

# Sylvia H Duncan

## List of Publications by Year in descending order

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82  
papers

23,838  
citations

22099

59  
h-index

56606

83  
g-index

87  
all docs

87  
docs citations

87  
times ranked

22661  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012, 3, 289-306.	4.3	1,611
2	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
3	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011, 5, 220-230.	4.4	1,352
4	The microbiology of butyrate formation in the human colon. <i>FEMS Microbiology Letters</i> , 2002, 217, 133-139.	0.7	1,105
5	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
6	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , 2014, 8, 1323-1335.	4.4	861
7	Phylogenetic Relationships of Butyrate-Producing Bacteria from the Human Gut. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1654-1661.	1.4	817
8	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , 2013, 69, 52-60.	3.1	817
9	<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
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	<i>Faecalibacterium prausnitzii</i> : from microbiology to diagnostics and prognostics. <i>ISME Journal</i> , 2017, 11, 841-852.	4.4	510
18	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

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19	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
20	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
21	Contribution of acetate to butyrate formation by human faecal bacteria. <i>British Journal of Nutrition</i> , 2004, 91, 915-923.	1.2	371
22	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
23	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
24	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	1.7	308
25	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
26	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
27	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
28	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.	0.6	246
29	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
30	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, 1331-1339.	6.1	232
31	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
32	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
33	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014, 22, 267-274.	3.5	194
34	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
35	<i>Faecalibacterium prausnitzii</i> 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
36	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

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37	Oxalobacter formigenes and Its Potential Role in Human Health. Applied and Environmental Microbiology, 2002, 68, 3841-3847.	1.4	172
38	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. Microbial Genomics, 2016, 2, e000043.	1.0	162
39	Probiotics and prebiotics and health in ageing populations. Maturitas, 2013, 75, 44-50.	1.0	157
40	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
41	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
42	Unique Organization of Extracellular Amylases into Amyloosomes in the Resistant Starch-Utilizing Human Colonic Firmicutes Bacterium Ruminococcus bromii. MBio, 2015, 6, e01058-15.	1.8	145
43	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. FEMS Microbiology Ecology, 2011, 76, 615-624.	1.3	129
44	Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid. Environmental Microbiology, 2016, 18, 2214-2225.	1.8	119
45	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. Environmental Microbiology, 2015, 17, 1615-1630.	1.8	118
46	Some are more equal than others. Gut Microbes, 2013, 4, 236-240.	4.3	117
47	Lactate has the potential to promote hydrogen sulphide formation in the human colon. FEMS Microbiology Letters, 2009, 299, 128-134.	0.7	115
48	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
49	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
50	The impact of nutrition on intestinal bacterial communities. Current Opinion in Microbiology, 2017, 38, 59-65.	2.3	111
51	Ruminococcal cellulosome systems from rumen to human. Environmental Microbiology, 2015, 17, 3407-3426.	1.8	104
52	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. MBio, 2020, 11, .	1.8	103
53	Mucosa-Associated Faecalibacterium prausnitzii Phylotype Richness Is Reduced in Patients with Inflammatory Bowel Disease. Applied and Environmental Microbiology, 2015, 81, 7582-7592.	1.4	89
54	Sporulation capability and amyloosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader Ruminococcus bromii. Environmental Microbiology, 2018, 20, 324-336.	1.8	79

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55	Anaerostipes hadrus comb. nov., a dominant species within the human colonic microbiota; reclassification of Eubacterium hadrum Moore et Åal. 1976. Anaerobe, 2012, 18, 523-529.	1.0	78
56	Rates of production and utilization of lactate by microbial communities from the human colon. FEMS Microbiology Ecology, 2011, 77, 107-119.	1.3	76
57	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. PLoS ONE, 2014, 9, e99221.	1.1	73
58	Anti-Inflammatory Implications of the Microbial Transformation of Dietary Phenolic Compounds. Nutrition and Cancer, 2008, 60, 636-642.	0.9	68
59	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. MSystems, 2020, 5, .	1.7	67
60	Formate cross-feeding and cooperative metabolic interactions revealed by transcriptomics in co-cultures of acetogenic and amylolytic human colonic bacteria. Environmental Microbiology, 2019, 21, 259-271.	1.8	58
61	Enzymatic profiling of cellulosomal enzymes from the human gut bacterium, <i>Ruminococcus champanellensis</i> , reveals a fine-tuned system for cohesin-dockerin recognition. Environmental Microbiology, 2016, 18, 542-556.	1.8	57
62	Proposal of a neotype strain (A1-86) for Eubacterium rectale. Request for an Opinion. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1735-1736.	0.8	57
63	Mutual Interaction of Phenolic Compounds and Microbiota: Metabolism of Complex Phenolic Apigenin-C- and Kaempferol-O-Derivatives by Human Fecal Samples. Journal of Agricultural and Food Chemistry, 2018, 66, 485-497.	2.4	42
64	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. BMC Microbiology, 2020, 20, 283.	1.3	41
65	Microbial lactate utilisation and the stability of the gut microbiome. Gut Microbiome, 2022, 3, .	0.8	41
66	Chlorogenic acid versus amaranth's caffeoylisocitric acid – Gut microbial degradation of caffeic acid derivatives. Food Research International, 2017, 100, 375-384.	2.9	30
67	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. British Journal of Nutrition, 2004, 91, 749-755.	1.2	28
68	The gut microbial metabolome: modulation of cancer risk in obese individuals. Proceedings of the Nutrition Society, 2013, 72, 178-188.	0.4	27
69	Availability and dose response of phytochemicals from a wheat bran rich cereal product in healthy human volunteers. Molecular Nutrition and Food Research, 2017, 61, 1600202.	1.5	23
70	Impact of protein on the composition and metabolism of the human gut microbiota and health. Proceedings of the Nutrition Society, 2021, 80, 173-185.	0.4	20
71	Lysozyme activity of the <i>Ruminococcus champanellensis</i> cellulosome. Environmental Microbiology, 2016, 18, 5112-5122.	1.8	19
72	Advanced analytical methodologies to study the microbial metabolome of the human gut. TrAC - Trends in Analytical Chemistry, 2013, 52, 54-60.	5.8	10

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73	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, .	1.8	10
74	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
75	Survival Strategies and Metabolic Interactions between <i>Ruminococcus gauvreauii</i> and <i>Ruminococcoides bili</i> , Isolated from Human Bile. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	10
76	Dietary effects on the microbiological safety of food. <i>Proceedings of the Nutrition Society</i> , 2001, 60, 247-255.	0.4	9
77	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
78	Dietary fibre complexity and its influence on functional groups of the human gut microbiota. <i>Proceedings of the Nutrition Society</i> , 2021, 80, 386-397.	0.4	9
79	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
80	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
81	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> , 2022, 16, 49-65.	1.6	6
82	Microorganisms in the human gut: Diversity and function. <i>Biochemist</i> , 2011, 33, 4-9.	0.2	0