

# Petra Louis

## List of Publications by Year in descending order

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88  
papers

24,413  
citations

31976

53  
h-index

53230

85  
g-index

91  
all docs

91  
docs citations

91  
times ranked

24656  
citing authors

#	ARTICLE	IF	CITATIONS
1	The gut microbiota, bacterial metabolites and colorectal cancer. <i>Nature Reviews Microbiology</i> , 2014, 12, 661-672.	28.6	2,007
2	Diversity, metabolism and microbial ecology of butyrate-producing bacteria from the human large intestine. <i>FEMS Microbiology Letters</i> , 2009, 294, 1-8.	1.8	1,612
3	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012, 3, 289-306.	9.8	1,611
4	Formation of propionate and butyrate by the human colonic microbiota. <i>Environmental Microbiology</i> , 2017, 19, 29-41.	3.8	1,597
5	The role of the gut microbiota in nutrition and health. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2012, 9, 577-589.	17.8	1,515
6	Dominant and diet-responsive groups of bacteria within the human colonic microbiota. <i>ISME Journal</i> , 2011, 5, 220-230.	9.8	1,352
7	Human colonic microbiota associated with diet, obesity and weight loss. <i>International Journal of Obesity</i> , 2008, 32, 1720-1724.	3.4	1,024
8	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.	3.1	882
9	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , 2014, 8, 1323-1335.	9.8	861
10	<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.	9.8	801
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.	3.1	687
12	Effect of inulin on the human gut microbiota: stimulation of <i>Bifidobacterium adolescentis</i> and <i>Faecalibacterium prausnitzii</i> . <i>British Journal of Nutrition</i> , 2009, 101, 541-550.	2.3	675
13	Understanding the effects of diet on bacterial metabolism in the large intestine. <i>Journal of Applied Microbiology</i> , 2007, 102, 1197-1208.	3.1	634
14	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.	3.8	599
15	The role of pH in determining the species composition of the human colonic microbiota. <i>Environmental Microbiology</i> , 2009, 11, 2112-2122.	3.8	587
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.	3.8	518
17	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. <i>ISME Journal</i> , 2014, 8, 2218-2230.	9.8	489
18	Restricted Distribution of the Butyrate Kinase Pathway among Butyrate-Producing Bacteria from the Human Colon. <i>Journal of Bacteriology</i> , 2004, 186, 2099-2106.	2.2	377

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19	A Diet Low in FODMAPs Reduces Symptoms in Patients With Irritable Bowel Syndrome and A Probiotic Restores Bifidobacterium Species: A Randomized Controlled Trial. <i>Gastroenterology</i> , 2017, 153, 936-947.	1.3	315
20	Modulation of the human gut microbiota by dietary fibres occurs at the species level. <i>BMC Biology</i> , 2016, 14, 3.	3.8	308
21	Cultivable bacterial diversity from the human colon. <i>Letters in Applied Microbiology</i> , 2007, 44, 343-350.	2.2	245
22	Microbiota of De-Novo Pediatric IBD: Increased Faecalibacterium Prausnitzii and Reduced Bacterial Diversity in Crohn's But Not in Ulcerative Colitis. <i>American Journal of Gastroenterology</i> , 2012, 107, 1913-1922.	0.4	245
23	Distribution of $\alpha$ -glucosidase and $\alpha$ -glucuronidase activity and of $\alpha$ -glucuronidase gene in human colonic bacteria. <i>FEMS Microbiology Ecology</i> , 2008, 66, 487-495.	2.7	240
24	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.	2.5	236
25	Prebiotic potential of pectin and pectic oligosaccharides to promote anti-inflammatory commensal bacteria in the human colon. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	203
26	Maturation of the gut microbiome during the first year of life contributes to the protective farm effect on childhood asthma. <i>Nature Medicine</i> , 2020, 26, 1766-1775.	30.7	202
27	Characterization of genes for the biosynthesis of the compatible solute ectoine from <i>Marinococcus halophilus</i> and osmoregulated expression in <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 1141-1149.	1.8	200
28	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.	1.7	200
29	Phylogeny, culturing, and metagenomics of the human gut microbiota. <i>Trends in Microbiology</i> , 2014, 22, 267-274.	7.7	194
30	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.	9.8	173
31	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.	3.1	166
32	Butyric acid-producing anaerobic bacteria as a novel probiotic treatment approach for inflammatory bowel disease. <i>Journal of Medical Microbiology</i> , 2010, 59, 141-143.	1.8	164
33	Unique Organization of Extracellular Amylases into Amyloosomes in the Resistant Starch-Utilizing Human Colonic <i>Firmicutes</i> Bacterium <i>Ruminococcus bromii</i> . <i>MBio</i> , 2015, 6, e01058-15.	4.1	145
34	Managing hypoosmotic stress: Aquaporins and medianosensitive channels in <i>Escherichia coli</i> . <i>Current Opinion in Microbiology</i> , 1999, 2, 166-169.	5.1	137
35	Relation between phylogenetic position, lipid metabolism and butyrate production by different <i>Butyrivibrio</i> -like bacteria from the rumen. <i>Antonie Van Leeuwenhoek</i> , 2007, 91, 417-422.	1.7	135
36	Butyrate production in phylogenetically diverse <i>Firmicutes</i> isolated from the chicken caecum. <i>Microbial Biotechnology</i> , 2011, 4, 503-512.	4.2	133

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37	Altered intestinal microbiota and blood T cell phenotype are shared by patients with Crohn's disease and their unaffected siblings. <i>Gut</i> , 2014, 63, 1578-1586.	12.1	127
38	Modelling the emergent dynamics and major metabolites of the human colonic microbiota. <i>Environmental Microbiology</i> , 2015, 17, 1615-1630.	3.8	118
39	Some are more equal than others. <i>Gut Microbes</i> , 2013, 4, 236-240.	9.8	117
40	A role for mechanosensitive channels in survival of stationary phase: Regulation of channel expression by RpoS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15959-15964.	7.1	111
41	The impact of nutrition on intestinal bacterial communities. <i>Current Opinion in Microbiology</i> , 2017, 38, 59-65.	5.1	111
42	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. <i>MBio</i> , 2020, 11, .	4.1	103
43	Phylogenetic distribution of genes encoding $\beta$ -glucuronidase activity in human colonic bacteria and the impact of diet on faecal glycosidase activities. <i>Environmental Microbiology</i> , 2012, 14, 1876-1887.	3.8	97
44	<i>Butyricoccus pullicaecorum</i> gen. nov., sp. nov., an anaerobic, butyrate-producing bacterium isolated from the caecal content of a broiler chicken. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2799-2802.	1.7	95
45	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.	3.8	79
46	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.	1.8	76
47	Does the Human Gut Microbiota Contribute to the Etiology of Autism Spectrum Disorders?. <i>Digestive Diseases and Sciences</i> , 2012, 57, 1987-1989.	2.3	75
48	How to Manipulate the Microbiota: Prebiotics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 902, 119-142.	1.6	69
49	Pivotal Roles for pH, Lactate, and Lactate-Utilizing Bacteria in the Stability of a Human Colonic Microbial Ecosystem. <i>MSystems</i> , 2020, 5, .	3.8	67
50	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. <i>Environmental Microbiology</i> , 2014, 16, 2879-2890.	3.8	62
51	Intestinal colonization: How key microbial players become established in this dynamic process. <i>BioEssays</i> , 2013, 35, 913-923.	2.5	61
52	Heterologous ectoine production in <i>Escherichia coli</i> : By-passing the metabolic bottle-neck. <i>Saline Systems</i> , 2008, 4, 12.	2.0	58
53	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.	3.8	58
54	Influence of cabbage processing methods and prebiotic manipulation of colonic microflora on glucosinolate breakdown in man. <i>British Journal of Nutrition</i> , 2007, 98, 364-372.	2.3	55

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55	Randomised clinical trial: <i>Bifidobacterium lactis</i> NCC2818 probiotic vs placebo, and impact on gut transit time, symptoms, and gut microbiology in chronic constipation. <i>Alimentary Pharmacology and Therapeutics</i> , 2019, 49, 251-264.	3.7	45
56	Organization of butyrate synthetic genes in human colonic bacteria: phylogenetic conservation and horizontal gene transfer. <i>FEMS Microbiology Letters</i> , 2007, 269, 240-247.	1.8	44
57	Extending colonic mucosal microbiome analysis—assessment of colonic lavage as a proxy for endoscopic colonic biopsies. <i>Microbiome</i> , 2016, 4, 61.	11.1	43
58	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.	5.2	42
59	Life in the Gut: Microbial responses to Stress in the Gastrointestinal Tract. <i>Science Progress</i> , 2010, 93, 7-36.	1.9	41
60	Microbial lactate utilisation and the stability of the gut microbiome. <i>Gut Microbiome</i> , 2022, 3, .	3.2	41
61	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.	3.3	34
62	Human Gut <i>Faecalibacterium prausnitzii</i> Deploys a Highly Efficient Conserved System To Cross-Fed on Î2-Mannan-Derived Oligosaccharides. <i>MBio</i> , 2021, 12, e0362820.	4.1	31
63	Long-term personalized low FODMAP diet improves symptoms and maintains luminal <i>Bifidobacteria</i> abundance in irritable bowel syndrome. <i>Neurogastroenterology and Motility</i> , 2022, 34, e14241.	3.0	31
64	Chlorogenic acid versus amaranth's caffeoylisocitric acid — Gut microbial degradation of caffeic acid derivatives. <i>Food Research International</i> , 2017, 100, 375-384.	6.2	30
65	Porcine Small and Large Intestinal Microbiota Rapidly Hydrolyze the Masked Mycotoxin Deoxynivalenol-3-Glucoside and Release Deoxynivalenol in Spiked Batch Cultures <i>In Vitro</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	30
66	Nutritional influences on the gut microbiota and the consequences for gastrointestinal health. <i>Biochemical Society Transactions</i> , 2011, 39, 1073-1078.	3.4	29
67	Anthocyanin-enriched bilberry extract attenuates glycaemic response in overweight volunteers without changes in insulin. <i>Journal of Functional Foods</i> , 2020, 64, 103597.	3.4	29
68	The effect of prunes on stool output, gut transit time and gastrointestinal microbiota: A randomised controlled trial. <i>Clinical Nutrition</i> , 2019, 38, 165-173.	5.0	27
69	Essential oils have different effects on human pathogenic and commensal bacteria in mixed faecal fermentations compared with pure cultures. <i>Microbiology (United Kingdom)</i> , 2015, 161, 441-449.	1.8	26
70	microPop: Modelling microbial populations and communities in R. <i>Methods in Ecology and Evolution</i> , 2018, 9, 399-409.	5.2	23
71	Î2-Glucan is a major growth substrate for human gut bacteria related to <i>Coprococcus eutactus</i> . <i>Environmental Microbiology</i> , 2020, 22, 2150-2164.	3.8	22
72	Prevalent Human Gut Bacteria Hydrolyse and Metabolise Important Food-Derived Mycotoxins and Masked Mycotoxins. <i>Toxins</i> , 2020, 12, 654.	3.4	14

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73	Immune Responsiveness to LPS Determines Risk of Childhood Wheeze and Asthma in 17q21 Risk Allele Carriers. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 205, 641-650.	5.6	13
74	Prebiotic fructans have greater impact on luminal microbiology and CD3+ T cells in healthy siblings than patients with Crohn's disease: A pilot study investigating the potential for primary prevention of inflammatory bowel disease. <i>Clinical Nutrition</i> , 2021, 40, 5009-5019.	5.0	12
75	Different Substrate Preferences Help Closely Related Bacteria To Coexist in the Gut. <i>MBio</i> , 2017, 8, .	4.1	10
76	Distribution, organization and expression of genes concerned with anaerobic lactate utilization in human intestinal bacteria. <i>Microbial Genomics</i> , 2022, 8, .	2.0	10
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.	1.7	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.	1.0	9
79	1133 The Low FODMAP Diet Reduces Symptoms in Irritable Bowel Syndrome Compared With Placebo Diet and the Microbiota Alterations May Be Prevented by Probiotic Co-Administration: A 2x2 Factorial Randomized Controlled Trial. <i>Gastroenterology</i> , 2016, 150, S230.	1.3	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, .	3.2	8
81	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.	4.2	6
82	Identification of Plasmids in the Genus <i>Marinococcus</i> and Complete Nucleotide Sequence of Plasmid pPL1 from <i>Marinococcus halophilus</i> . <i>Plasmid</i> , 1997, 38, 107-114.	1.4	5
83	How our gut microbes influence our behaviour. <i>Journal of Neuroendocrinology</i> , 2013, 25, 517-518.	2.6	3
84	Gut Microbiome and Obesity. , 2014, , 73-82.		3
85	Impact of Intestinal Microbial Communities upon Health. , 2012, , 243-252.		2
86	Gut microbial ecology. , 2009, , 38-67.		1
87	Functional Metagenomics of Human Intestinal Microbiome $\beta$ -Glucuronidase Activity. , 2013, , 1-8.		0
88	Microorganisms in the human gut: Diversity and function. <i>Biochemist</i> , 2011, 33, 4-9.	0.5	0