

Karen P Scott

List of Publications by Year in descending order

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75
papers

17,764
citations

61945

43
h-index

79644

73
g-index

77
all docs

77
docs citations

77
times ranked

20621
citing authors

#	ARTICLE	IF	CITATIONS
1	Expert consensus document: The International Scientific Association for Probiotics and Prebiotics (ISAPP) consensus statement on the definition and scope of prebiotics. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2017, 14, 491-502.	8.2	3,192
2	Microbial degradation of complex carbohydrates in the gut. <i>Gut Microbes</i> , 2012, 3, 289-306.	4.3	1,611
3	Gut microbiota functions: metabolism of nutrients and other food components. <i>European Journal of Nutrition</i> , 2018, 57, 1-24.	1.8	1,608
4	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
5	Phylogenetic distribution of three pathways for propionate production within the human gut microbiota. <i>ISME Journal</i> , 2014, 8, 1323-1335.	4.4	861
6	The International Scientific Association for Probiotics and Prebiotics (ISAPP) consensus statement on the definition and scope of synbiotics. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020, 17, 687-701.	8.2	826
7	The influence of diet on the gut microbiota. <i>Pharmacological Research</i> , 2013, 69, 52-60.	3.1	817
8	Understanding the effects of diet on bacterial metabolism in the large intestine. <i>Journal of Applied Microbiology</i> , 2007, 102, 1197-1208.	1.4	634
9	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
10	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
11	Dietary prebiotics: current status and new definition. <i>Food Science and Technology Bulletin</i> , 2010, 7, 1-19.	0.5	432
12	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
13	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
14	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
15	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
16	Restoring Specific Lactobacilli Levels Decreases Inflammation and Muscle Atrophy Markers in an Acute Leukemia Mouse Model. <i>PLoS ONE</i> , 2012, 7, e37971.	1.1	186
17	Manipulating the gut microbiota to maintain health and treat disease. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 25877.	3.8	162
18	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

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19	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
20	Optimization of a high-throughput CTAB-based protocol for the extraction of qPCR-grade DNA from rumen fluid, plant and bacterial pure cultures. <i>FEMS Microbiology Letters</i> , 2011, 325, 162-169.	0.7	149
21	First-Pass Meconium Samples from Healthy Term Vaginally-Delivered Neonates: An Analysis of the Microbiota. <i>PLoS ONE</i> , 2015, 10, e0133320.	1.1	134
22	Occurrence of the New Tetracycline Resistance Gene <i>tet (W)</i> in Bacteria from the Human Gut. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 775-777.	1.4	128
23	Substrate-driven gene expression in <i>Roseburia inulinivorans</i> : Importance of inducible enzymes in the utilization of inulin and starch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4672-4679.	3.3	119
24	Evidence for recent intergeneric transfer of a new tetracycline resistance gene, <i>tet(W)</i> , isolated from <i>Butyrivibrio fibrisolvens</i> , and the occurrence of <i>tet(O)</i> in ruminal bacteria. <i>Environmental Microbiology</i> , 1999, 1, 53-64.	1.8	112
25	Estimation of the Relative Abundance of Different <i>Bacteroides</i> and <i>Prevotella</i> Ribotypes in Gut Samples by Restriction Enzyme Profiling of PCR-Amplified 16S rRNA Gene Sequences. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3683-3689.	1.4	106
26	Fate of Free DNA and Transformation of the Oral Bacterium <i>Streptococcus gordonii</i> DL1 by Plasmid DNA in Human Saliva. <i>Applied and Environmental Microbiology</i> , 1999, 65, 6-10.	1.4	102
27	Distribution of Tetracycline and Erythromycin Resistance Genes Among Human Oral and Fecal Metagenomic DNA. <i>Microbial Drug Resistance</i> , 2009, 15, 159-166.	0.9	101
28	Altered Colonic Bacterial Fermentation as a Potential Pathophysiological Factor in Irritable Bowel Syndrome. <i>American Journal of Gastroenterology</i> , 2015, 110, 1339-1346.	0.2	101
29	Comparative Analysis of Sequences Flanking <i>tet (W)</i> Resistance Genes in Multiple Species of Gut Bacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 2632-2639.	1.4	93
30	Influence of tetracycline exposure on tetracycline resistance and the carriage of tetracycline resistance genes within commensal <i>Escherichia coli</i> populations. <i>Journal of Applied Microbiology</i> , 2003, 94, 1087-1097.	1.4	89
31	Developments in understanding and applying prebiotics in research and practice – an ISAPP conference paper. <i>Journal of Applied Microbiology</i> , 2020, 128, 934-949.	1.4	85
32	Tetracycline Resistome of the Organic Pig Gut. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1717-1722.	1.4	83
33	Novel Tetracycline Resistance Gene, <i>tet (32)</i> , in the <i>Clostridium</i> -Related Human Colonic Anaerobe K10 and Its Transmission In Vitro to the Rumen Anaerobe <i>Butyrivibrio fibrisolvens</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 3246-3249.	1.4	82
34	Distribution of specific tetracycline and erythromycin resistance genes in environmental samples assessed by microarray detection. <i>Environmental Microbiology</i> , 2007, 9, 703-715.	1.8	82
35	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
36	Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	78

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37	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 (<i>cesA</i>) and AJ272430 (<i>xynE</i>).. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1391-1397.	0.7	78
38	A xylanase produced by the rumen anaerobic protozoan <i>Polyplastron multivesiculatum</i> shows close sequence similarity to family 11 xylanases from Gram-positive bacteria. <i>FEMS Microbiology Letters</i> , 1999, 181, 145-152.	0.7	53
39	Transformation of an oral bacterium via chromosomal integration of free DNA in the presence of human saliva. <i>FEMS Microbiology Letters</i> , 2001, 200, 163-167.	0.7	50
40	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
41	EndB, a Multidomain Family 44 Cellulase from <i>Ruminococcus flavefaciens</i> 17, Binds to Cellulose via a Novel Cellulose-Binding Module and to Another <i>R. flavefaciens</i> Protein via a Dockerin Domain. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4426-4431.	1.4	47
42	Qualitatively distinct patterns of cytokines are released by human dendritic cells in response to different pathogens. <i>Immunology</i> , 2005, 116, 245-254.	2.0	47
43	Can prebiotics and probiotics improve therapeutic outcomes for undernourished individuals?. <i>Gut Microbes</i> , 2014, 5, 74-82.	4.3	47
44	A New Tetracycline Efflux Gene, <i>tet(40)</i> , Is Located in Tandem with <i>tet(O/32/O)</i> in a Human Gut Firmicute Bacterium and in Metagenomic Library Clones. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 4001-4009.	1.4	45
45	Characterization of XYN10B, a modular xylanase from the ruminal protozoan <i>Polyplastron multivesiculatum</i> , with a family 22 carbohydrate-binding module that binds to cellulose. <i>Biochemical Journal</i> , 2003, 373, 495-503.	1.7	44
46	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
47	The green fluorescent protein as a visible marker for lactic acid bacteria in complex ecosystems. <i>FEMS Microbiology Ecology</i> , 1998, 26, 219-230.	1.3	42
48	Chromosomal integration of the green fluorescent protein gene in lactic acid bacteria and the survival of marked strains in human gut simulations. <i>FEMS Microbiology Letters</i> , 2000, 182, 23-27.	0.7	42
49	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
50	Natural genetic transformation in the rumen bacterium <i>Streptococcus bovis</i> JB1. <i>FEMS Microbiology Letters</i> , 1999, 179, 485-490.	0.7	41
51	Tetracycline susceptibility of the ingested <i>Lactobacillus acidophilus</i> LaCH-5 and <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Bb-12 strains during antibiotic/probiotic intervention. <i>International Journal of Antimicrobial Agents</i> , 2007, 29, 271-280.	1.1	40
52	The <i>Butyrivibrio fibrisolvens tet(W)</i> 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
53	Evaluation of novel assays to assess the influence of different iron sources on the growth of <i>Clostridium difficile</i> . <i>Anaerobe</i> , 2012, 18, 298-304.	1.0	35
54	Transfer of plasmids between strains of <i>Escherichia coli</i> under rumen conditions. <i>Journal of Applied Bacteriology</i> , 1995, 78, 189-193.	1.1	34

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55	The agronomic performance and nutritional content of oat and barley varieties grown in a northern maritime environment depends on variety and growing conditions. <i>Journal of Cereal Science</i> , 2017, 74, 1-10.	1.8	34
56	Hybrid tet Genes and tet Gene Nomenclature: Request for Opinion. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 1265-1266.	1.4	33
57	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
58	16S sequencing and functional analysis of the fecal microbiome during treatment of newly diagnosed pediatric inflammatory bowel disease. <i>Medicine (United States)</i> , 2017, 96, e7347.	0.4	30
59	Nutritional influences on the gut microbiota and the consequences for gastrointestinal health. <i>Biochemical Society Transactions</i> , 2011, 39, 1073-1078.	1.6	29
60	Probiotic and prebiotic claims in Europe: seeking a clear roadmap. <i>British Journal of Nutrition</i> , 2011, 106, 1765-1767.	1.2	23
61	Antibiotics and Resistance Genes: Influencing the Microbial Ecosystem in the Gut. <i>Advances in Applied Microbiology</i> , 2007, 62, 269-292.	1.3	15
62	Organisation and Variable Incidence of Genes Concerned with the Utilization of Xylans in the Rumen Cellulolytic Bacterium <i>Ruminococcus flavefaciens</i> . <i>Anaerobe</i> , 2000, 6, 333-340.	1.0	12
63	Changes in the gut microbiota of Nigerian infants within the first year of life. <i>PLoS ONE</i> , 2022, 17, e0265123.	1.1	11
64	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
65	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
66	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
67	Daily Fermented Whey Consumption Alters the Fecal Short-Chain Fatty Acid Profile in Healthy Adults. <i>Frontiers in Nutrition</i> , 2020, 7, 165.	1.6	7
68	The Microbiota of the Human Gastrointestinal Tract. , 2015, , 1-15.		5
69	G116(P)â€¦The human gut is probably sterile at birth. <i>Archives of Disease in Childhood</i> , 2015, 100, A50.3-A51.	1.0	2
70	Chromosomal integration of the green fluorescent protein gene in lactic acid bacteria and the survival of marked strains in human gut simulations. <i>FEMS Microbiology Letters</i> , 2000, 182, 23-27.	0.7	2
71	Conjugation Protocol Optimised for <i>Roseburia inulinivorans</i> and <i>Eubacterium rectale</i> . <i>Bio-protocol</i> , 2020, 10, e3575.	0.2	2
72	Fermentation of oats (<i>Avena sativa</i>) by the faecal microbiota using an <i>in vitro</i> colonic fermentor system. <i>Proceedings of the Nutrition Society</i> , 2015, 74, .	0.4	1

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73	Natural genetic transformation in the rumen bacterium <i>Streptococcus bovis</i> JB1. <i>FEMS Microbiology Letters</i> , 1999, 179, 485-490.	0.7	1
74	The impact of antimicrobials on gut bacteria: an interview with Karen Scott. <i>Future Microbiology</i> , 2019, 14, 1081-1082.	1.0	0
75	Microorganisms in the human gut: Diversity and function. <i>Biochemist</i> , 2011, 33, 4-9.	0.2	0