

Sylvia H Duncan

List of Publications by Citations

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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.

83 papers	17,303 citations	54 h-index	87 g-index
87 ext. papers	21,198 ext. citations	5.7 avg, IF	6.65 L-index

#	Paper	IF	Citations
83	The role of the gut microbiota in nutrition and health. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2012 , 9, 577-89	24.2	1119
82	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012 , 3, 289-306	8.8	1085
81	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011 , 5, 220-30	11.9	1081
80	The microbiology of butyrate formation in the human colon. <i>FEMS Microbiology Letters</i> , 2002 , 217, 133-9	2.9	911
79	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
78	Phylogenetic relationships of butyrate-producing bacteria from the human gut. <i>Applied and Environmental Microbiology</i> , 2000 , 66, 1654-61	4.8	653
77	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
76	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , 2013 , 69, 52-60	10.2	594
75	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , 2014 , 8, 1323-35	11.9	561
74	Ruminococcus bromii 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
73	Two routes of metabolic cross-feeding between Bifidobacterium adolescentis and butyrate-producing anaerobes from the human gut. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 3593-9	4.8	541
72	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
71	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
70	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
69	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
68	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
67	Targeted restoration of the intestinal microbiota with a simple, defined bacteriotherapy resolves relapsing Clostridium difficile disease in mice. <i>PLoS Pathogens</i> , 2012 , 8, e1002995	7.6	403

66	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
65	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
64	Contribution of acetate to butyrate formation by human faecal bacteria. <i>British Journal of Nutrition</i> , 2004 , 91, 915-23	3.6	271
63	Prebiotic stimulation of human colonic butyrate-producing bacteria and bifidobacteria, in vitro. <i>FEMS Microbiology Ecology</i> , 2014 , 87, 30-40	4.3	249
62	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
61	<i>Faecalibacterium prausnitzii</i> : from microbiology to diagnostics and prognostics. <i>ISME Journal</i> , 2017 , 11, 841-852	11.9	240
60	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016 , 14, 3	7.3	214
59	The gut anaerobe <i>Faecalibacterium prausnitzii</i> uses an extracellular electron shuttle to grow at oxic-anoxic interphases. <i>ISME Journal</i> , 2012 , 6, 1578-85	11.9	201
58	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
57	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
56	Translocation of Crohn's disease <i>Escherichia coli</i> across M-cells: contrasting effects of soluble plant fibres and emulsifiers. <i>Gut</i> , 2010 , 59, 1331-9	19.2	172
55	Enhanced butyrate formation by cross-feeding between <i>Faecalibacterium prausnitzii</i> and <i>Bifidobacterium adolescentis</i> . <i>FEMS Microbiology Letters</i> , 2015 , 362,	2.9	167
54	Circulating and Tissue-Resident CD4 T Cells With Reactivity to Intestinal Microbiota Are Abundant in Healthy Individuals and Function Is Altered During Inflammation. <i>Gastroenterology</i> , 2017 , 153, 1320-1337.e16	13.3	150
53	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014 , 22, 267-74	12.4	148
52	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	2.2	142
51	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
50	<i>Oxalobacter formigenes</i> and its potential role in human health. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 3841-7	4.8	141
49	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

48	Probiotics and prebiotics and health in ageing populations. <i>Maturitas</i> , 2013 , 75, 44-50	5	132
47	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
46	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
45	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
44	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic Firmicutes Bacterium Ruminococcus bromii. <i>MBio</i> , 2015 , 6, e01058-15	7.8	99
43	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
42	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
41	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
40	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
39	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
38	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , 2015 , 17, 1615-30	5.2	86
37	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
36	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, 464-75	3.7	83
35	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , 2017 , 38, 59-65	7.9	78
34	Faecalibacterium prausnitzii 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
33	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015 , 17, 3407-26	5.2	67
32	Mucosa-associated Faecalibacterium prausnitzii phylotype richness is reduced in patients with inflammatory bowel disease. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7582-92	4.8	66
31	Rumen cellulosomics: divergent fiber-degrading strategies revealed by comparative genome-wide analysis of six ruminococcal strains. <i>PLoS ONE</i> , 2014 , 9, e99221	3.7	55

30	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
29	Anti-inflammatory implications of the microbial transformation of dietary phenolic compounds. <i>Nutrition and Cancer</i> , 2008 , 60, 636-42	2.8	54
28	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
27	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
26	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
25	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
24	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , 2020 , 11,	7.8	40
23	Mutual Interaction of Phenolic Compounds and Microbiota: Metabolism of Complex Phenolic Apigenin-C- and Kaempferol-O-Derivatives by Human Fecal Samples. <i>Journal of Agricultural and Food Chemistry</i> , 2018 , 66, 485-497	5.7	28
22	The gut microbial metabolome: modulation of cancer risk in obese individuals. <i>Proceedings of the Nutrition Society</i> , 2013 , 72, 178-88	2.9	24
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	5.2	24
20	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020 , 5,	7.6	22
19	Effects of esculin and esculetin on the survival of Escherichia coli O157 in human faecal slurries, continuous-flow simulations of the rumen and colon and in calves. <i>British Journal of Nutrition</i> , 2004 , 91, 749-55	3.6	21
18	Chlorogenic acid versus amaranthyl caffeoylsuccinic acid - Gut microbial degradation of caffeic acid derivatives. <i>Food Research International</i> , 2017 , 100, 375-384	7	20
17	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> , 2020 , 20, 283	4.5	18
16	Availability and dose response of phytochemicals from a wheat bran rich cereal product in healthy human volunteers. <i>Molecular Nutrition and Food Research</i> , 2017 , 61, 1600202	5.9	16
15	Lysozyme activity of the Ruminococcus champanellensis cellulosome. <i>Environmental Microbiology</i> , 2016 , 18, 5112-5122	5.2	12
14	Advanced analytical methodologies to study the microbial metabolome of the human gut. <i>TrAC - Trends in Analytical Chemistry</i> , 2013 , 52, 54-60	14.6	9
13	Dietary effects on the microbiological safety of food. <i>Proceedings of the Nutrition Society</i> , 2001 , 60, 247-55		7

12	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	2.2	7
11	Impact of protein on the composition and metabolism of the human gut microbiota and health. <i>Proceedings of the Nutrition Society</i> , 2021 , 80, 173-185	2.9	5
10	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria.. <i>Microbial Genomics</i> , 2022 , 8,	4.4	3
9	Dietary fibre complexity and its influence on functional groups of the human gut microbiota. <i>Proceedings of the Nutrition Society</i> , 1-27	2.9	3
8	Roseburia 2015 , 1-7		2
7	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	3.2	2
6	Invasive Plants Are a Valuable Alternate Protein Source and Can Contribute to Meeting Climate Change Targets. <i>Frontiers in Sustainable Food Systems</i> , 2021 , 5,	4.8	2
5	Higher total faecal short chain fatty concentrations correlate with increasing proportions of butyrate and decreasing proportions of branched chain fatty acids across multiple human studies 1-23		1
4	High throughput method development and optimised production of leaf protein concentrates with potential to support the agri-industry. <i>Journal of Food Measurement and Characterization</i> , 1	2.8	0
3	MS-based Methodologies to Study the Microbial Metabolome 2013 , 221-243		
2	Faecalibacterium 2015 , 1-6		
1	Microorganisms in the human gut: Diversity and function. <i>Biochemist</i> , 2011 , 33, 4-9	0.5	