

Harry J Flint

List of Publications by Citations

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217
papers

34,536
citations

86
h-index

185
g-index

225
ext. papers

42,334
ext. citations

5.4
avg, IF

7.48
L-index

#	Paper	IF	Citations
217	Expert consensus document. The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2014 , 11, 506-14	24.2	3614
216	The gut microbiota, bacterial metabolites and colorectal cancer. <i>Nature Reviews Microbiology</i> , 2014 , 12, 661-72	22.2	1390
215	The role of the gut microbiota in nutrition and health. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2012 , 9, 577-89	24.2	1119
214	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012 , 3, 289-306	8.8	1085
213	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011 , 5, 220-30	11.9	1081
212	Diversity, metabolism and microbial ecology of butyrate-producing bacteria from the human large intestine. <i>FEMS Microbiology Letters</i> , 2009 , 294, 1-8	2.9	1078
211	Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. <i>Nature Reviews Microbiology</i> , 2008 , 6, 121-31	22.2	1070
210	The microbiology of butyrate formation in the human colon. <i>FEMS Microbiology Letters</i> , 2002 , 217, 133-92.9		911
209	Formation of propionate and butyrate by the human colonic microbiota. <i>Environmental Microbiology</i> , 2017 , 19, 29-41	5.2	831
208	Lactate-utilizing bacteria, isolated from human feces, that produce butyrate as a major fermentation product. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 5810-7	4.8	673
207	Phylogenetic relationships of butyrate-producing bacteria from the human gut. <i>Applied and Environmental Microbiology</i> , 2000 , 66, 1654-61	4.8	653
206	Reduced dietary intake of carbohydrates by obese subjects results in decreased concentrations of butyrate and butyrate-producing bacteria in feces. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 1073-8	4.8	624
205	Intestinal microbiota in functional bowel disorders: a Rome foundation report. <i>Gut</i> , 2013 , 62, 159-76	19.2	607
204	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , 2013 , 69, 52-60	10.2	594
203	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , 2014 , 8, 1323-35	11.9	561
202	<i>Ruminococcus bromii</i> is a keystone species for the degradation of resistant starch in the human colon. <i>ISME Journal</i> , 2012 , 6, 1535-43	11.9	551
201	Two routes of metabolic cross-feeding between <i>Bifidobacterium adolescentis</i> and butyrate-producing anaerobes from the human gut. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 3593-9	4.8	541

200	pH and peptide supply can radically alter bacterial populations and short-chain fatty acid ratios within microbial communities from the human colon. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 3692-700	4.8	485
199	High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health. <i>American Journal of Clinical Nutrition</i> , 2011 , 93, 1062-72	7	456
198	Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA:acetate CoA-transferase gene. <i>Environmental Microbiology</i> , 2010 , 12, 304-14	5.2	445
197	Interactions and competition within the microbial community of the human colon: links between diet and health. <i>Environmental Microbiology</i> , 2007 , 9, 1101-11	5.2	430
196	The role of pH in determining the species composition of the human colonic microbiota. <i>Environmental Microbiology</i> , 2009 , 11, 2112-22	5.2	416
195	Acetate utilization and butyryl coenzyme A (CoA):acetate-CoA transferase in butyrate-producing bacteria from the human large intestine. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 5186-90	4.8	407
194	Targeted restoration of the intestinal microbiota with a simple, defined bacteriotherapy resolves relapsing <i>Clostridium difficile</i> disease in mice. <i>PLoS Pathogens</i> , 2012 , 8, e1002995	7.6	403
193	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016 , 10, 2557-2568	11.9	380
192	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. <i>ISME Journal</i> , 2014 , 8, 2218-30	11.9	356
191	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355
190	Growth requirements and fermentation products of <i>Fusobacterium prausnitzii</i> , and a proposal to reclassify it as <i>Faecalibacterium prausnitzii</i> gen. nov., comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002 , 52, 2141-2146	2.2	352
189	Comparative metabolomics in vegans and omnivores reveal constraints on diet-dependent gut microbiota metabolite production. <i>Gut</i> , 2016 , 65, 63-72	19.2	307
188	Restricted distribution of the butyrate kinase pathway among butyrate-producing bacteria from the human colon. <i>Journal of Bacteriology</i> , 2004 , 186, 2099-106	3.5	295
187	Assessment of microbial diversity in human colonic samples by 16S rDNA sequence analysis. <i>FEMS Microbiology Ecology</i> , 2002 , 39, 33-9	4.3	279
186	Contribution of acetate to butyrate formation by human faecal bacteria. <i>British Journal of Nutrition</i> , 2004 , 91, 915-23	3.6	271
185	Prebiotic stimulation of human colonic butyrate-producing bacteria and bifidobacteria, in vitro. <i>FEMS Microbiology Ecology</i> , 2014 , 87, 30-40	4.3	249
184	Cultured representatives of two major phylogroups of human colonic <i>Faecalibacterium prausnitzii</i> can utilize pectin, uronic acids, and host-derived substrates for growth. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 420-8	4.8	247
183	Colonic bacterial metabolites and human health. <i>Current Opinion in Microbiology</i> , 2013 , 16, 246-54	7.9	243

182	From cellulosomes to cellulosomes. <i>Chemical Record</i> , 2008 , 8, 364-77	6.6	237
181	Roseburia intestinalis sp. nov., a novel saccharolytic, butyrate-producing bacterium from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002 , 52, 1615-1620	2.2	237
180	Contribution of diet to the composition of the human gut microbiota. <i>Microbial Ecology in Health and Disease</i> , 2015 , 26, 26164		227
179	Oligonucleotide probes that detect quantitatively significant groups of butyrate-producing bacteria in human feces. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 4320-4	4.8	226
178	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016 , 14, 3	7.3	214
177	The gut anaerobe Faecalibacterium prausnitzii uses an extracellular electron shuttle to grow at oxic-anoxic interphases. <i>ISME Journal</i> , 2012 , 6, 1578-85	11.9	201
176	Microbiota of de-novo pediatric IBD: increased Faecalibacterium prausnitzii and reduced bacterial diversity in Crohn's but not in ulcerative colitis. <i>American Journal of Gastroenterology</i> , 2012 , 107, 1913-22	9.7	201
175	Selective colonization of insoluble substrates by human faecal bacteria. <i>Environmental Microbiology</i> , 2007 , 9, 667-79	5.2	197
174	The impact of different DNA extraction kits and laboratories upon the assessment of human gut microbiota composition by 16S rRNA gene sequencing. <i>PLoS ONE</i> , 2014 , 9, e88982	3.7	177
173	The impact of nutrition on the human microbiome. <i>Nutrition Reviews</i> , 2012 , 70 Suppl 1, S10-3	6.4	174
172	Major phenylpropanoid-derived metabolites in the human gut can arise from microbial fermentation of protein. <i>Molecular Nutrition and Food Research</i> , 2013 , 57, 523-35	5.9	172
171	Enhanced butyrate formation by cross-feeding between Faecalibacterium prausnitzii and Bifidobacterium adolescentis. <i>FEMS Microbiology Letters</i> , 2015 , 362,	2.9	167
170	Whole-genome transcription profiling reveals genes up-regulated by growth on fucose in the human gut bacterium "Roseburia inulinivorans". <i>Journal of Bacteriology</i> , 2006 , 188, 4340-9	3.5	161
169	16S rRNA gene-based profiling of the human infant gut microbiota is strongly influenced by sample processing and PCR primer choice. <i>Microbiome</i> , 2015 , 3, 26	16.6	153
168	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014 , 22, 267-74	12.4	148
167	Bacterial diversity within the equine large intestine as revealed by molecular analysis of cloned 16S rRNA genes. <i>FEMS Microbiology Ecology</i> , 2001 , 38, 141-151	4.3	145
166	Proposal of Roseburia faecis sp. nov., Roseburia hominis sp. nov. and Roseburia inulinivorans sp. nov., based on isolates from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2437-2441	2.2	142
165	Effects of alternative dietary substrates on competition between human colonic bacteria in an anaerobic fermentor system. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 1136-42	4.8	141

164	Development of a semiquantitative degenerate real-time pcr-based assay for estimation of numbers of butyryl-coenzyme A (CoA) CoA transferase genes in complex bacterial samples. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 2009-12	4.8	140
163	Cellulosomal scaffoldin-like proteins from <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2001 , 183, 1945-53	3.5	137
162	Impact of pH on lactate formation and utilization by human fecal microbial communities. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 6526-33	4.8	136
161	Probiotics and prebiotics and health in ageing populations. <i>Maturitas</i> , 2013 , 75, 44-50	5	132
160	Plant cell wall breakdown by anaerobic microorganisms from the Mammalian digestive tract. <i>Annals of the New York Academy of Sciences</i> , 2008 , 1125, 280-8	6.5	131
159	Molecular analysis of the microbial diversity present in the colonic wall, colonic lumen, and cecal lumen of a pig. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 5372-7	4.8	129
158	Gut microbiota signatures predict host and microbiota responses to dietary interventions in obese individuals. <i>PLoS ONE</i> , 2014 , 9, e9702	3.7	127
157	Faecalibacterium prausnitzii A2-165 has a high capacity to induce IL-10 in human and murine dendritic cells and modulates T cell responses. <i>Scientific Reports</i> , 2016 , 6, 18507	4.9	119
156	Prebiotic potential of pectin and pectic oligosaccharides to promote anti-inflammatory commensal bacteria in the human colon. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	117
155	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , 2008 , 10, 3275-83	5.2	109
154	Alterations in microbiota and fermentation products in equine large intestine in response to dietary variation and intestinal disease. <i>British Journal of Nutrition</i> , 2012 , 107, 989-95	3.6	108
153	Biomass utilization by gut microbiomes. <i>Annual Review of Microbiology</i> , 2014 , 68, 279-96	17.5	107
152	Occurrence of the new tetracycline resistance gene tet(W) in bacteria from the human gut. <i>Antimicrobial Agents and Chemotherapy</i> , 2000 , 44, 775-7	5.9	107
151	Anaerostipes caccae gen. nov., sp. nov., a new saccharolytic, acetate-utilising, butyrate-producing bacterium from human faeces. <i>Systematic and Applied Microbiology</i> , 2002 , 25, 46-51	4.2	101
150	Oral treatment with improves insulin sensitivity in mice. <i>Npj Biofilms and Microbiomes</i> , 2016 , 2, 16009	8.2	101
149	Obesity and the gut microbiota. <i>Journal of Clinical Gastroenterology</i> , 2011 , 45 Suppl, S128-32	3	100
148	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic Firmicutes Bacterium <i>Ruminococcus bromii</i> . <i>MBio</i> , 2015 , 6, e01058-15	7.8	99
147	Some are more equal than others: the role of "keystone" species in the degradation of recalcitrant substrates. <i>Gut Microbes</i> , 2013 , 4, 236-40	8.8	98

146	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic. <i>Microbial Genomics</i> , 2016 , 2, e000043	4.4	98
145	Specific substrate-driven changes in human faecal microbiota composition contrast with functional redundancy in short-chain fatty acid production. <i>ISME Journal</i> , 2018 , 12, 610-622	11.9	98
144	The rumen microbial ecosystem--some recent developments. <i>Trends in Microbiology</i> , 1997 , 5, 483-8	12.4	97
143	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	3.7	97
142	Molecular diversity, cultivation, and improved detection by fluorescent in situ hybridization of a dominant group of human gut bacteria related to <i>Roseburia</i> spp. or <i>Eubacterium rectale</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 6371-6	4.8	96
141	Lactate has the potential to promote hydrogen sulphide formation in the human colon. <i>FEMS Microbiology Letters</i> , 2009 , 299, 128-34	2.9	90
140	Estimation of the relative abundance of different <i>Bacteroides</i> and <i>Prevotella</i> ribotypes in gut samples by restriction enzyme profiling of PCR-amplified 16S rRNA gene sequences. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 3683-9	4.8	90
139	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. <i>FEMS Microbiology Ecology</i> , 2011 , 76, 615-24	4.3	87
138	Substrate-driven gene expression in <i>Roseburia inulinivorans</i> : importance of inducible enzymes in the utilization of inulin and starch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4672-9	11.5	87
137	Evidence for recent intergeneric transfer of a new tetracycline resistance gene, <i>tet(W)</i> , isolated from <i>Butyrivibrio fibrisolvens</i> , and the occurrence of <i>tet(O)</i> in ruminal bacteria. <i>Environmental Microbiology</i> , 1999 , 1, 53-64	5.2	87
136	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , 2015 , 17, 1615-30	5.2	86
135	Lytic and lysogenic infection of diverse <i>Escherichia coli</i> and <i>Shigella</i> strains with a verocytotoxigenic bacteriophage. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 4335-7	4.8	86
134	Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. <i>Environmental Microbiology</i> , 2016 , 18, 2214-25	5.2	86
133	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014 , 15, 160	4.5	85
132	Comparative analysis of sequences flanking <i>tet(W)</i> resistance genes in multiple species of gut bacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 2006 , 50, 2632-9	5.9	84
131	Unravelling the genetic diversity of ruminal bacteria belonging to the CFB phylum. <i>FEMS Microbiology Ecology</i> , 2000 , 33, 69-79	4.3	84
130	Mucosa-associated <i>Faecalibacterium prausnitzii</i> and <i>Escherichia coli</i> co-abundance can distinguish Irritable Bowel Syndrome and Inflammatory Bowel Disease phenotypes. <i>International Journal of Medical Microbiology</i> , 2014 , 304, 464-75	3.7	83
129	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012 , 14, 207-27	5.2	82

128	A bifunctional xylanase encoded by the xynA gene of the rumen cellulolytic bacterium <i>Ruminococcus flavefaciens</i> 17 comprises two dissimilar domains linked by an asparagine/glutamine-rich sequence. <i>Molecular Microbiology</i> , 1992 , 6, 1013-23	4.1	81
127	Fate of free DNA and transformation of the oral bacterium <i>Streptococcus gordonii</i> DL1 by plasmid DNA in human saliva. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 6-10	4.8	79
126	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , 2017 , 38, 59-65	7.9	78
125	Unconventional mode of attachment of the <i>Ruminococcus flavefaciens</i> cellulosome to the cell surface. <i>Journal of Bacteriology</i> , 2005 , 187, 7569-78	3.5	75
124	Inhibitory activity of gut bacteria against <i>Escherichia coli</i> O157 mediated by dietary plant metabolites. <i>FEMS Microbiology Letters</i> , 1998 , 164, 283-8	2.9	74
123	<i>Faecalibacterium prausnitzii</i> Strain HTF-F and Its Extracellular Polymeric Matrix Attenuate Clinical Parameters in DSS-Induced Colitis. <i>PLoS ONE</i> , 2015 , 10, e0123013	3.7	74
122	Changes in the Abundance of <i>Faecalibacterium prausnitzii</i> Phylogroups I and II in the Intestinal Mucosa of Inflammatory Bowel Disease and Patients with Colorectal Cancer. <i>Inflammatory Bowel Diseases</i> , 2016 , 22, 28-41	4.5	73
121	Mechanistic Insights Into the Cross-Feeding of and on Host and Dietary Carbohydrates. <i>Frontiers in Microbiology</i> , 2018 , 9, 2558	5.7	71
120	Phylogenetic distribution of genes encoding β -glucuronidase activity in human colonic bacteria and the impact of diet on faecal glycosidase activities. <i>Environmental Microbiology</i> , 2012 , 14, 1876-87	5.2	68
119	Novel organization and divergent dockerin specificities in the cellulosome system of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2003 , 185, 703-13	3.5	68
118	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015 , 17, 3407-26.2	5.2	67
117	Three multidomain esterases from the cellulolytic rumen anaerobe <i>Ruminococcus flavefaciens</i> 17 that carry divergent dockerin sequences. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 6), 1391-1397	2.9	67
116	Mucosa-associated <i>Faecalibacterium prausnitzii</i> phylotype richness is reduced in patients with inflammatory bowel disease. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7582-92	4.8	66
115	Cell-associated alpha-amylases of butyrate-producing Firmicute bacteria from the human colon. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 3281-3290	2.9	65
114	Novel tetracycline resistance gene, tet(32), in the <i>Clostridium</i> -related human colonic anaerobe K10 and its transmission in vitro to the rumen anaerobe <i>Butyrivibrio fibrisolvens</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2001 , 45, 3246-9	5.9	62
113	A novel class of CoA-transferase involved in short-chain fatty acid metabolism in butyrate-producing human colonic bacteria. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 179-185	2.9	60
112	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	3.7	56
111	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

110	Anaerostipes hadrus comb. nov., a dominant species within the human colonic microbiota; reclassification of Eubacterium hadrum Moore et al. 1976. <i>Anaerobe</i> , 2012 , 18, 523-9	2.8	54
109	Rates of production and utilization of lactate by microbial communities from the human colon. <i>FEMS Microbiology Ecology</i> , 2011 , 77, 107-19	4.3	53
108	Application of 16S rRNA gene-targeted fluorescence in situ hybridization and restriction fragment length polymorphism to study porcine microbiota along the gastrointestinal tract in response to different sources of dietary fibre. <i>FEMS Microbiology Ecology</i> , 2007 , 59, 138-46	4.3	51
107	Conservation and divergence in cellulosome architecture between two strains of Ruminococcus flavefaciens. <i>Journal of Bacteriology</i> , 2006 , 188, 7971-6	3.5	50
106	Bacteroides (Fibrobacter) succinogenes, a cellulolytic anaerobic bacterium from the gastrointestinal tract. <i>Applied Microbiology and Biotechnology</i> , 1989 , 30, 433	5.7	49
105	Lack of flagella disadvantages Salmonella enterica serovar Enteritidis during the early stages of infection in the rat. <i>Journal of Medical Microbiology</i> , 2003 , 52, 91-99	3.2	48
104	Dockerin-like sequences in cellulases and xylanases from the rumen cellulolytic bacterium Ruminococcus flavefaciens. <i>FEMS Microbiology Letters</i> , 1997 , 149, 213-9	2.9	47
103	ScaC, an adaptor protein carrying a novel cohesin that expands the dockerin-binding repertoire of the Ruminococcus flavefaciens 17 cellulosome. <i>Journal of Bacteriology</i> , 2004 , 186, 2576-85	3.5	47
102	Transformation of an oral bacterium via chromosomal integration of free DNA in the presence of human saliva. <i>FEMS Microbiology Letters</i> , 2001 , 200, 163-7	2.9	47
101	Sporulation capability and amylosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader Ruminococcus bromii. <i>Environmental Microbiology</i> , 2018 , 20, 324-336	5.2	46
100	A xylanase produced by the rumen anaerobic protozoan Polyplastron multivesiculatum shows close sequence similarity to family 11 xylanases from gram-positive bacteria. <i>FEMS Microbiology Letters</i> , 1999 , 181, 145-52	2.9	45
99	How to Manipulate the Microbiota: Prebiotics. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 902, 119-42	3.6	45
98	Proposal of a neotype strain (A1-86) for Eubacterium rectale. Request for an opinion. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 1735-6	2.2	44
97	Enzymatic profiling of cellulosomal enzymes from the human gut bacterium, Ruminococcus champanellensis, reveals a fine-tuned system for cohesin-dockerin recognition. <i>Environmental Microbiology</i> , 2016 , 18, 542-56	5.2	43
96	Expression of two xylanase genes from the rumen cellulolytic bacterium Ruminococcus flavefaciens 17 cloned in pUC13. <i>Microbiology (United Kingdom)</i> , 1991 , 137, 123-9	2.9	42
95	Discovery of a novel lantibiotic nisin O from Blautia obeum A2-162, isolated from the human gastrointestinal tract. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1292-1305	2.9	41
94	Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota (Ruminococcus bicirculans) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014 , 16, 2879-90	5.2	40
93	A novel cell surface-anchored cellulose-binding protein encoded by the sca gene cluster of Ruminococcus flavefaciens. <i>Journal of Bacteriology</i> , 2007 , 189, 4774-83	3.5	40

92	Polysaccharide breakdown by anaerobic microorganisms inhabiting the Mammalian gut. <i>Advances in Applied Microbiology</i> , 2004 , 56, 89-120	4.9	40
91	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , 2020 , 11,	7.8	40
90	A new tetracycline efflux gene, tet(40), is located in tandem with tet(O/32/O) in a human gut firmicute bacterium and in metagenomic library clones. <i>Antimicrobial Agents and Chemotherapy</i> , 2008 , 52, 4001-9	5.9	39
89	Organization of butyrate synthetic genes in human colonic bacteria: phylogenetic conservation and horizontal gene transfer. <i>FEMS Microbiology Letters</i> , 2007 , 269, 240-7	2.9	39
88	Cellulosome gene cluster analysis for gauging the diversity of the ruminal cellulolytic bacterium <i>Ruminococcus flavefaciens</i> . <i>FEMS Microbiology Letters</i> , 2008 , 285, 188-94	2.9	39
87	Assessment of metabolic diversity within the intestinal microbiota from healthy humans using combined molecular and cultural approaches. <i>FEMS Microbiology Ecology</i> , 2008 , 66, 496-504	4.3	39
86	Characterization of XYN10B, a modular xylanase from the ruminal protozoan <i>Polyplastron multivesiculatum</i> , with a family 22 carbohydrate-binding module that binds to cellulose. <i>Biochemical Journal</i> , 2003 , 373, 495-503	3.8	39
85	Chromosomal integration of the green fluorescent protein gene in lactic acid bacteria and the survival of marked strains in human gut simulations. <i>FEMS Microbiology Letters</i> , 2000 , 182, 23-7	2.9	39
84	Mosaic tetracycline resistance genes are widespread in human and animal fecal samples. <i>Antimicrobial Agents and Chemotherapy</i> , 2007 , 51, 1115-8	5.9	38
83	EndB, a multidomain family 44 cellulase from <i>Ruminococcus flavefaciens</i> 17, binds to cellulose via a novel cellulose-binding module and to another <i>R. flavefaciens</i> protein via a dockerin domain. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 4426-31	4.8	38
82	Natural genetic transformation in the rumen bacterium <i>Streptococcus bovis</i> JB1. <i>FEMS Microbiology Letters</i> , 1999 , 179, 485-90	2.9	38
81	Electroporation induced transformation of <i>Bacteroides ruminicola</i> and <i>Bacteroides uniformis</i> by plasmid DNA. <i>FEMS Microbiology Letters</i> , 1989 , 61, 101-104	2.9	38
80	The green fluorescent protein as a visible marker for lactic acid bacteria in complex ecosystems. <i>FEMS Microbiology Ecology</i> , 1998 , 26, 219-230	4.3	35
79	Involvement of the multidomain regulatory protein XynR in positive control of xylanase gene expression in the ruminal anaerobe <i>Prevotella bryantii</i> B(1)4. <i>Journal of Bacteriology</i> , 2003 , 185, 2219-26	3.5	35
78	Heterologous expression of an endoglucanase gene (endA) from the ruminal anaerobe <i>Ruminococcus flavefaciens</i> 17 in <i>Streptococcus bovis</i> and <i>Streptococcus sanguis</i> . <i>FEMS Microbiology Letters</i> , 1995 , 126, 165-9	2.9	34
77	Hybrid tet genes and tet gene nomenclature: request for opinion. <i>Antimicrobial Agents and Chemotherapy</i> , 2005 , 49, 1265-6	5.9	33
76	The <i>Butyrivibrio fibrisolvens</i> tet(W) gene is carried on the novel conjugative transposon TnB1230, which contains duplicated nitroreductase coding sequences. <i>Journal of Bacteriology</i> , 2004 , 186, 3656-9	3.5	32
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