

Harry J Flint

List of Publications by Year in descending order

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Version: 2024-02-01

215
papers

47,916
citations

2795

94
h-index

2027

205
g-index

227
all docs

227
docs citations

227
times ranked

37950
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 506-514.	8.2	5,773
2	The gut microbiota, bacterial metabolites and colorectal cancer. <i>Nature Reviews Microbiology</i> , 2014, 12, 661-672.	13.6	2,007
3	Diversity, metabolism and microbial ecology of butyrate-producing bacteria from the human large intestine. <i>FEMS Microbiology Letters</i> , 2009, 294, 1-8.	0.7	1,612
4	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012, 3, 289-306.	4.3	1,611
5	Formation of propionate and butyrate by the human colonic microbiota. <i>Environmental Microbiology</i> , 2017, 19, 29-41.	1.8	1,597
6	The role of the gut microbiota in nutrition and health. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2012, 9, 577-589.	8.2	1,515
7	Polysaccharide utilization by gut bacteria: potential for new insights from genomic analysis. <i>Nature Reviews Microbiology</i> , 2008, 6, 121-131.	13.6	1,407
8	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011, 5, 220-230.	4.4	1,352
9	The microbiology of butyrate formation in the human colon. <i>FEMS Microbiology Letters</i> , 2002, 217, 133-139.	0.7	1,105
10	Lactate-Utilizing Bacteria, Isolated from Human Feces, That Produce Butyrate as a Major Fermentation Product. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5810-5817.	1.4	882
11	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , 2014, 8, 1323-1335.	4.4	861
12	Phylogenetic Relationships of Butyrate-Producing Bacteria from the Human Gut. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1654-1661.	1.4	817
13	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , 2013, 69, 52-60.	3.1	817
14	<i>Ruminococcus bromii</i> is a keystone species for the degradation of resistant starch in the human colon. <i>ISME Journal</i> , 2012, 6, 1535-1543.	4.4	801
15	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, 1073-1078.	1.4	795
16	Intestinal microbiota in functional bowel disorders: a Rome foundation report. <i>Gut</i> , 2013, 62, 159-176.	6.1	776
17	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, 3593-3599.	1.4	687
18	Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA:acetate CoA-transferase gene. <i>Environmental Microbiology</i> , 2010, 12, 304-314.	1.8	599

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19	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, 3692-3700.	1.4	596
20	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, 1062-1072.	2.2	589
21	The role of pH in determining the species composition of the human colonic microbiota. <i>Environmental Microbiology</i> , 2009, 11, 2112-2122.	1.8	587
22	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
23	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	4.4	570
24	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, 5186-5190.	1.4	569
25	Interactions and competition within the microbial community of the human colon: links between diet and health. <i>Environmental Microbiology</i> , 2007, 9, 1101-1111.	1.8	518
26	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.	2.1	504
27	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. <i>ISME Journal</i> , 2014, 8, 2218-2230.	4.4	489
28	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.	0.8	479
29	Comparative metabolomics in vegans and omnivores reveal constraints on diet-dependent gut microbiota metabolite production. <i>Gut</i> , 2016, 65, 63-72.	6.1	428
30	Restricted Distribution of the Butyrate Kinase Pathway among Butyrate-Producing Bacteria from the Human Colon. <i>Journal of Bacteriology</i> , 2004, 186, 2099-2106.	1.0	377
31	Contribution of acetate to butyrate formation by human faecal bacteria. <i>British Journal of Nutrition</i> , 2004, 91, 915-923.	1.2	371
32	Prebiotic stimulation of human colonic butyrate-producing bacteria and bifidobacteria, <i>in vitro</i> . <i>FEMS Microbiology Ecology</i> , 2014, 87, 30-40.	1.3	348
33	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, 420-428.	1.4	341
34	Assessment of microbial diversity in human colonic samples by 16S rDNA sequence analysis. <i>FEMS Microbiology Ecology</i> , 2002, 39, 33-39.	1.3	324
35	Contribution of diet to the composition of the human gut microbiota. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 26164.	3.8	310
36	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	1.7	308

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37	Colonic bacterial metabolites and human health. <i>Current Opinion in Microbiology</i> , 2013, 16, 246-254.	2.3	293
38	<i>Roseburia intestinalis</i> sp. nov., a novel saccharolytic, butyrate-producing bacterium from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1615-1620.	0.8	285
39	Oligonucleotide Probes That Detect Quantitatively Significant Groups of Butyrate-Producing Bacteria in Human Feces. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4320-4324.	1.4	284
40	Major phenylpropanoid-derived metabolites in the human gut can arise from microbial fermentation of protein. <i>Molecular Nutrition and Food Research</i> , 2013, 57, 523-535.	1.5	268
41	From cellulosomes to cellulosomes. <i>Chemical Record</i> , 2008, 8, 364-377.	2.9	267
42	The gut anaerobe <i>Faecalibacterium prausnitzii</i> uses an extracellular electron shuttle to grow at oxic-anoxic interphases. <i>ISME Journal</i> , 2012, 6, 1578-1585.	4.4	260
43	Enhanced butyrate formation by cross-feeding between <i>Faecalibacterium prausnitzii</i> and <i>Bifidobacterium adolescentis</i> . <i>FEMS Microbiology Letters</i> , 2015, 362, fmv176.	0.7	250
44	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> , 2012, 107, 1913-1922.	0.2	245
45	Selective colonization of insoluble substrates by human faecal bacteria. <i>Environmental Microbiology</i> , 2007, 9, 667-679.	1.8	238
46	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.	1.1	236
47	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> , 2006, 188, 4340-4349.	1.0	225
48	The impact of nutrition on the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S10-S13.	2.6	213
49	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.	4.9	208
50	Prebiotic potential of pectin and pectic oligosaccharides to promote anti-inflammatory commensal bacteria in the human colon. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	203
51	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> , 2006, 56, 2437-2441.	0.8	200
52	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014, 22, 267-274.	3.5	194
53	Impact of pH on Lactate Formation and Utilization by Human Fecal Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6526-6533.	1.4	182
54	Plant Cell Wall Breakdown by Anaerobic Microorganisms from the Mammalian Digestive Tract. <i>Annals of the New York Academy of Sciences</i> , 2008, 1125, 280-288.	1.8	181

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55	Faecalibacterium prausnitzii A2-165 has a high capacity to induce IL-10 in human and murine dendritic cells and modulates T cell responses. Scientific Reports, 2016, 6, 18507.	1.6	174
56	Bacterial diversity within the equine large intestine as revealed by molecular analysis of cloned 16S rRNA genes. FEMS Microbiology Ecology, 2001, 38, 141-151.	1.3	173
57	Specific substrate-driven changes in human faecal microbiota composition contrast with functional redundancy in short-chain fatty acid production. ISME Journal, 2018, 12, 610-622.	4.4	173
58	Cellulosomal Scaffoldin-Like Proteins from Ruminococcus flavefaciens. Journal of Bacteriology, 2001, 183, 1945-1953.	1.0	166
59	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. Applied and Environmental Microbiology, 2007, 73, 2009-2012.	1.4	166
60	Butyric acid-producing anaerobic bacteria as a novel probiotic treatment approach for inflammatory bowel disease. Journal of Medical Microbiology, 2010, 59, 141-143.	0.7	164
61	Gut Microbiota Signatures Predict Host and Microbiota Responses to Dietary Interventions in Obese Individuals. PLoS ONE, 2014, 9, e90702.	1.1	163
62	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. Microbial Genomics, 2016, 2, e000043.	1.0	162
63	Biomass Utilization by Gut Microbiomes. Annual Review of Microbiology, 2014, 68, 279-296.	2.9	161
64	Oral treatment with Eubacterium hallii improves insulin sensitivity in db/db mice. Npj Biofilms and Microbiomes, 2016, 2, 16009.	2.9	159
65	Probiotics and prebiotics and health in ageing populations. Maturitas, 2013, 75, 44-50.	1.0	157
66	Alterations in microbiota and fermentation products in equine large intestine in response to dietary variation and intestinal disease. British Journal of Nutrition, 2012, 107, 989-995.	1.2	156
67	Effects of Alternative Dietary Substrates on Competition between Human Colonic Bacteria in an Anaerobic Fermentor System. Applied and Environmental Microbiology, 2003, 69, 1136-1142.	1.4	151
68	Anaerostipes caccae gen. nov., sp. nov., a New Saccharolytic, Acetate-utilising, Butyrate-producing Bacterium from Human Faeces. Systematic and Applied Microbiology, 2002, 25, 46-51.	1.2	150
69	Functional genomics reveals that Clostridium difficile Spo0A coordinates sporulation, virulence and metabolism. BMC Genomics, 2014, 15, 160.	1.2	145
70	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic Firmicutes Bacterium Ruminococcus bromii. MBio, 2015, 6, e01058-15.	1.8	145
71	Molecular Analysis of the Microbial Diversity Present in the Colonic Wall, Colonic Lumen, and Cecal Lumen of a Pig. Applied and Environmental Microbiology, 1999, 65, 5372-5377.	1.4	145
72	The rumen microbial ecosystem—some recent developments. Trends in Microbiology, 1997, 5, 483-488.	3.5	135

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73	The species composition of the human intestinal microbiota differs between particle-associated and liquid phase communities. <i>Environmental Microbiology</i> , 2008, 10, 3275-3283.	1.8	135
74	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. <i>FEMS Microbiology Ecology</i> , 2011, 76, 615-624.	1.3	129
75	Occurrence of the New Tetracycline Resistance Gene tet (W) in Bacteria from the Human Gut. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 775-777.	1.4	128
76	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 207-227.	1.8	128
77	Mechanistic Insights Into the Cross-Feeding of <i>Ruminococcus gnavus</i> and <i>Ruminococcus bromii</i> on Host and Dietary Carbohydrates. <i>Frontiers in Microbiology</i> , 2018, 9, 2558.	1.5	125
78	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.	1.1	124
79	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, 4672-4679.	3.3	119
80	Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. <i>Environmental Microbiology</i> , 2016, 18, 2214-2225.	1.8	119
81	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , 2015, 17, 1615-1630.	1.8	118
82	Some are more equal than others. <i>Gut Microbes</i> , 2013, 4, 236-240.	4.3	117
83	Lactate has the potential to promote hydrogen sulphide formation in the human colon. <i>FEMS Microbiology Letters</i> , 2009, 299, 128-134.	0.7	115
84	Obesity and the Gut Microbiota. <i>Journal of Clinical Gastroenterology</i> , 2011, 45, S128-S132.	1.1	115
85	Faecalibacterium prausnitzii Strain HTF-F and Its Extracellular Polymeric Matrix Attenuate Clinical Parameters in DSS-Induced Colitis. <i>PLoS ONE</i> , 2015, 10, e0123013.	1.1	115
86	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> , 2014, 304, 464-475.	1.5	114
87	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, 6371-6376.	1.4	113
88	Evidence for recent intergeneric transfer of a new tetracycline resistance gene, tet(W), isolated from <i>Butyrivibrio fibrisolvens</i> , and the occurrence of tet(O) in ruminal bacteria. <i>Environmental Microbiology</i> , 1999, 1, 53-64.	1.8	112
89	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , 2017, 38, 59-65.	2.3	111
90	Changes in the Abundance of Faecalibacterium prausnitzii 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.	0.9	108

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91	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, 3683-3689.	1.4	106
92	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015, 17, 3407-3426.	1.8	104
93	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , 2020, 11, .	1.8	103
94	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.	1.4	102
95	Unravelling the genetic diversity of ruminal bacteria belonging to the CFB phylum. <i>FEMS Microbiology Ecology</i> , 2000, 33, 69-79.	1.3	97
96	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, 4335-4337.	1.4	97
97	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, 1876-1887.	1.8	97
98	Comparative Analysis of Sequences Flanking tet (W) Resistance Genes in Multiple Species of Gut Bacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 2632-2639.	1.4	93
99	Mucosa-Associated Faecalibacterium prausnitzii Phylotype Richness Is Reduced in Patients with Inflammatory Bowel Disease. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7582-7592.	1.4	89
100	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, 1013-1023.	1.2	87
101	Unconventional Mode of Attachment of the <i>Ruminococcus flavefaciens</i> Cellulosome to the Cell Surface. <i>Journal of Bacteriology</i> , 2005, 187, 7569-7578.	1.0	87
102	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, 3246-3249.	1.4	82
103	Cell-associated α -amylases of butyrate-producing Firmicute bacteria from the human colon. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3281-3290.	0.7	81
104	Inhibitory activity of gut bacteria against <i>Escherichia coli</i> O157 mediated by dietary plant metabolites. <i>FEMS Microbiology Letters</i> , 1998, 164, 283-288.	0.7	79
105	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> , 2018, 20, 324-336.	1.8	79
106	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> , 2017, 163, 1292-1305.	0.7	79
107	Novel Organization and Divergent Dockerin Specificities in the Cellulosome System of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2003, 185, 703-713.	1.0	78
108	<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> , 2012, 18, 523-529.	1.0	78

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109	Three multidomain esterases from the cellulolytic rumen anaerobe <i>Ruminococcus flavefaciens</i> 17 that carry divergent dockerin sequences The GenBank accession numbers for the sequences reported in this paper are AJ238716 (<i>cesA</i>) and AJ272430 (<i>xynE</i>). <i>Microbiology (United Kingdom)</i> , 2000, 146, 1391-1397.	0.7	78
110	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.	0.7	76
111	Rates of production and utilization of lactate by microbial communities from the human colon. <i>FEMS Microbiology Ecology</i> , 2011, 77, 107-119.	1.3	76
112	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six <i>Ruminococcal</i> Strains. <i>PLoS ONE</i> , 2014, 9, e99221.	1.1	73
113	How to Manipulate the Microbiota: Prebiotics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 902, 119-142.	0.8	69
114	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020, 5, .	1.7	67
115	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.	1.1	65
116	Complete genome of a new <i>Firmicutes</i> species belonging to the dominant human colonic microbiota (<i>Ruminococcus bicirculans</i>) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014, 16, 2879-2890.	1.8	62
117	<i>Bacteroides (Fibrobacter) succinogenes</i> , a cellulolytic anaerobic bacterium from the gastrointestinal tract. <i>Applied Microbiology and Biotechnology</i> , 1989, 30, 433.	1.7	59
118	Formate cross-feeding and cooperative metabolic interactions revealed by transcriptomics in co-cultures of acetogenic and amylolytic human colonic bacteria. <i>Environmental Microbiology</i> , 2019, 21, 259-271.	1.8	58
119	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, 138-146.	1.3	57
120	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> , 2016, 18, 542-556.	1.8	57
121	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> , 2008, 58, 1735-1736.	0.8	57
122	ScaC, an Adaptor Protein Carrying a Novel Cohesin That Expands the Dockerin-Binding Repertoire of the <i>Ruminococcus flavefaciens</i> 17 Cellulosome. <i>Journal of Bacteriology</i> , 2004, 186, 2576-2585.	1.0	56
123	Cellulosome gene cluster analysis for gauging the diversity of the ruminal cellulolytic bacterium <i>Ruminococcus flavefaciens</i> . <i>FEMS Microbiology Letters</i> , 2008, 285, 188-194.	0.7	56
124	Polysaccharide Breakdown by Anaerobic Microorganisms Inhabiting the Mammalian Gut. <i>Advances in Applied Microbiology</i> , 2004, 56, 89-120.	1.3	55
125	A xylanase produced by the rumen anaerobic protozoan <i>Polyplastron multivesiculatum</i> shows close sequence similarity to family 11 xylanases from Gram-positive bacteria. <i>FEMS Microbiology Letters</i> , 1999, 181, 145-152.	0.7	53
126	Conservation and Divergence in Cellulosome Architecture between Two Strains of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7971-7976.	1.0	52

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127	Lack of flagella disadvantages <i>Salmonella enterica</i> serovar Enteritidis during the early stages of infection in the rat. <i>Journal of Medical Microbiology</i> , 2003, 52, 91-99.	0.7	52
128	Dockerin-like sequences in cellulases and xylanases from the rumen cellulolytic bacterium <i>Ruminococcus flavefaciens</i> . <i>FEMS Microbiology Letters</i> , 2006, 149, 213-219.	0.7	51
129	Transformation of an oral bacterium via chromosomal integration of free DNA in the presence of human saliva. <i>FEMS Microbiology Letters</i> , 2001, 200, 163-167.	0.7	50
130	Expression of two xylanase genes from the rumen cellulolytic bacterium <i>Ruminococcus flavefaciens</i> 17 cloned in pUC13. <i>Microbiology (United Kingdom)</i> , 1991, 137, 123-129.	0.7	49
131	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.	1.3	49
132	A Novel Cell Surface-Anchored Cellulose-Binding Protein Encoded by the sca Gene Cluster of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2007, 189, 4774-4783.	1.0	48
133	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, 4426-4431.	1.4	47
134	A New Tetracycline Efflux Gene, <i>tet</i> (40), Is Located in Tandem with <i>O</i> (32/O) in a Human Gut Firmicute Bacterium and in Metagenomic Library Clones. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 4001-4009.	1.4	45
135	Heterologous expression of an endoglucanase gene (<i>endA</i>) 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, 165-169.	0.7	44
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