

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	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
2	Higher total faecal short-chain fatty acid concentrations correlate with increasing proportions of butyrate and decreasing proportions of branched-chain fatty acids across multiple human studies. <i>Gut Microbiome</i> , 2022, 3, .	0.8	8
3	Type IV pili are widespread among non-pathogenic Gram-positive gut bacteria with diverse carbohydrate utilization patterns. <i>Environmental Microbiology</i> , 2021, 23, 1527-1540.	1.8	3
4	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , 2020, 11, .	1.8	103
5	Relative abundance of the <i>Prevotella</i> 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> , 2020, 20, 283.	1.3	41
6	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
7	Nondigestible Carbohydrates Affect Metabolic Health and Gut Microbiota in Overweight Adults after Weight Loss. <i>Journal of Nutrition</i> , 2020, 150, 1859-1870.	1.3	16
8	β-Glucan is a major growth substrate for human gut bacteria related to <i>Coprococcus eutactus</i> . <i>Environmental Microbiology</i> , 2020, 22, 2150-2164.	1.8	22
9	Comparative genetic and physiological characterisation of <i>Pectinatus</i> species reveals shared tolerance to beer-associated stressors but halotolerance specific to pickle-associated strains. <i>Food Microbiology</i> , 2020, 90, 103462.	2.1	6
10	Variability and Stability of the Human Gut Microbiome. <i>Fascinating Life Sciences</i> , 2020, , 63-79.	0.5	4
11	How Gut Micro-organisms Make Use of Available Carbohydrates. <i>Fascinating Life Sciences</i> , 2020, , 81-96.	0.5	1
12	Who Inhabits Our Gut? Introducing the Human Gut Microbiota. <i>Fascinating Life Sciences</i> , 2020, , 47-61.	0.5	0
13	Evaluation of bacterial biomarkers to aid in challenging inflammatory bowel diseases diagnostics and subtype classification. <i>World Journal of Gastrointestinal Pathophysiology</i> , 2020, 11, 64-77.	0.5	8
14	How Microbes Gain Energy with and Without Oxygen. <i>Fascinating Life Sciences</i> , 2020, , 31-45.	0.5	0
15	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> , 2020, , 97-108.	0.5	0
16	How to Analyse Microbial Communities?. <i>Fascinating Life Sciences</i> , 2020, , 15-29.	0.5	0
17	Gut Microbes and Metabolites. <i>Fascinating Life Sciences</i> , 2020, , 109-118.	0.5	1
18	Perspectives and Prospects. <i>Fascinating Life Sciences</i> , 2020, , 137-146.	0.5	0

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19	Impact of carbohydrate substrate complexity on the diversity of the human colonic microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	28
20	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> , 2019, 59, 131-140.	1.0	8
21	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
22	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
23	microPop: Modelling microbial populations and communities in R. <i>Methods in Ecology and Evolution</i> , 2018, 9, 399-409.	2.2	23
24	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.	4.4	173
25	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
26	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> , 2018, 8, 15566.	1.6	34
27	Complexity of the <i>Ruminococcus flavefaciens</i> FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. <i>Scientific Reports</i> , 2017, 7, 42355.	1.6	31
28	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
29	Formation of propionate and butyrate by the human colonic microbiota. <i>Environmental Microbiology</i> , 2017, 19, 29-41.	1.8	1,597
30	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
31	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , 2017, 38, 59-65.	2.3	111
32	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
33	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.	0.9	108
34	Oral treatment with <i>Eubacterium hallii</i> improves insulin sensitivity in db/db mice. <i>Npj Biofilms and Microbiomes</i> , 2016, 2, 16009.	2.9	159
35	Challenges in microbial ecology: building predictive understanding of community function and dynamics. <i>ISME Journal</i> , 2016, 10, 2557-2568.	4.4	570
36	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

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37	Gut microbial metabolites in health and disease. <i>Gut Microbes</i> , 2016, 7, 187-188.	4.3	34
38	How to Manipulate the Microbiota: Prebiotics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 902, 119-142.	0.8	69
39	Lysozyme activity of the <i>Ruminococcus champanellensis</i> cellulosome. <i>Environmental Microbiology</i> , 2016, 18, 5112-5122.	1.8	19
40	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.	1.6	174
41	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
42	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
43	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	1.7	308
44	Objections to the proposed reclassification of <i>Eubacterium rectale</i> as <i>Agathobacter rectalis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2106-2106.	0.8	9
45	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. <i>Microbial Genomics</i> , 2016, 2, e000043.	1.0	162
46	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
47	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
48	Functional phylotyping approach for assessing intraspecific diversity of <i>Ruminococcus albus</i> within the rumen microbiome. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-10.	0.7	12
49	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015, 17, 3407-3426.	1.8	104
50	Complete Genome Sequence of the Human Gut Symbiont <i>Roseburia hominis</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	8
51	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic <i>Firmicutes</i> Bacterium <i>Ruminococcus bromii</i> . <i>MBio</i> , 2015, 6, e01058-15.	1.8	145
52	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
53	Mucosa-Associated <i>Faecalibacterium prausnitzii</i> Phylotype Richness Is Reduced in Patients with Inflammatory Bowel Disease. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7582-7592.	1.4	89
54	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , 2015, 17, 1615-1630.	1.8	118

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55	Faecalibacterium prausnitzii Strain HTF-F and Its Extracellular Polymeric Matrix Attenuate Clinical Parameters in DSS-Induced Colitis. PLoS ONE, 2015, 10, e0123013.	1.1	115
56	The Impact of Different DNA Extraction Kits and Laboratories upon the Assessment of Human Gut Microbiota Composition by 16S rRNA Gene Sequencing. PLoS ONE, 2014, 9, e88982.	1.1	236
57	Gut Microbiota Signatures Predict Host and Microbiota Responses to Dietary Interventions in Obese Individuals. PLoS ONE, 2014, 9, e90702.	1.1	163
58	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. PLoS ONE, 2014, 9, e99221.	1.1	73
59	Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota (<i>Ruminococcus bicirculans</i>) reveals two chromosomes and a selective capacity to utilize plant glucans. Environmental Microbiology, 2014, 16, 2879-2890.	1.8	62
60	Prebiotic stimulation of human colonic butyrate-producing bacteria and bifidobacteria, in vitro. FEMS Microbiology Ecology, 2014, 87, 30-40.	1.3	348
61	Phylogeny, culturing, and metagenomics of the human gut microbiota. Trends in Microbiology, 2014, 22, 267-274.	3.5	194
62	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. ISME Journal, 2014, 8, 1323-1335.	4.4	861
63	The gut microbiota, bacterial metabolites and colorectal cancer. Nature Reviews Microbiology, 2014, 12, 661-672.	13.6	2,007
64	Mucosa-associated Faecalibacterium prausnitzii and Escherichia coli co-abundance can distinguish Irritable Bowel Syndrome and Inflammatory Bowel Disease phenotypes. International Journal of Medical Microbiology, 2014, 304, 464-475.	1.5	114
65	The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. Nature Reviews Gastroenterology and Hepatology, 2014, 11, 506-514.	8.2	5,773
66	Functional genomics reveals that Clostridium difficile Spo0A coordinates sporulation, virulence and metabolism. BMC Genomics, 2014, 15, 160.	1.2	145
67	pH feedback and phenotypic diversity within bacterial functional groups of the human gut. Journal of Theoretical Biology, 2014, 342, 62-69.	0.8	13
68	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. ISME Journal, 2014, 8, 2218-2230.	4.4	489
69	Biomass Utilization by Gut Microbiomes. Annual Review of Microbiology, 2014, 68, 279-296.	2.9	161
70	Gut Microbiome and Obesity. , 2014, , 73-82.		3
71	A representative of the dominant human colonic Firmicutes, Roseburia faecis M72/1, forms a novel bacteriocin-like substance. Anaerobe, 2013, 23, 5-8.	1.0	28
72	Colonic bacterial metabolites and human health. Current Opinion in Microbiology, 2013, 16, 246-254.	2.3	293

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73	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , 2013, 69, 52-60.	3.1	817
74	The gut microbial metabolome: modulation of cancer risk in obese individuals. <i>Proceedings of the Nutrition Society</i> , 2013, 72, 178-188.	0.4	27
75	Probiotics and prebiotics and health in ageing populations. <i>Maturitas</i> , 2013, 75, 44-50.	1.0	157
76	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
77	Intestinal microbiota in functional bowel disorders: a Rome foundation report. <i>Gut</i> , 2013, 62, 159-176.	6.1	776
78	Some are more equal than others. <i>Gut Microbes</i> , 2013, 4, 236-240.	4.3	117
79	Expression of Cellulosome Components and Type IV Pili within the Extracellular Proteome of <i>Ruminococcus flavefaciens</i> 007. <i>PLoS ONE</i> , 2013, 8, e65333.	1.1	25
80	Pro-Inflammatory Flagellin Proteins of Prevalent Motile Commensal Bacteria Are Variably Abundant in the Intestinal Microbiome of Elderly Humans. <i>PLoS ONE</i> , 2013, 8, e68919.	1.1	42
81	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
82	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, 989-995.	1.2	156
83	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
84	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
85	The impact of nutrition on the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S10-S13.	2.6	213
86	Antibiotics and adiposity. <i>Nature</i> , 2012, 488, 601-602.	13.7	8
87	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
88	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
89	<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
90	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012, 3, 289-306.	4.3	1,611

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91	<i>Ruminococcus bromii</i> is a keystone species for the degradation of resistant starch in the human colon. ISME Journal, 2012, 6, 1535-1543.	4.4	801
92	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. Environmental Microbiology, 2012, 14, 207-227.	1.8	128
93	Phylogenetic distribution of genes encoding β -glucuronidase activity in human colonic bacteria and the impact of diet on faecal glycosidase activities. Environmental Microbiology, 2012, 14, 1876-1887.	1.8	97
94	Impact of Intestinal Microbial Communities upon Health. , 2012, , 243-252.		2
95	Molecular Biology: Microbial. , 2011, , 798-801.		0
96	Obesity and the Gut Microbiota. Journal of Clinical Gastroenterology, 2011, 45, S128-S132.	1.1	115
97	Nutritional influences on the gut microbiota and the consequences for gastrointestinal health. Biochemical Society Transactions, 2011, 39, 1073-1078.	1.6	29
98	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. FEMS Microbiology Ecology, 2011, 76, 615-624.	1.3	129
99	Rates of production and utilization of lactate by microbial communities from the human colon. FEMS Microbiology Ecology, 2011, 77, 107-119.	1.3	76
100	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. ISME Journal, 2011, 5, 220-230.	4.4	1,352
101	Substrate-driven gene expression in <i>Roseburia inulinivorans</i> : Importance of inducible enzymes in the utilization of inulin and starch. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4672-4679.	3.3	119
102	High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health. American Journal of Clinical Nutrition, 2011, 93, 1062-1072.	2.2	589
103	Cellulosomics, a Gene-Centric Approach to Investigating the Intraspecific Diversity and Adaptation of <i>Ruminococcus flavefaciens</i> within the Rumen. PLoS ONE, 2011, 6, e25329.	1.1	28
104	Microorganisms in the human gut: Diversity and function. Biochemist, 2011, 33, 4-9.	0.2	0
105	Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA:acetate Co-transferase gene. Environmental Microbiology, 2010, 12, 304-314.	1.8	599
106	Abundance and Diversity of Dockerin-Containing Proteins in the Fiber-Degrading Rumen Bacterium, <i>Ruminococcus flavefaciens</i> FD-1. PLoS ONE, 2010, 5, e12476.	1.1	65
107	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
108	Cohesin diversity revealed by the crystal structure of the anchoring cohesin from <i>Ruminococcus flavefaciens</i> . Proteins: Structure, Function and Bioinformatics, 2009, 77, 699-709.	1.5	16

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109	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
110	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
111	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
112	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
113	From cellulosomes to cellulosomes. <i>Chemical Record</i> , 2008, 8, 364-377.	2.9	267
114	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
115	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
116	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
117	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
118	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
119	Transfer of Conjugative Elements from Rumen and Human Firmicutes Bacteria to <i>Roseburia inulinivorans</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 3915-3917.	1.4	33
120	A New Tetracycline Efflux Gene, <i>tet</i> (40), Is Located in Tandem with <i>tet</i> (O/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
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	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
123	A Novel Cell Surface-Anchored Cellulose-Binding Protein Encoded by the <i>sca</i> Gene Cluster of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2007, 189, 4774-4783.	1.0	48
124	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
125	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, 2009-2012.	1.4	166
126	Mosaic Tetracycline Resistance Genes Are Widespread in Human and Animal Fecal Samples. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 1115-1118.	1.4	43

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127	Selective colonization of insoluble substrates by human faecal bacteria. <i>Environmental Microbiology</i> , 2007, 9, 667-679.	1.8	238
128	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
129	Application of 16S rRNA gene-targetted 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
130	Organization of butyrate synthetic genes in human colonic bacteria: phylogenetic conservation and horizontal gene transfer. <i>FEMS Microbiology Letters</i> , 2007, 269, 240-247.	0.7	44
131	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
132	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
133	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
134	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
135	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
136	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
137	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
138	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
139	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
140	Hybrid tet Genes and tet Gene Nomenclature: Request for Opinion. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 1265-1266.	1.4	33
141	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
142	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
143	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
144	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, 3656-3659.	1.0	36

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145	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
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148	Effects of esculin and esculetin on the survival of <i>Escherichia coli</i> O157 in human faecal slurries, continuous-flow simulations of the rumen and colon and in calves. <i>British Journal of Nutrition</i> , 2004, 91, 749-755.	1.2	28
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150	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, 2219-2226.	1.0	37
151	Effects of Alternative Dietary Substrates on Competition between Human Colonic Bacteria in an Anaerobic Fermentor System. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1136-1142.	1.4	151
152	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
153	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
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156	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
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158	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
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161	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
162	Title is missing!. <i>Biotechnology Letters</i> , 2002, 24, 735-741.	1.1	4

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180	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 (cesA) and AJ272430 (xynE).. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1391-1397.	0.7	78

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