

Sylvia H Duncan

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

23,838
citations

22099

59
h-index

56606

83
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87
all docs

87
docs citations

87
times ranked

22661
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
3	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
4	Microbial lactate utilisation and the stability of the gut microbiome. <i>Gut Microbiome</i> , 2022, 3, .	0.8	41
5	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
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, .	1.8	10
7	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.	0.4	20
8	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
9	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , 2020, 11, .	1.8	103
10	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
11	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
12	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
13	Formate cross-feeding and cooperative metabolic interactions revealed by transcriptomics in co-cultures of acetogenic and amyolytic human colonic bacteria. <i>Environmental Microbiology</i> , 2019, 21, 259-271.	1.8	58
14	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
15	Mutual Interaction of Phenolic Compounds and Microbiota: Metabolism of Complex Phenolic Apigenin- <i>C</i> - and Kaempferol- <i>O</i> -Derivatives by Human Fecal Samples. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 485-497.	2.4	42
16	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
17	Chlorogenic acid versus amaranth's caffeoylisocitric acid – Gut microbial degradation of caffeic acid derivatives. <i>Food Research International</i> , 2017, 100, 375-384.	2.9	30
18	<i>Faecalibacterium prausnitzii</i> : from microbiology to diagnostics and prognostics. <i>ISME Journal</i> , 2017, 11, 841-852.	4.4	510

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19	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
20	Availability and dose response of phytophenols from a wheat bran rich cereal product in healthy human volunteers. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1600202.	1.5	23
21	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
22	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , 2017, 38, 59-65.	2.3	111
23	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
24	Lysozyme activity of the <i>Ruminococcus champanellensis</i> cellulosome. <i>Environmental Microbiology</i> , 2016, 18, 5112-5122.	1.8	19
25	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
26	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
27	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	1.7	308
28	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
29	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
30	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015, 17, 3407-3426.	1.8	104
31	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
32	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
33	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
34	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , 2015, 17, 1615-1630.	1.8	118
35	<i>Faecalibacterium prausnitzii</i> 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
36	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

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37	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. PLoS ONE, 2014, 9, e99221.	1.1	73
38	Prebiotic stimulation of human colonic butyrate-producing bacteria and bifidobacteria, <i>in vitro</i> . FEMS Microbiology Ecology, 2014, 87, 30-40.	1.3	348
39	Phylogeny, culturing, and metagenomics of the human gut microbiota. Trends in Microbiology, 2014, 22, 267-274.	3.5	194
40	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. ISME Journal, 2014, 8, 1323-1335.	4.4	861
41	Mucosa-associated <i>Faecalibacterium prausnitzii</i> and <i>Escherichia coli</i> co-abundance can distinguish Irritable Bowel Syndrome and Inflammatory Bowel Disease phenotypes. International Journal of Medical Microbiology, 2014, 304, 464-475.	1.5	114
42	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
43	Advanced analytical methodologies to study the microbial metabolome of the human gut. TrAC - Trends in Analytical Chemistry, 2013, 52, 54-60.	5.8	10
44	The influence of diet on the gut microbiota. Pharmacological Research, 2013, 69, 52-60.	3.1	817
45	The gut microbial metabolome: modulation of cancer risk in obese individuals. Proceedings of the Nutrition Society, 2013, 72, 178-188.	0.4	27
46	Probiotics and prebiotics and health in ageing populations. Maturitas, 2013, 75, 44-50.	1.0	157
47	Major phenylpropanoid-derived metabolites in the human gut can arise from microbial fermentation of protein. Molecular Nutrition and Food Research, 2013, 57, 523-535.	1.5	268
48	Some are more equal than others. Gut Microbes, 2013, 4, 236-240.	4.3	117
49	Targeted Restoration of the Intestinal Microbiota with a Simple, Defined Bacteriotherapy Resolves Relapsing <i>Clostridium difficile</i> Disease in Mice. PLoS Pathogens, 2012, 8, e1002995.	2.1	504
50	Cultured Representatives of Two Major Phylogroups of Human Colonic <i>Faecalibacterium prausnitzii</i> Can Utilize Pectin, Uronic Acids, and Host-Derived Substrates for Growth. Applied and Environmental Microbiology, 2012, 78, 420-428.	1.4	341
51	The role of the gut microbiota in nutrition and health. Nature Reviews Gastroenterology and Hepatology, 2012, 9, 577-589.	8.2	1,515
52	The gut anaerobe <i>Faecalibacterium prausnitzii</i> uses an extracellular electron shuttle to grow at oxic-anoxic interphases. ISME Journal, 2012, 6, 1578-1585.	4.4	260
53	<i>Anaerostipes hadrus</i> comb. nov., a dominant species within the human colonic microbiota; reclassification of <i>Eubacterium hadrum</i> Moore et al. 1976. Anaerobe, 2012, 18, 523-529.	1.0	78
54	Microbial degradation of complex carbohydrates in the gut. Gut Microbes, 2012, 3, 289-306.	4.3	1,611

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55	<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
56	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. FEMS Microbiology Ecology, 2011, 76, 615-624.	1.3	129
57	Rates of production and utilization of lactate by microbial communities from the human colon. FEMS Microbiology Ecology, 2011, 77, 107-119.	1.3	76
58	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. ISME Journal, 2011, 5, 220-230.	4.4	1,352
59	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
60	Microorganisms in the human gut: Diversity and function. Biochemist, 2011, 33, 4-9.	0.2	0
61	Translocation of Crohn's disease <i>Escherichia coli</i> across M-cells: contrasting effects of soluble plant fibres and emulsifiers. Gut, 2010, 59, 1331-1339.	6.1	232
62	Lactate has the potential to promote hydrogen sulphide formation in the human colon. FEMS Microbiology Letters, 2009, 299, 128-134.	0.7	115
63	The role of pH in determining the species composition of the human colonic microbiota. Environmental Microbiology, 2009, 11, 2112-2122.	1.8	587
64	Anti-Inflammatory Implications of the Microbial Transformation of Dietary Phenolic Compounds. Nutrition and Cancer, 2008, 60, 636-642.	0.9	68
65	Proposal of a neotype strain (A1-86) for <i>Eubacterium rectale</i> . Request for an Opinion. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1735-1736.	0.8	57
66	Reduced Dietary Intake of Carbohydrates by Obese Subjects Results in Decreased Concentrations of Butyrate and Butyrate-Producing Bacteria in Feces. Applied and Environmental Microbiology, 2007, 73, 1073-1078.	1.4	795
67	Impact of pH on Lactate Formation and Utilization by Human Fecal Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 6526-6533.	1.4	182
68	Interactions and competition within the microbial community of the human colon: links between diet and health. Environmental Microbiology, 2007, 9, 1101-1111.	1.8	518
69	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. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2437-2441.	0.8	200
70	Two Routes of Metabolic Cross-Feeding between <i>Bifidobacterium adolescentis</i> and Butyrate-Producing Anaerobes from the Human Gut. Applied and Environmental Microbiology, 2006, 72, 3593-3599.	1.4	687
71	pH and Peptide Supply Can Radically Alter Bacterial Populations and Short-Chain Fatty Acid Ratios within Microbial Communities from the Human Colon. Applied and Environmental Microbiology, 2005, 71, 3692-3700.	1.4	596
72	Lactate-Utilizing Bacteria, Isolated from Human Feces, That Produce Butyrate as a Major Fermentation Product. Applied and Environmental Microbiology, 2004, 70, 5810-5817.	1.4	882

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73	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
74	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
75	Contribution of acetate to butyrate formation by human faecal bacteria. <i>British Journal of Nutrition</i> , 2004, 91, 915-923.	1.2	371
76	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
77	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
78	<i>Oxalobacter formigenes</i> and Its Potential Role in Human Health. <i>Applied and Environmental Microbiology</i> , 2002, 68, 3841-3847.	1.4	172
79	<i>Anaerostipes caccae</i> 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.	1.2	150
80	The microbiology of butyrate formation in the human colon. <i>FEMS Microbiology Letters</i> , 2002, 217, 133-139.	0.7	1,105
81	Dietary effects on the microbiological safety of food. <i>Proceedings of the Nutrition Society</i> , 2001, 60, 247-255.	0.4	9
82	Phylogenetic Relationships of Butyrate-Producing Bacteria from the Human Gut. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1654-1661.	1.4	817