investigation of bacterial communities on the inner and outer surfaces of peripheral venous catheters. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013 , 32, 1083-90	5.3	16
90	Isolation of Genetically Tractable Most-Wanted Bacteria by Metaparental Mating. <i>Scientific Reports</i> , 2015 , 5, 13282	4.9	16
89	Partial characterization of a DNA restriction endonuclease from <i>Ruminococcus flavefaciens</i> FD-1 and its inhibition by site-specific adenine methylation. <i>Applied and Environmental Microbiology</i> , 1992 , 58, 66-9	4.8	16
88	Gene and genome-centric analyses of koala and wombat fecal microbiomes point to metabolic specialization for digestion. <i>PeerJ</i> , 2017 , 5, e4075	3.1	16

87	Duodenal bacterial load as determined by quantitative polymerase chain reaction in asymptomatic controls, functional gastrointestinal disorders and inflammatory bowel disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2020 , 52, 155-167	6.1	15
86	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, 105-8	3.8	15
85	Gastroduodenal "Dysbiosis": a New Clinical Entity. <i>Current Treatment Options in Gastroenterology</i> , 2018 , 16, 591-604	2.5	15
84	Towards an integrated understanding of the therapeutic utility of exclusive enteral nutrition in the treatment of Crohn's disease. <i>Food and Function</i> , 2016 , 7, 1741-51	6.1	14
83	Effects of feeding fiber-fermenting bacteria to pigs on nutrient digestion, fecal output, and plasma energy metabolites. <i>Journal of Animal Science</i> , 2012 , 90, 4020-7	0.7	14
82	Subcellular distribution of glycanases and related components in <i>Ruminococcus albus</i> SY3 and their role in cell adhesion to cellulose. <i>Journal of Applied Microbiology</i> , 2001 , 91, 677-85	4.7	14
81	Adhesion to cellulose by <i>Ruminococcus albus</i> : a combination of cellulosomes and Pil-proteins?. <i>FEMS Microbiology Letters</i> , 2000 , 185, 109-115	2.9	14
80	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Microbiomes. <i>MBio</i> , 2018 , 9,	7.8	14
79	The NAD(P)H-utilizing glutamate dehydrogenase of <i>Bacteroides thetaiotaomicron</i> belongs to enzyme family I, and its activity is affected by trans-acting gene(s) positioned downstream of <i>gdhA</i> . <i>Journal of Bacteriology</i> , 1996 , 178, 7212-20	3.5	13
78	An (Anti)-Inflammatory Microbiota: Defining the Role in Inflammatory Bowel Disease?. <i>Digestive Diseases</i> , 2016 , 34, 64-71	3.2	12
77	The symbiotic rumen microbiome and cattle performance: a brief review. <i>Animal Production Science</i> , 2013 , 53, 876	1.4	12
76	Production and Utilization of Methane Biogas as Renewable Fuel	403-433	12
75	The FibRumBa database: a resource for biologists with interests in gastrointestinal microbial ecology, plant biomass degradation, and anaerobic microbiology. <i>Microbial Ecology</i> , 2010 , 59, 212-3	4.4	12
74	Glutamate dehydrogenase activity profiles for type strains of ruminal <i>Prevotella</i> spp. <i>Applied and Environmental Microbiology</i> , 1997 , 63, 3314-7	4.8	12
73	Small Intestinal Bacterial Overgrowth in Functional Dyspepsia: A Systematic Review and Meta-Analysis. <i>American Journal of Gastroenterology</i> , 2021 , 116, 935-942	0.7	12
72	Development of Multiwell-Plate Methods Using Pure Cultures of Methanogens To Identify New Inhibitors for Suppressing Ruminant Methane Emissions. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	11
71	Phenylacetic and phenylpropionic acids do not affect xylan degradation by <i>Ruminococcus albus</i> . <i>Applied and Environmental Microbiology</i> , 2003 , 69, 6954-8	4.8	11
70	Breastfeeding: a key modulator of gut microbiota characteristics in late infancy. <i>Journal of Developmental Origins of Health and Disease</i> , 2019 , 10, 206-213	2.4	11

69	AHG0090 is a Genetically Tractable Bacterium and Produces a Secreted Peptidic Bioactive that Suppresses Nuclear Factor Kappa B Activation in Human Gut Epithelial Cells. <i>Frontiers in Immunology</i> , 2018 , 9, 790	8.4	10
68	Draft genome sequence of <i>Bacteroides vulgatus</i> PC510, a strain isolated from human feces. <i>Journal of Bacteriology</i> , 2011 , 193, 4025-6	3.5	10
67	Genomic differences between <i>Fibrobacter succinogenes</i> S85 and <i>Fibrobacter intestinalis</i> DR7, identified by suppression subtractive hybridization. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 987-93	4.8	10
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65	Transplant associated infections-The role of the gastrointestinal microbiota and potential therapeutic options. <i>Nephrology</i> , 2020 , 25, 5-13	2.2	10
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