Mark Morrison

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

105 12,039 55 212 h-index g-index citations papers 6.58 15,210 229 5.3 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
212	Successful Manipulation of the Gut Microbiome to Treat Spontaneous and Induced Murine Models of Colitis 2022 , 1, 359-374		O
211	Journal of Renal Nutrition Prebiotic supplementation in kidney transplant recipients for preventing infections and gastrointestinal upset: a randomized controlled feasibility study <i>Journal of Renal Nutrition</i> , 2022 ,	3	1
210	Secreted NF- B suppressive microbial metabolites modulate gut inflammation <i>Cell Reports</i> , 2022 , 39, 110646	10.6	3
209	Secreted Toxins From Strains Isolated From Keratinocyte Skin Cancers Mediate Pro-tumorigenic Inflammatory Responses in the Skin <i>Frontiers in Microbiology</i> , 2021 , 12, 789042	5.7	1
208	Is a Fundamental Design Change for Gastrointestinal Endoscopes Required?. <i>Journal of Clinical Gastroenterology</i> , 2021 , 55, 21-24	3	1
207	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
206	Pregnant women who develop preeclampsia have lower abundance of the butyrate-producer Coprococcus in their gut microbiota. <i>Pregnancy Hypertension</i> , 2021 , 23, 211-219	2.6	9
205	Microbiome-immune interactions in tuberculosis. <i>PLoS Pathogens</i> , 2021 , 17, e1009377	7.6	8
204	From trash to gold: gastrointestinal microbiome research in patients with functional gastrointestinal disorders. <i>Journal of Investigative Medicine</i> , 2021 , 69, 793-795	2.9	
203	Wheat-based food form has a greater effect than amylose content on fermentation outcomes and microbial community shifts in an in vitro fermentation model. <i>Food Hydrocolloids</i> , 2021 , 114, 106560	10.6	3
202	Novel strain-level resolution of Crohn's disease mucosa-associated microbiota via an ex vivo combination of microbe culture and metagenomic sequencing. <i>ISME Journal</i> , 2021 , 15, 3326-3338	11.9	7
201	Elucidation of Proteus mirabilis as a Key Bacterium in Crohn's Disease Inflammation. <i>Gastroenterology</i> , 2021 , 160, 317-330.e11	13.3	17
200	Chemoradiation therapy changes oral microbiome and metabolomic profiles in patients with oral cavity cancer and oropharyngeal cancer. <i>Head and Neck</i> , 2021 , 43, 1521-1534	4.2	3
199	Characteristics of the gastrointestinal microbiota in paired live kidney donors and recipients. <i>Nephrology</i> , 2021 , 26, 471-478	2.2	2
198	Concomitant Irritable Bowel Syndrome Does Not Influence the Response to Antimicrobial Therapy in Patients with Functional Dyspepsia. <i>Digestive Diseases and Sciences</i> , 2021 , 1	4	5
197	Draft Genome Sequence of Streptococcus salivarius AGIRA0003, Isolated from Functional Gastrointestinal Disorder Duodenal Tissue. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0075821	1.3	1
196	Methane positive small intestinal bacterial overgrowth in inflammatory bowel disease and irritable bowel syndrome: A systematic review and meta-analysis. <i>Gut Microbes</i> , 2021 , 13, 1933313	8.8	9

195	species enriched in the oral cavity of patients with RA are a source of peptidoglycan-polysaccharide polymers that can induce arthritis in mice. <i>Annals of the Rheumatic Diseases</i> , 2021 , 80, 573-581	2.4	6
194	Chronic High-Fat Diet Induces Early Barrett's Esophagus in Mice through Lipidome Remodeling. <i>Biomolecules</i> , 2020 , 10,	5.9	5
193	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
192	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
191	Targeting the Gut Microbiome as a Treatment for Primary Sclerosing Cholangitis: A Conceptional Framework. <i>American Journal of Gastroenterology</i> , 2020 , 115, 814-822	0.7	25
190	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
189	Helminths, polyparasitism, and the gut microbiome in the Philippines. <i>International Journal for Parasitology</i> , 2020 , 50, 217-225	4.3	7
188	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
187	Secretome Components from Faecalibacterium prausnitzii Strains A2-165 and AHMP21 Modulate Cutaneous Wound Inflammation. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 2312-2315.e6	4.3	4
186	fermentation outcomes of arabinoxylan and galactoxyloglucan depend on fecal inoculum more than substrate chemistry. <i>Food and Function</i> , 2020 , 11, 7892-7904	6.1	10
185	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
184	Transplant associated infections-The role of the gastrointestinal microbiota and potential therapeutic options. <i>Nephrology</i> , 2020 , 25, 5-13	2.2	10
183	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
182	The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers. <i>Nutrients</i> , 2019 , 11,	6.7	37
181	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
180	Analysis of the Effects of Dietary Pattern on the Oral Microbiome of Elite Endurance Athletes. <i>Nutrients</i> , 2019 , 11,	6.7	35
179	P837 The common food additives sodium sulfite and polysorbate 80 have a profound inhibitory effect on the commensal, anti-inflammatory bacterium Faecalibacterium prausnitzii: the ENIGMA study. <i>Journal of Crohnis and Colitis</i> , 2019 , 13, S542-S543	1.5	О
178	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

177	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
176	P849 Urease-positive proteobacteria in Crohn disease identified by novel ex vivo mucosal microbe culture combined with metagenomic sequencing (MC-MGS): the ENIGMA study. <i>Journal of Crohnis and Colitis</i> , 2019 , 13, S548-S549	1.5	Ο
175	Infectious Complications Following Kidney Transplantation-A Focus on Hepatitis C Infection, Cytomegalovirus Infection and Novel Developments in the Gut Microbiota. <i>Medicina (Lithuania)</i> , 2019 , 55,	3.1	5
174	Dysbiosis of the Duodenal Mucosal Microbiota Is Associated With Increased Small Intestinal Permeability in Chronic Liver Disease. <i>Clinical and Translational Gastroenterology</i> , 2019 , 10, e00068	4.2	9
173	P834 Proteus is a key candidate in the pathogenesis of Crohn® disease: mucosa, stool genomics and functional analysis: the ENIGMA study. <i>Journal of Crohnis and Colitis</i> , 2019 , 13, S541-S541	1.5	1
172	Microbiota and Body Composition During the Period of Complementary Feeding. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019 , 69, 726-732	2.8	4
171	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
170	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
169	Growth and protein-rich food intake in infancy is associated with fat-free mass index at 2-3 years of age. <i>Journal of Paediatrics and Child Health</i> , 2018 , 54, 770-775	1.3	2
168	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
167	Male-specific Association Between Fat-Free Mass Index and Fecal Microbiota in 2- to 3-Year-Old Australian Children. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2018 , 66, 147-151	2.8	9
166	Culture- and metagenomics-enabled analyses of the Methanosphaera genus reveals their monophyletic origin and differentiation according to genome size. <i>ISME Journal</i> , 2018 , 12, 2942-2953	11.9	9
165	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
164	A Vegetarian Diet Is a Major Determinant of Gut Microbiota Composition in Early Pregnancy. <i>Nutrients</i> , 2018 , 10,	6.7	50
163	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
162	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
161	Proteus spp. as Putative Gastrointestinal Pathogens. Clinical Microbiology Reviews, 2018, 31,	34	51
160	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

(2017-2018)

159	Gastroduodenal "Dysbiosis": a New Clinical Entity. <i>Current Treatment Options in Gastroenterology</i> , 2018 , 16, 591-604	2.5	15
158	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Microbiomes. <i>MBio</i> , 2018 , 9,	7.8	14
157	Influence of cigarette smoking on the human duodenal mucosa-associated microbiota. <i>Microbiome</i> , 2018 , 6, 150	16.6	37
156	Food Starch Structure Impacts Gut Microbiome Composition. <i>MSphere</i> , 2018 , 3,	5	72
155	Diet and the Microbiome. Gastroenterology Clinics of North America, 2017, 46, 49-60	4.4	18
154	Dyspepsia and the microbiome: time to focus on the small intestine. <i>Gut</i> , 2017 , 66, 1168-1169	19.2	100
153	Antibiotic treatment at delivery shapes the initial oral microbiome in neonates. <i>Scientific Reports</i> , 2017 , 7, 43481	4.9	52
152	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
151	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
150	The gut bacterium and pathobiont Bacteroides vulgatus activates NF- 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
149	Is There a Link Between H. Pylori and the Epidemiology of Crohn's Disease?. <i>Digestive Diseases and Sciences</i> , 2017 , 62, 2472-2480	4	8
148	Translating our microbiome into medicine. <i>Medical Journal of Australia</i> , 2017 , 206, 287-288	4	
147	The saliva microbiome profiles are minimally affected by collection method or DNA extraction protocols. <i>Scientific Reports</i> , 2017 , 7, 8523	4.9	62
146	Life in the small intestine: the forgotten microbiome?. Microbiology Australia, 2017, 38, 116	0.8	
145	Emerging pathogenic links between microbiota and the gut-lung axis. <i>Nature Reviews Microbiology</i> , 2017 , 15, 55-63	22.2	579
144	Pathophysiology of Functional Gastrointestinal Disorders: A Holistic Overview. <i>Digestive Diseases</i> , 2017 , 35 Suppl 1, 5-13	3.2	69
143	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
142	Oral Microbiome: A New Biomarker Reservoir for Oral and Oropharyngeal Cancers. <i>Theranostics</i> , 2017 , 7, 4313-4321	12.1	60

141	New Insights into the Diversity of the Genus. Frontiers in Microbiology, 2017, 8, 1790	5.7	30
140	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
139	Methane matters: from blue-tinged moos, to boozy roos, and the health of humans too. <i>Animal Frontiers</i> , 2016 , 6, 15-21	5.5	1
138	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
137	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
136	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
135	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
134	An (Anti)-Inflammatory Microbiota: Defining the Role in Inflammatory Bowel Disease?. <i>Digestive Diseases</i> , 2016 , 34, 64-71	3.2	12
133	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
132	Microbial biofilms associated with intravascular catheter-related bloodstream infections in adult intensive care patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016 , 35, 201-5	5.3	8
131	Mothers Secretor Status Affects Development of Childrens Microbiota Composition and Function: A Pilot Study. <i>PLoS ONE</i> , 2016 , 11, e0161211	3.7	47
130	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016 , 4, 36	16.6	322
129	Exploring the Bioactive Landscape of the Gut Microbiota to Identify Metabolites Underpinning Human Health 2016 , 49-82		
128	Letter: investigating the intestinal mucosa-associated microbiota - relevance and potential pitfalls. Authors' reply. <i>Alimentary Pharmacology and Therapeutics</i> , 2016 , 44, 648-9	6.1	
127	Differences down-under: alcohol-fueled methanogenesis by archaea present in Australian macropodids. <i>ISME Journal</i> , 2016 , 10, 2376-88	11.9	20
126	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
125	633 The Relative Abundances of Dorea and Faecalibacterium spp. in the Mucosa Associated Microbiome of Newly Diagnosed Children With Crohn's Disease Are Differentially Affected by Exclusive Enteral Nutrition. <i>Gastroenterology</i> , 2016 , 150, S132-S133	13.3	2
124	The Microbiome in Obesity, Diabetes, and NAFLD: What is Your Gut Telling Us?. <i>Current Hepatology Reports</i> , 2016 , 15, 96-102	1	4

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123	Inflammasome signaling affects anxiety- and depressive-like behavior and gut microbiome composition. <i>Molecular Psychiatry</i> , 2016 , 21, 797-805	15.1	268
122	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
121	Isolation of Genetically Tractable Most-Wanted Bacteria by Metaparental Mating. <i>Scientific Reports</i> , 2015 , 5, 13282	4.9	16
120	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
119	Microbial diversity on intravascular catheters from paediatric patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2015 , 34, 2463-70	5.3	2
118	Methane matters in animals and man: from beginning to end. <i>Microbiology Australia</i> , 2015 , 36, 4	0.8	
117	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. Frontiers in Microbiology, 2015, 6, 1469	5.7	48
116	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
115	Molecular investigation of bacterial communities on intravascular catheters: no longer just Staphylococcus. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2014 , 33, 1189-98	5.3	20
114	Letter: inverse correlation between Helicobacter pylori and obesity - a conclusion too early? Authors' reply. <i>Alimentary Pharmacology and Therapeutics</i> , 2014 , 40, 1120	6.1	
113	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
112	Rumen cellulosomics: divergent fiber-degrading strategies revealed by comparative genome-wide analysis of six ruminococcal strains. <i>PLoS ONE</i> , 2014 , 9, e99221	3.7	55
111	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
110	Development of a phylogenetic microarray for comprehensive analysis of ruminal bacterial communities. <i>Journal of Applied Microbiology</i> , 2014 , 117, 949-60	4.7	8
109	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
108	Review article: Associations between Helicobacter pylori and obesityan ecological study. <i>Alimentary Pharmacology and Therapeutics</i> , 2014 , 40, 24-31	6.1	65
107	Investigation of a new acetogen isolated from an enrichment of the tammar wallaby forestomach. <i>BMC Microbiology</i> , 2014 , 14, 314	4.5	22
106	The symbiotic rumen microbiome and cattle performance: a brief review. <i>Animal Production Science</i> , 2013 , 53, 876	1.4	12

105	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
104	Looking large, to make more, out of gut metagenomics. Current Opinion in Microbiology, 2013, 16, 630-	5 7.9	6
103	Bacterial census of poultry intestinal microbiome. <i>Poultry Science</i> , 2013 , 92, 671-83	3.9	245
102	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
101	Draft Genome Sequence of Enterococcus faecalis PC1.1, a Candidate Probiotic Strain Isolated from Human Feces. <i>Genome Announcements</i> , 2013 , 1,		9
100	Genome Sequence of Stenotrophomonas maltophilia Strain AU12-09, Isolated from an Intravascular Catheter. <i>Genome Announcements</i> , 2013 , 1,		9
99	Extending the cellulosome paradigm: the modular Clostridium thermocellum cellulosomal serpin PinA is a broad-spectrum inhibitor of subtilisin-like proteases. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6173-5	4.8	9
98	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
97	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
96	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
95	Characterization of the gastrointestinal microbiota in health and inflammatory bowel disease. <i>Inflammatory Bowel Diseases</i> , 2012 , 18, 372-90	4.5	79
94	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
93	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
92	Genome sequence of Staphylococcus epidermidis strain AU12-03, isolated from an intravascular catheter. <i>Journal of Bacteriology</i> , 2012 , 194, 6639	3.5	2
91	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
90	Draft genome sequence of Treponema sp. strain JC4, a novel spirochete isolated from the bovine rumen. <i>Journal of Bacteriology</i> , 2012 , 194, 4130	3.5	18
89	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
88	Metagenomics of the Svalbard reindeer rumen microbiome reveals abundance of polysaccharide utilization loci. <i>PLoS ONE</i> , 2012 , 7, e38571	3.7	130

(2011-2011)

87	Sequence-Based Characterization of Microbiomes by Serial Analysis of Ribosomal Sequence Tags (SARST) 2011 , 265-273		О
86	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
85	Isolation of Succinivibrionaceae implicated in low methane emissions from Tammar wallabies. <i>Science</i> , 2011 , 333, 646-8	33.3	119
84	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
83	Status of the phylogenetic diversity census of ruminal microbiomes. <i>FEMS Microbiology Ecology</i> , 2011 , 76, 49-63	4.3	226
82	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011 , 8, 191-2	21.6	161
81	Muramidases found in the foregut microbiome of the Tammar wallaby can direct cell aggregation and biofilm formation. <i>ISME Journal</i> , 2011 , 5, 341-50	11.9	7
80	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
79	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
78	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
77	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
76	Highlighting new phylogenetic specificities of Crohn's disease microbiota. <i>Inflammatory Bowel Diseases</i> , 2011 , 17, 185-92	4.5	191
75	A meta-analysis of the microbial diversity observed in anaerobic digesters. <i>Bioresource Technology</i> , 2011 , 102, 3730-9	11	328
74	Draft genome sequence of Turicibacter sanguinis PC909, isolated from human feces. <i>Journal of Bacteriology</i> , 2011 , 193, 1288-9	3.5	43
73	Draft genome sequence of Bacteroides vulgatus PC510, a strain isolated from human feces. <i>Journal of Bacteriology</i> , 2011 , 193, 4025-6	3.5	10
72	Strategy for modular tagged high-throughput amplicon sequencing. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6310-2	4.8	19
71	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
70	Biochemical characterization and relative expression levels of multiple carbohydrate esterases of the xylanolytic rumen bacterium Prevotella ruminicola 23 grown on an ester-enriched substrate. Applied and Environmental Microbiology, 2011 , 77, 5671-81	4.8	42

69	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
68	Overestimation of the abundance of sulfate-reducing bacteria in human feces by quantitative PCR targeting the Desulfovibrio 16S rRNA gene. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3544-6	4.8	30
67	Selection and Sequencing of Strains as References for Human Microbiome Studies 2011 , 79-90		
66	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
65	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
64	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
63	Occurrence and persistence of erythromycin resistance genes (erm) and tetracycline resistance genes (tet) in waste treatment systems on swine farms. <i>Microbial Ecology</i> , 2010 , 60, 479-86	4.4	68
62	Comparative genome analysis of Prevotella ruminicola and Prevotella bryantii: insights into their environmental niche. <i>Microbial Ecology</i> , 2010 , 60, 721-9	4.4	192
61	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
60	Recent developments in nucleic acid based techniques for use in rumen manipulation. <i>Revista Brasileira De Zootecnia</i> , 2009 , 38, 341-351	1.2	5
59	Community composition and density of methanogens in the foregut of the Tammar wallaby (Macropus eugenii). <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2598-602	4.8	51
58	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
57	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
56	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
55	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
54	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
53	Cell surface enzyme attachment is mediated by family 37 carbohydrate-binding modules, unique to Ruminococcus albus. <i>Journal of Bacteriology</i> , 2008 , 190, 8220-2	3.5	41
52	Genomic differences between Fibrobacter succinogenes S85 and Fibrobacter intestinalis DR7, identified by suppression subtractive hybridization. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 987-93	4.8	10

(2004-2008)

51	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
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37	Strain-specific genomic regions of Ruminococcus flavefaciens 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
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35	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
34	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

33	Improved extraction of PCR-quality community DNA from digesta and fecal samples. <i>BioTechniques</i> , 2004 , 36, 808-12	2.5	990
32	Phenylacetic and phenylpropionic acids do not affect xylan degradation by Ruminococcus albus. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 6954-8	4.8	11
31	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
30	Opportunities to improve fiber degradation in the rumen: microbiology, ecology, and genomics. <i>FEMS Microbiology Reviews</i> , 2003 , 27, 663-93	15.1	284
29	The glutamine synthetase of Prevotella bryantii B(1)4 is a family III enzyme (GlnN) and glutamine supports growth of mutants lacking glutamate dehydrogenase activity. <i>FEMS Microbiology Letters</i> , 2003 , 229, 15-21	2.9	7
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26	Subcellular distribution of glycanases and related components in Ruminococcus albus SY3 and their role in cell adhesion to cellulose. <i>Journal of Applied Microbiology</i> , 2001 , 91, 677-85	4.7	14
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23	Adhesion to cellulose by Ruminococcus albus: a combination of cellulosomes and Pil-proteins?. <i>FEMS Microbiology Letters</i> , 2000 , 185, 109-15	2.9	82
22	Adhesion to cellulose by Ruminococcus albus: a combination of cellulosomes and Pil-proteins?. <i>FEMS Microbiology Letters</i> , 2000 , 185, 109-115	2.9	14
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20	Adherence of the gram-positive bacterium Ruminococcus albus 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
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17	Biochemical and mutational analysis of a gingipain-like peptidase activity from Prevotella ruminicola B(1)4 and its role in ammonia production by ruminal bacteria. <i>Applied and Environmental Microbiology</i> , 1997 , 63, 670-5	4.8	9
16	Glutamate dehydrogenase activity profiles for type strains of ruminal Prevotella spp. <i>Applied and Environmental Microbiology</i> , 1997 , 63, 3314-7	4.8	12

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15	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
14	Do ruminal bacteria exchange genetic material?. <i>Journal of Dairy Science</i> , 1996 , 79, 1476-86	4	20
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12	Nitrogen metabolism by ruminal microorganisms: current understanding and future perspectives. <i>Australian Journal of Agricultural Research</i> , 1996 , 47, 227		35
11	The NAD(P)H-dependent glutamate dehydrogenase activities of Prevotella ruminicola B(1)4 can be attributed to one enzyme (GdhA), and gdhA 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
10	Alteration of supplement nitrogen:Sulphur ratio by increasing sulphate supplementation affects the rate rather than the extent of fibre degradation in cattle fed a matured tropical grass hay. Journal of the Science of Food and Agriculture, 1994, 65, 449-455	4.3	
9	The restriction endonuclease RflFII, isolated from Ruminococcus flavefaciens FD-1, recognizes the sequence 5'-AGTACT-3', and is inhibited by site-specific adenine methylation. <i>FEMS Microbiology Letters</i> , 1994 , 122, 181-5	2.9	7
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4	Production and Utilization of Methane Biogas as Renewable Fuel403-433		12
3	The Gut Microbiome: Current Understanding and Future Perspectives19-40		1
2	Secreted microbial metabolites modulate gut immunity and inflammatory tone		1
1	Shotgun metagenomics reveals an enrichment of potentially cross-reactive bacterial epitopes in ankylosing spondylitis patients, as well as the effects of TNFi therapy and the host! genotype upon microbiome composition		3