L Hoyles

List of Publications by Year
in descending order

85 papers	7,772 citations	109137 35 h-index	66788 78 g-index
107 all docs	107 docs citations	107 times ranked	11608 citing authors

#	Article	IF	Citations
1	A hostâ€“gut microbial amino acid co-metabolite, p-cresol glucuronide, promotes bloodâ€“brain barrier integrity in vivo. Tissue Barriers, 2023, 11, .	1.6	15
2	Commentary on: prebiotic effects: metabolic and health benefits. British Journal of Nutrition, 2022, 127, 554-555.	1.2	7
3	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. Gut, 2022, 71, 2463-2480.	6.1	53
4	The microbiotaâ€“gutâ€“brain axis: pathways to better brain health. Perspectives on what we know, what we need to investigate and how to put knowledge into practice. Cellular and Molecular Life Sciences, 2022, 79, 80.	2.4	60
5	ITCH E3 ubiquitin ligase downregulation compromises hepatic degradation of branched-chain amino acids. Molecular Metabolism, 2022, 59, 101454.	3.0	5
6	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	15.2	102
7	Altered immunity to microbiota, B cell activation and depleted Î³Î´/resident memory T cells in colorectal cancer. Cancer Immunology, Immunotherapy, 2022, 71, 2619-2629.	2.0	9
8	O8: DIRECT MANIPULATION OF THE INTESTINAL MICROBIOME TO INFLUENCE POST-OPERATIVE OUTCOMES. British Journal of Surgery, 2021, 108, .	0.1	1
9	Human and preclinical studies of the hostâ€“gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. Gut, 2021, 70, 2105-2114.	6.1	58
10	Iron status influences non-alcoholic fatty liver disease in obesity through the gut microbiome. Microbiome, 2021, 9, 104.	4.9	70
11	Improved molecular characterization of the Klebsiella oxytoca complex reveals the prevalence of the kleboxymycin biosynthetic gene cluster. Microbial Genomics, 2021, 7, .	1.0	10
12	Comparison of PCR versus PCR-Free DNA Library Preparation for Characterising the Human Faecal Virome. Viruses, 2021, 13, 2093.	1.5	9
13	Advancing tools for human early lifecourse exposome research and translation (ATHLETE). Environmental Epidemiology, 2021, 5, e166.	1.4	24
14	An integrated workflow for enhanced taxonomic and functional coverage of the mouse fecal metaproteome. Gut Microbes, 2021, 13, 1994836.	4.3	6
15	Regulation of bloodâ€“brain barrier integrity by microbiome-associated methylamines and cognition by trimethylamine N-oxide. Microbiome, 2021, 9, 235.	4.9	65
16	Combinatorial, additive and dose-dependent drugâ€“microbiome associations. Nature, 2021, 600, 500-505.	13.7	102
17	Deficient Resident Memory T Cell and CD8 T Cell Response to Commensals in Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2020, 14, 525-537.	0.6	60
18	Rapid MinION profiling of preterm microbiota and antimicrobial-resistant pathogens. Nature Microbiology, 2020, 5, 430-442.	5.9	113

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19	Succession of Bifidobacterium longum Strains in Response to a Changing Early Life Nutritional Environment Reveals Dietary Substrate Adaptations. IScience, 2020, 23, 101368.	1.9	26
20	Genome Characterization of a Novel Wastewater Bacteroides fragilis Bacteriophage (vB_BfrS_23) and its Host GB124. Frontiers in Microbiology, 2020, 11, 583378.	1.5	5
21	A Two-Way Interaction between Methotrexate and the Gut Microbiota of Male Sprague–Dawley Rats. Journal of Proteome Research, 2020, 19, 3326-3339.	1.8	35
22	Bacteroides thetaiotaomicron-derived outer membrane vesicles promote regulatory dendritic cell responses in health but not in inflammatory bowel disease. Microbiome, 2020, 8, 88.	4.9	76
23	The APOA1bp–SREBF–NOTCH axis is associated with reduced atherosclerosis risk in morbidly obese patients. Clinical Nutrition, 2020, 39, 3408-3418.	2.3	7
24	Bacteriophages of spp., their diversity and potential therapeutic uses. Journal of Medical Microbiology, 2020, 69, 176-194.	0.7	49
25	Preterm infants harbour diverse Klebsiella populations, including atypical species that encode and produce an array of antimicrobial resistance- and virulence-associated factors. Microbial Genomics, 2020, 6, .	1.0	35
26	Faecal microbiota transplant from aged donor mice affects spatial learning and memory via modulating hippocampal synaptic plasticity- and neurotransmission-related proteins in young recipients. Microbiome, 2020, 8, 140.	4.9	134
27	Gastrointestinal Tract: Fat Metabolism in the Colon. , 2020, , 359-367.		0
28	Gastrointestinal Tract: Intestinal Fatty Acid Metabolism and Implications for Health. , 2020, , 369-387.		0
29	Batch effect exerts a bigger influence on the rat urinary metabolome and gut microbiota than uraemia: a cautionary tale. Microbiome, 2019, 7, 127.	4.9	17
30	Draft Genome Sequences of Citrobacter freundii and Citrobacter murliniae Strains Isolated from the Feces of Preterm Infants. Microbiology Resource Announcements, 2019, 8, .	0.3	6
31	Influence of the Human Gut Microbiome on the Metabolic Phenotype. , 2019, , 535-560.		13
32	Gastrointestinal Tract: Intestinal Fatty Acid Metabolism and Implications for Health. , 2019, , 1-19.		1
33	Gastrointestinal Tract: Fat Metabolism in the Colon. , 2019, , 1-9.		0
34	Draft Genome Sequence of Raoultella ornithinolytica P079F W, Isolated from the Feces of a Preterm Infant. Microbiology Resource Announcements, 2019, 8, .	0.3	2
35	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota. Microbiome, 2018, 6, 73.	4.9	127
36	Molecular phenomics and metagenomics of hepatic steatosis in non-diabetic obese women. Nature Medicine, 2018, 24, 1070-1080.	15.2	465

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37	Microbiomeâ€“host systems interactions: protective effects of propionate upon the bloodâ€“brain barrier. Microbiome, 2018, 6, 55.	4.9	324
38	A Data Integration Multi-Omics Approach to Study Calorie Restriction-Induced Changes in Insulin Sensitivity. Frontiers in Physiology, 2018, 9, 1958.	1.3	39
39	Review article: the human intestinal virome in health and disease. Alimentary Pharmacology and Therapeutics, 2017, 46, 800-815.	1.9	187
40	Microbial-Host Co-metabolites Are Prodromal Markers Predicting Phenotypic Heterogeneity in Behavior, Obesity, and Impaired Glucose Tolerance. Cell Reports, 2017, 20, 136-148.	2.9	78
41	Kroppenstedtia pulmonis sp. nov. and Kroppenstedtia sanguinis sp. nov., isolated from human patients. Antonie Van Leeuwenhoek, 2016, 109, 603-610.	0.7	12
42	Akkermansia muciniphilaand improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. Gut, 2016, 65, 426-436.	6.1	1,379
43	Dynamics and diversity of the â€˜Atopobium cluster' in the human faecal microbiota, and phenotypic characterization of â€˜Atopobium cluster' isolates. Microbiology (United Kingdom), 2015, 161, 565-579.	0.7	22
44	Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome. Cell Metabolism, 2015, 22, 320-331.	7.2	345
45	Klebsiella pneumoniaesubsp.pneumoniaeâ€“bacteriophage combination from the caecal effluent of a healthy woman. PeerJ, 2015, 3, e1061.	0.9	38
46	Characterization of virus-like particles associated with the human faecal and caecal microbiota. Research in Microbiology, 2014, 165, 803-812.	1.0	169
47	Colonic bacterial metabolites and human health. Current Opinion in Microbiology, 2013, 16, 246-254.	2.3	293
48	Biodiversity of lactococcal bacteriophages isolated from 3 Gouda-type cheese-producing plants. Journal of Dairy Science, 2013, 96, 4945-4957.	1.4	42
49	Corynebacterium uterequi sp. nov., a non-lipophilic bacterium isolated from urogenital samples from horses. Veterinary Microbiology, 2013, 165, 469-474.	0.8	16
50	Use of denaturing gradient gel electrophoresis to detect Actinobacteria associated with the human faecal microbiota. Anaerobe, 2013, 22, 90-96.	1.0	12
51	Recognition of greater diversity of Bacillus species and related bacteria in human faeces. Research in Microbiology, 2012, 163, 3-13.	1.0	53
52	Investigation of the impact of feeding Lactobacillus plantarum CRL 1815 encapsulated in microbially derived polymers on the rat faecal microbiota. Journal of Applied Microbiology, 2012, 113, 399-410.	1.4	7
53	Isolation of Actinomyces hyovaginalis from sheep and comparison with isolates obtained from pigs. Veterinary Microbiology, 2012, 157, 471-475.	0.8	7
54	In vitro fermentation of rice bran combined with Lactobacillus acidophilus 14 150B or Bifidobacterium longum 05 by the canine faecal microbiota. FEMS Microbiology Ecology, 2011, 75, 365-376.	1.3	17

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55	Evaluation of the inclusion of a mixture of organic acids or lactulose into the feed of pigs experimentally challenged with Salmonella Typhimurium. Veterinary Microbiology, 2010, 142, 337-345.	0.8	36
56	Prebiotic effects: metabolic and health benefits. British Journal of Nutrition, 2010, 104, S1-S63.	1.2	1,745
57	Examination of faecal Bifidobacterium populations in breast- and formula-fed infants during the first 18 months of life. Microbiology (United Kingdom), 2010, 156, 3329-3341.	0.7	244
58	Gastrointestinal Tract: Intestinal Fatty Acid Metabolism and Implications for Health. , 2010, , 3119-3132.		9
59	Gastrointestinal Tract: Fat Metabolism in the Colon. , 2010, , 3111-3118.		1
60	What do we mean when we refer toBacteroidetesÃ¢Â€Âƒpopulations in the human gastrointestinal microbiota?. FEMS Microbiology Letters, 2009, 299, 175-183.	0.7	39
61	Diet, Immunity and Functional Foods. Advances in Experimental Medicine and Biology, 2008, 635, 79-92.	0.8	25
62	Survivability of a probiotic Lactobacillus casei in the gastrointestinal tract of healthy human volunteers and its impact on the faecal microflora. Journal of Applied Microbiology, 2006, 102, 061120055200066-???.	1.4	63
63	â€˜List of Changes in Taxonomic Opinionâ€™: making use of the new lists. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1429-1430.	0.8	7
64	Corynebacterium caspium sp. nov., from a Caspian seal (Phoca caspica). International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 925-928.	0.8	71
65	Jeotgalicoccus pinnipedialis sp. nov., from a southern elephant seal (Mirounga leonina). International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 745-748.	0.8	23
66	Transfer of Members of the Genus Falcivibrio to the Genus Mobiluncus, and Emended Description of the Genus Mobiluncus. Systematic and Applied Microbiology, 2004, 27, 72-83.	1.2	42
67	Bifidobacterium scardovii sp. nov., from human sources. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 995-999.	0.8	28
68	Actinomyces coleocanis sp. nov., from the vagina of a dog. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1201-1203.	0.8	16
69	Arthrobacter nasiphocae sp. nov., from the common seal (Phoca vitulina).. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 569-571.	0.8	23
70	Arcanobacterium hippocoleae sp. nov., from the vagina of a horse.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 617-619.	0.8	31
71	Characterization of some Strains from Human Clinical Sources which resemble â€œLeptotrichia sanguinegensâ€ Description of Sneathia sanguinegens sp. nov., gen. nov.. Systematic and Applied Microbiology, 2001, 24, 358-361.	1.2	57
72	Streptococcus ovis sp. nov., isolated from sheep.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 1147-1150.	0.8	31

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73	Corynebacterium capitovis sp. nov., from a sheep.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 857-860.	0.8	25
74	Actinomyces marimammalium sp. nov., from marine mammals.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 151-156.	0.8	29
75	Actinomyces catuli sp. nov., from dogs.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 679-682.	0.8	17
76	Actinomyces suimastitidis sp. nov., isolated from pig mastitis.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 1323-1326.	0.8	25
77	Corynebacterium testudinoris sp. nov., from a tortoise, and Corynebacterium felinum sp. nov., from a Scottish wild cat.. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 1349-1352.	0.8	40
78	Facklamia miroungae sp. nov., from a juvenile southern elephant seal (Mirounga leonina).. International Journal of Systematic and Evolutionary Microbiology, 2001, 51, 1401-1403.	0.8	21
79	Arcanobacterium/Corynebacterium-like bacterial isolates from sheep. Veterinary Record, 2001, 148, 284.	0.2	0
80	Vagococcus fessus sp. nov., isolated from a seal and a harbour porpoise.. International Journal of Systematic and Evolutionary Microbiology, 2000, 50, 1151-1154.	0.8	30
81	Characterization of Actinomyces isolates from samples from the human urogenital tract: description of Actinomyces urogenitalis sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2000, 50, 1649-1654.	0.8	51
82	Actinomyces canis sp. nov., isolated from dogs.. International Journal of Systematic and Evolutionary Microbiology, 2000, 50, 1547-1551.	0.8	31
83	Characterization of a Gemella-like organism isolated from an abscess of a rabbit: description of Gemella cunicula sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2000, 50, 2037-2041.	0.8	34
84	Characterization of Actinomyces Isolates from Infected Root Canals of Teeth: Description of Actinomyces radicidentis sp. nov.. Journal of Clinical Microbiology, 2000, 38, 3399-3403.	1.8	60
85	Phenotypic and Phylogenetic Characterization of a New Corynebacterium Species from Dogs: Description of Corynebacterium auriscanis sp. nov. Journal of Clinical Microbiology, 1999, 37, 3443-3447.	1.8	40