

# Harry J Flint

## 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.

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	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria.. <i>Microbial Genomics</i> , <b>2022</b> , 8,	4.4	3
216	Type IV pili are widespread among non-pathogenic Gram-positive gut bacteria with diverse carbohydrate utilization patterns. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 1527-1540	5.2	0
215	Nondigestible Carbohydrates Affect Metabolic Health and Gut Microbiota in Overweight Adults after Weight Loss. <i>Journal of Nutrition</i> , <b>2020</b> , 150, 1859-1870	4.1	6
214	βGlucan is a major growth substrate for human gut bacteria related to Coprococcus eutactus. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 2150-2164	5.2	13
213	Comparative genetic and physiological characterisation of Pectinatus species reveals shared tolerance to beer-associated stressors but halotolerance specific to pickle-associated strains. <i>Food Microbiology</i> , <b>2020</b> , 90, 103462	6	3
212	How Microbes Gain Energy with and Without Oxygen. <i>Fascinating Life Sciences</i> , <b>2020</b> , 31-45	1.1	
211	Do My Microbes Make Me Fat? Potential for the Gut Microbiota to Influence Energy Balance, Obesity and Metabolic Health in Humans. <i>Fascinating Life Sciences</i> , <b>2020</b> , 97-108	1.1	
210	How to Analyse Microbial Communities?. <i>Fascinating Life Sciences</i> , <b>2020</b> , 15-29	1.1	
209	Gut Microbes and Metabolites. <i>Fascinating Life Sciences</i> , <b>2020</b> , 109-118	1.1	
208	Perspectives and Prospects. <i>Fascinating Life Sciences</i> , <b>2020</b> , 137-146	1.1	
207	How Gut Micro-organisms Make Use of Available Carbohydrates. <i>Fascinating Life Sciences</i> , <b>2020</b> , 81-96	1.1	0
206	Who Inhabits Our Gut? Introducing the Human Gut Microbiota. <i>Fascinating Life Sciences</i> , <b>2020</b> , 47-61	1.1	
205	Evaluation of bacterial biomarkers to aid in challenging inflammatory bowel diseases diagnostics and subtype classification. <i>World Journal of Gastrointestinal Pathophysiology</i> , <b>2020</b> , 11, 64-77	3.2	2
204	Treating the Gut Microbiome as a System. <i>Fascinating Life Sciences</i> , <b>2020</b> , 127-135	1.1	
203	Variability and Stability of the Human Gut Microbiome. <i>Fascinating Life Sciences</i> , <b>2020</b> , 63-79	1.1	1
202	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , <b>2020</b> , 11,	7.8	40
201	Relative abundance of the Prevotella genus within the human gut microbiota of elderly volunteers determines the inter-individual responses to dietary supplementation with wheat bran arabinoxylan-oligosaccharides. <i>BMC Microbiology</i> , <b>2020</b> , 20, 283	4.5	18

200	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , <b>2020</b> , 5,	7.6	22
199	Heterologous gene expression in the human gut bacteria <i>Eubacterium rectale</i> and <i>Roseburia inulinivorans</i> by means of conjugative plasmids. <i>Anaerobe</i> , <b>2019</b> , 59, 131-140	2.8	5
198	Formate cross-feeding and cooperative metabolic interactions revealed by transcriptomics in co-cultures of acetogenic and amyolytic human colonic bacteria. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 259-271	5.2	24
197	Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , <b>2019</b> , 95,	4.3	16
196	Sporulation capability and amylosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader <i>Ruminococcus bromii</i> . <i>Environmental Microbiology</i> , <b>2018</b> , 20, 324-336	5.2	46
195	microPop: Modelling microbial populations and communities in R. <i>Methods in Ecology and Evolution</i> , <b>2018</b> , 9, 399-409	7.7	11
194	Specific substrate-driven changes in human faecal microbiota composition contrast with functional redundancy in short-chain fatty acid production. <i>ISME Journal</i> , <b>2018</b> , 12, 610-622	11.9	98
193	Mechanistic Insights Into the Cross-Feeding of and on Host and Dietary Carbohydrates. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2558	5.7	71
192	Dietary fibers inhibit obesity in mice, but host responses in the cecum and liver appear unrelated to fiber-specific changes in cecal bacterial taxonomic composition. <i>Scientific Reports</i> , <b>2018</b> , 8, 15566	4.9	22
191	Complexity of the <i>Ruminococcus flavefaciens</i> FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. <i>Scientific Reports</i> , <b>2017</b> , 7, 42355	4.9	20
190	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1069-1076	44.5	355
189	Formation of propionate and butyrate by the human colonic microbiota. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 29-41	5.2	831
188	Prebiotic potential of pectin and pectic oligosaccharides to promote anti-inflammatory commensal bacteria in the human colon. <i>FEMS Microbiology Ecology</i> , <b>2017</b> , 93,	4.3	117
187	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , <b>2017</b> , 38, 59-65	7.9	78
186	Discovery of a novel lantibiotic nisin O from <i>Blautia obeum</i> A2-162, isolated from the human gastrointestinal tract. <i>Microbiology (United Kingdom)</i> , <b>2017</b> , 163, 1292-1305	2.9	41
185	Lysozyme activity of the <i>Ruminococcus champanellensis</i> cellulosome. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 5112-5122	5.2	12
184	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> , <b>2016</b> , 6, 18507	4.9	119
183	Enzymatic profiling of cellulosomal enzymes from the human gut bacterium, <i>Ruminococcus champanellensis</i> , reveals a fine-tuned system for cohesin-dockerin recognition. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 542-56	5.2	43

182	Comparative metabolomics in vegans and omnivores reveal constraints on diet-dependent gut microbiota metabolite production. <i>Gut</i> , <b>2016</b> , 65, 63-72	19.2	307
181	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , <b>2016</b> , 14, 3	7.3	214
180	Objections to the proposed reclassification of <i>Eubacterium rectale</i> as <i>Agathobacter rectalis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2016</b> , 66, 2106	2.2	7
179	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000043	4.4	98
178	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> , <b>2016</b> , 22, 28-41	4.5	73
177	Oral treatment with improves insulin sensitivity in mice. <i>Npj Biofilms and Microbiomes</i> , <b>2016</b> , 2, 16009	8.2	101
176	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , <b>2016</b> , 10, 2557-2568	11.9	380
175	Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 2214-25	5.2	86
174	How to Manipulate the Microbiota: Prebiotics. <i>Advances in Experimental Medicine and Biology</i> , <b>2016</b> , 902, 119-42	3.6	45
173	16S rRNA gene-based profiling of the human infant gut microbiota is strongly influenced by sample processing and PCR primer choice. <i>Microbiome</i> , <b>2015</b> , 3, 26	16.6	153
172	Functional phylotyping approach for assessing intraspecific diversity of <i>Ruminococcus albus</i> within the rumen microbiome. <i>FEMS Microbiology Letters</i> , <b>2015</b> , 362, 1-10	2.9	8
171	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 3407-26.2	6.2	67
170	Complete Genome Sequence of the Human Gut Symbiont <i>Roseburia hominis</i> . <i>Genome Announcements</i> , <b>2015</b> , 3,		7
169	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic Firmicutes Bacterium <i>Ruminococcus bromii</i> . <i>MBio</i> , <b>2015</b> , 6, e01058-15	7.8	99
168	Enhanced butyrate formation by cross-feeding between <i>Faecalibacterium prausnitzii</i> and <i>Bifidobacterium adolescentis</i> . <i>FEMS Microbiology Letters</i> , <b>2015</b> , 362,	2.9	167
167	Mucosa-associated <i>Faecalibacterium prausnitzii</i> phylotype richness is reduced in patients with inflammatory bowel disease. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 7582-92	4.8	66
166	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 1615-30	5.2	86
165	<i>Faecalibacterium</i> <b>2015</b> , 1-6		

164	Roseburia <b>2015</b> , 1-7		2
163	Contribution of diet to the composition of the human gut microbiota. <i>Microbial Ecology in Health and Disease</i> , <b>2015</b> , 26, 26164		227
162	Faecalibacterium prausnitzii Strain HTF-F and Its Extracellular Polymeric Matrix Attenuate Clinical Parameters in DSS-Induced Colitis. <i>PLoS ONE</i> , <b>2015</b> , 10, e0123013	3.7	74
161	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , <b>2014</b> , 22, 267-74	12.4	148
160	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , <b>2014</b> , 8, 1323-35	11.9	561
159	The gut microbiota, bacterial metabolites and colorectal cancer. <i>Nature Reviews Microbiology</i> , <b>2014</b> , 12, 661-72	22.2	1390
158	Mucosa-associated Faecalibacterium prausnitzii and Escherichia coli co-abundance can distinguish Irritable Bowel Syndrome and Inflammatory Bowel Disease phenotypes. <i>International Journal of Medical Microbiology</i> , <b>2014</b> , 304, 464-75	3.7	83
157	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> , <b>2014</b> , 11, 506-14	24.2	3614
156	Functional genomics reveals that Clostridium difficile Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , <b>2014</b> , 15, 160	4.5	85
155	pH feedback and phenotypic diversity within bacterial functional groups of the human gut. <i>Journal of Theoretical Biology</i> , <b>2014</b> , 342, 62-9	2.3	12
154	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. <i>ISME Journal</i> , <b>2014</b> , 8, 2218-30	11.9	356
153	Biomass utilization by gut microbiomes. <i>Annual Review of Microbiology</i> , <b>2014</b> , 68, 279-96	17.5	107
152	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> , <b>2014</b> , 9, e88982	3.7	177
151	Gut microbiota signatures predict host and microbiota responses to dietary interventions in obese individuals. <i>PLoS ONE</i> , <b>2014</b> , 9, e90702	3.7	127
150	Rumen cellulose-degrading strategies revealed by comparative genome-wide analysis of six ruminococcal strains. <i>PLoS ONE</i> , <b>2014</b> , 9, e99221	3.7	55
149	Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota ( <i>Akkermansia muciniphila</i> ) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 2879-90	5.2	40
148	Prebiotic stimulation of human colonic butyrate-producing bacteria and bifidobacteria, in vitro. <i>FEMS Microbiology Ecology</i> , <b>2014</b> , 87, 30-40	4.3	249
147	Gut Microbiome and Obesity <b>2014</b> , 73-82		3

146	A representative of the dominant human colonic Firmicutes, Roseburia faecis M72/1, forms a novel bacteriocin-like substance. <i>Anaerobe</i> , <b>2013</b> , 23, 5-8	2.8	20
145	Colonic bacterial metabolites and human health. <i>Current Opinion in Microbiology</i> , <b>2013</b> , 16, 246-54	7.9	243
144	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , <b>2013</b> , 69, 52-60	10.2	594
143	The gut microbial metabolome: modulation of cancer risk in obese individuals. <i>Proceedings of the Nutrition Society</i> , <b>2013</b> , 72, 178-88	2.9	24
142	Probiotics and prebiotics and health in ageing populations. <i>Maturitas</i> , <b>2013</b> , 75, 44-50	5	132
141	Major phenylpropanoid-derived metabolites in the human gut can arise from microbial fermentation of protein. <i>Molecular Nutrition and Food Research</i> , <b>2013</b> , 57, 523-35	5.9	172
140	Intestinal microbiota in functional bowel disorders: a Rome foundation report. <i>Gut</i> , <b>2013</b> , 62, 159-76	19.2	607
139	Some are more equal than others: the role of "keystone" species in the degradation of recalcitrant substrates. <i>Gut Microbes</i> , <b>2013</b> , 4, 236-40	8.8	98
138	The Microbiology of Resistant Starch Fermentation in the Human Large Intestine: A Host of Unanswered Questions <b>2013</b> , 251-266		1
137	Expression of cellulosome components and type IV pili within the extracellular proteome of <i>Ruminococcus flavefaciens</i> 007. <i>PLoS ONE</i> , <b>2013</b> , 8, e65333	3.7	22
136	Pro-inflammatory flagellin proteins of prevalent motile commensal bacteria are variably abundant in the intestinal microbiome of elderly humans. <i>PLoS ONE</i> , <b>2013</b> , 8, e68919	3.7	30
135	Phylogenetic distribution of genes encoding $\beta$ -glucuronidase activity in human colonic bacteria and the impact of diet on faecal glycosidase activities. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 1876-87	5.2	68
134	The impact of nutrition on the human microbiome. <i>Nutrition Reviews</i> , <b>2012</b> , 70 Suppl 1, S10-3	6.4	174
133	The role of the gut microbiota in nutrition and health. <i>Nature Reviews Gastroenterology and Hepatology</i> , <b>2012</b> , 9, 577-89	24.2	1119
132	The gut anaerobe <i>Faecalibacterium prausnitzii</i> uses an extracellular electron shuttle to grow at oxic-anoxic interphases. <i>ISME Journal</i> , <b>2012</b> , 6, 1578-85	11.9	201
131	<i>Anaerostipes hadrus</i> comb. nov., a dominant species within the human colonic microbiota; reclassification of <i>Eubacterium hadrum</i> Moore et al. 1976. <i>Anaerobe</i> , <b>2012</b> , 18, 523-9	2.8	54
130	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , <b>2012</b> , 3, 289-306	8.8	1085
129	<i>Ruminococcus bromii</i> is a keystone species for the degradation of resistant starch in the human colon. <i>ISME Journal</i> , <b>2012</b> , 6, 1535-43	11.9	551

128	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 207-27	5.2	82
127	Targeted restoration of the intestinal microbiota with a simple, defined bacteriotherapy resolves relapsing <i>Clostridium difficile</i> disease in mice. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002995	7.6	403
126	Alterations in microbiota and fermentation products in equine large intestine in response to dietary variation and intestinal disease. <i>British Journal of Nutrition</i> , <b>2012</b> , 107, 989-95	3.6	108
125	Microbiota of de-novo pediatric IBD: increased <i>Faecalibacterium prausnitzii</i> and reduced bacterial diversity in Crohn's but not in ulcerative colitis. <i>American Journal of Gastroenterology</i> , <b>2012</b> , 107, 1913-22	9.7	201
124	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> , <b>2012</b> , 78, 420-8	4.8	247
123	Impact of Intestinal Microbial Communities upon Health <b>2012</b> , 243-252		1
122	Molecular Biology: Microbial <b>2011</b> , 798-801		
121	Obesity and the gut microbiota. <i>Journal of Clinical Gastroenterology</i> , <b>2011</b> , 45 Suppl, S128-32	3	100
120	Nutritional influences on the gut microbiota and the consequences for gastrointestinal health. <i>Biochemical Society Transactions</i> , <b>2011</b> , 39, 1073-8	5.1	24
119	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. <i>FEMS Microbiology Ecology</i> , <b>2011</b> , 76, 615-24	4.3	87
118	Rates of production and utilization of lactate by microbial communities from the human colon. <i>FEMS Microbiology Ecology</i> , <b>2011</b> , 77, 107-19	4.3	53
117	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , <b>2011</b> , 5, 220-30	11.9	1081
116	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> , <b>2011</b> , 108 Suppl 1, 4672-9	11.5	87
115	High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health. <i>American Journal of Clinical Nutrition</i> , <b>2011</b> , 93, 1062-72	7	456
114	Cellulosomics, a gene-centric approach to investigating the intraspecific diversity and adaptation of <i>Ruminococcus flavefaciens</i> within the rumen. <i>PLoS ONE</i> , <b>2011</b> , 6, e25329	3.7	23
113	Microorganisms in the human gut: Diversity and function. <i>Biochemist</i> , <b>2011</b> , 33, 4-9	0.5	
112	Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA:acetate CoA-transferase gene. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 304-14	5.2	445
111	Abundance and diversity of dockerin-containing proteins in the fiber-degrading rumen bacterium, <i>Ruminococcus flavefaciens</i> FD-1. <i>PLoS ONE</i> , <b>2010</b> , 5, e12476	3.7	56

110	Cohesin diversity revealed by the crystal structure of the anchoring cohesin from <i>Ruminococcus flavefaciens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 77, 699-709	4.2	15
109	Diversity, metabolism and microbial ecology of butyrate-producing bacteria from the human large intestine. <i>FEMS Microbiology Letters</i> , <b>2009</b> , 294, 1-8	2.9	1078
108	Lactate has the potential to promote hydrogen sulphide formation in the human colon. <i>FEMS Microbiology Letters</i> , <b>2009</b> , 299, 128-34	2.9	90
107	The role of pH in determining the species composition of the human colonic microbiota. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 2112-22	5.2	416
106	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> , <b>2009</b> , 4, e6650	3.7	97
105	Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. <i>Nature Reviews Microbiology</i> , <b>2008</b> , 6, 121-31	22.2	1070
104	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 3275-83	5.2	109
103	Transfer of conjugative elements from rumen and human Firmicutes bacteria to <i>Roseburia inulinivorans</i> . <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 3915-7	4.8	9
102	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> , <b>2008</b> , 52, 4001-9	5.9	39
101	From cellulosomes to cellulosomes. <i>Chemical Record</i> , <b>2008</b> , 8, 364-77	6.6	237
100	Plant cell wall breakdown by anaerobic microorganisms from the Mammalian digestive tract. <i>Annals of the New York Academy of Sciences</i> , <b>2008</b> , 1125, 280-8	6.5	131
99	Cellulosome gene cluster analysis for gauging the diversity of the ruminal cellulolytic bacterium <i>Ruminococcus flavefaciens</i> . <i>FEMS Microbiology Letters</i> , <b>2008</b> , 285, 188-94	2.9	39
98	Assessment of metabolic diversity within the intestinal microbiota from healthy humans using combined molecular and cultural approaches. <i>FEMS Microbiology Ecology</i> , <b>2008</b> , 66, 496-504	4.3	39
97	Proposal of a neotype strain (A1-86) for <i>Eubacterium rectale</i> . Request for an opinion. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2008</b> , 58, 1735-6	2.2	44
96	Selective colonization of insoluble substrates by human faecal bacteria. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 667-79	5.2	197
95	Interactions and competition within the microbial community of the human colon: links between diet and health. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 1101-11	5.2	430
94	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> , <b>2007</b> , 59, 138-46	4.3	51
93	Organization of butyrate synthetic genes in human colonic bacteria: phylogenetic conservation and horizontal gene transfer. <i>FEMS Microbiology Letters</i> , <b>2007</b> , 269, 240-7	2.9	39

92	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> , <b>2007</b> , 73, 1073-8	4.8	624
91	A novel cell surface-anchored cellulose-binding protein encoded by the sca gene cluster of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 4774-83	3.5	40
90	Impact of pH on lactate formation and utilization by human fecal microbial communities. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 6526-33	4.8	136
89	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> , <b>2007</b> , 73, 2009-12	4.8	140
88	Mosaic tetracycline resistance genes are widespread in human and animal fecal samples. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2007</b> , 51, 1115-8	5.9	38
87	A novel class of CoA-transferase involved in short-chain fatty acid metabolism in butyrate-producing human colonic bacteria. <i>Microbiology (United Kingdom)</i> , <b>2006</b> , 152, 179-185	2.9	60
86	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> , <b>2006</b> , 72, 6371-6	4.8	96
85	Conservation and divergence in cellulosome architecture between two strains of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 7971-6	3.5	50
84	Proposal of <i>Roseburia faecis</i> sp. nov., <i>Roseburia hominis</i> sp. nov. and <i>Roseburia inulinivorans</i> sp. nov., based on isolates from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2006</b> , 56, 2437-2441	2.2	142
83	Comparative analysis of sequences flanking tet(W) resistance genes in multiple species of gut bacteria. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2006</b> , 50, 2632-9	5.9	84
82	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> , <b>2006</b> , 72, 3593-9	4.8	541
81	Whole-genome transcription profiling reveals genes up-regulated by growth on fucose in the human gut bacterium " <i>Roseburia inulinivorans</i> ". <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 4340-9	3.5	161
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