Julian Marchesi

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62 19,883 140 209 h-index g-index citations papers 6.89 24,386 225 7.5 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
209	Gut microbiota composition correlates with diet and health in the elderly. <i>Nature</i> , 2012 , 488, 178-84	50.4	1987
208	Design and evaluation of useful bacterium-specific PCR primers that amplify genes coding for bacterial 16S rRNA. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 795-9	4.8	1211
207	The gut microbiota and host health: a new clinical frontier. <i>Gut</i> , 2016 , 65, 330-9	19.2	1182
206	Composition, variability, and temporal stability of the intestinal microbiota of the elderly. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108 Suppl 1, 4586	5- 5 4-5	1105
205	Early life stress alters behavior, immunity, and microbiota in rats: implications for irritable bowel syndrome and psychiatric illnesses. <i>Biological Psychiatry</i> , 2009 , 65, 263-7	7.9	781
204	Comparative analysis of pyrosequencing and a phylogenetic microarray for exploring microbial community structures in the human distal intestine. <i>PLoS ONE</i> , 2009 , 4, e6669	3.7	606
203	Functional and comparative metagenomic analysis of bile salt hydrolase activity in the human gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 13580-5	11.5	565
202	The composition of the gut microbiota throughout life, with an emphasis on early life. <i>Microbial Ecology in Health and Disease</i> , 2015 , 26, 26050		505
201	The vocabulary of microbiome research: a proposal. <i>Microbiome</i> , 2015 , 3, 31	16.6	500
200	A bacterial driver-passenger model for colorectal cancer: beyond the usual suspects. <i>Nature Reviews Microbiology</i> , 2012 , 10, 575-82	22.2	475
199	Rapid and noninvasive metabonomic characterization of inflammatory bowel disease. <i>Journal of Proteome Research</i> , 2007 , 6, 546-51	5.6	456
198	Diversity of bifidobacteria within the infant gut microbiota. <i>PLoS ONE</i> , 2012 , 7, e36957	3.7	415
197	Towards the human colorectal cancer microbiome. <i>PLoS ONE</i> , 2011 , 6, e20447	3.7	384
196	Gut microbiota modulation of chemotherapy efficacy and toxicity. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2017 , 14, 356-365	24.2	382
195	Metabolic surgery profoundly influences gut microbial-host metabolic cross-talk. <i>Gut</i> , 2011 , 60, 1214-23	319.2	319
194	Next-generation probiotics: the spectrum from probiotics to live biotherapeutics. <i>Nature Microbiology</i> , 2017 , 2, 17057	26.6	317
193	Gut microbiota composition and activity in relation to host metabolic phenotype and disease risk. <i>Cell Metabolism</i> , 2012 , 16, 559-64	24.6	316

(2009-2015)

192	The vaginal microbiome during pregnancy and the postpartum period in a European population. <i>Scientific Reports</i> , 2015 , 5, 8988	4.9	288
191	Culture-independent analyses of temporal variation of the dominant fecal microbiota and targeted bacterial subgroups in Crohnß disease. <i>Journal of Clinical Microbiology</i> , 2006 , 44, 3980-8	9.7	237
190	Micro-eukaryotic diversity of the human distal gut microbiota: qualitative assessment using culture-dependent and -independent analysis of faeces. <i>ISME Journal</i> , 2008 , 2, 1183-93	11.9	229
189	A molecular analysis of fecal and mucosal bacterial communities in irritable bowel syndrome. <i>Digestive Diseases and Sciences</i> , 2010 , 55, 392-7	4	200
188	The human urinary microbiome; bacterial DNA in voided urine of asymptomatic adults. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013 , 3, 41	5.9	199
187	Culture-independent analysis of the gut microbiota in colorectal cancer and polyposis. <i>Environmental Microbiology</i> , 2008 , 10, 789-98	5.2	193
186	Cervical intraepithelial neoplasia disease progression is associated with increased vaginal microbiome diversity. <i>Scientific Reports</i> , 2015 , 5, 16865	4.9	191
185	Disturbance of the gut microbiota in early-life selectively affects visceral pain in adulthood without impacting cognitive or anxiety-related behaviors in male rats. <i>Neuroscience</i> , 2014 , 277, 885-901	3.9	185
184	Metabonomic and microbiological analysis of the dynamic effect of vancomycin-induced gut microbiota modification in the mouse. <i>Journal of Proteome Research</i> , 2008 , 7, 3718-28	5.6	185
183	The interaction between vaginal microbiota, cervical length, and vaginal progesterone treatment for preterm birth risk. <i>Microbiome</i> , 2017 , 5, 6	16.6	180
182	Desulfovibrio profundus sp. nov., a novel barophilic sulfate-reducing bacterium from deep sediment layers in the Japan Sea. <i>International Journal of Systematic Bacteriology</i> , 1997 , 47, 515-21		175
181	The vaginal microbiota, human papillomavirus infection and cervical intraepithelial neoplasia: what do we know and where are we going next?. <i>Microbiome</i> , 2016 , 4, 58	16.6	170
180	Marine metagenomics: strategies for the discovery of novel enzymes with biotechnological applications from marine environments. <i>Microbial Cell Factories</i> , 2008 , 7, 27	6.4	159
179	Colonic mucosa-associated diffusely adherent afaC+ Escherichia coli expressing lpfA and pks are increased in inflammatory bowel disease and colon cancer. <i>Gut</i> , 2014 , 63, 761-70	19.2	157
178	Species variation in the fecal metabolome gives insight into differential gastrointestinal function. Journal of Proteome Research, 2008 , 7, 352-60	5.6	156
177	Methanogen and bacterial diversity and distribution in deep gas hydrate sediments from the Cascadia Margin as revealed by 16S rRNA molecular analysis. <i>FEMS Microbiology Ecology</i> , 2001 , 34, 221-	2 2 8	141
176	The gut microbiome: the role of a virtual organ in the endocrinology of the host. <i>Journal of Endocrinology</i> , 2013 , 218, R37-47	4.7	140
175	Isolation and analysis of bacteria with antimicrobial activities from the marine sponge Haliclona simulans collected from Irish waters. <i>Marine Biotechnology</i> , 2009 , 11, 384-96	3.4	139

174	Host-microbiota interactions: from holobiont theory to analysis. <i>Microbiome</i> , 2019 , 7, 5	16.6	136
173	Dietary supplementation with inulin-propionate ester or inulin improves insulin sensitivity in adults with overweight and obesity with distinct effects on the gut microbiota, plasma metabolome and systemic inflammatory responses: a randomised cross-over trial. <i>Gut</i> , 2019 , 68, 1430-1438	19.2	134
172	Human methanogen diversity and incidence in healthy and diseased colonic groups using mcrA gene analysis. <i>BMC Microbiology</i> , 2008 , 8, 79	4.5	129
171	Vaginal dysbiosis increases risk of preterm fetal membrane rupture, neonatal sepsis and is exacerbated by erythromycin. <i>BMC Medicine</i> , 2018 , 16, 9	11.4	122
170	Microbiomic analysis of the bifidobacterial population in the human distal gut. <i>ISME Journal</i> , 2009 , 3, 745-51	11.9	111
169	Differences in fungi present in induced sputum samples from asthma patients and non-atopic controls: a community based case control study. <i>BMC Infectious Diseases</i> , 2013 , 13, 69	4	106
168	Long term effect of gut microbiota transfer on diabetes development. <i>Journal of Autoimmunity</i> , 2014 , 53, 85-94	15.5	105
167	Interactions between multiple helminths and the gut microbiota in wild rodents. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370,	5.8	102
166	International Cancer Microbiome Consortium consensus statement on the role of the human microbiome in carcinogenesis. <i>Gut</i> , 2019 , 68, 1624-1632	19.2	101
165	Microbial bile salt hydrolases mediate the efficacy of faecal microbiota transplant in the treatment of recurrent infection. <i>Gut</i> , 2019 , 68, 1791-1800	19.2	100
164	The normal intestinal microbiota. <i>Current Opinion in Infectious Diseases</i> , 2007 , 20, 508-13	5.4	97
163	Optimized Sample Handling Strategy for Metabolic Profiling of Human Feces. <i>Analytical Chemistry</i> , 2016 , 88, 4661-8	7.8	97
162	Metagenomic approaches to exploit the biotechnological potential of the microbial consortia of marine sponges. <i>Applied Microbiology and Biotechnology</i> , 2007 , 75, 11-20	5.7	93
161	Relationship between vaginal microbial dysbiosis, inflammation, and pregnancy outcomes in cervical cerclage. <i>Science Translational Medicine</i> , 2016 , 8, 350ra102	17.5	92
160	Transposon-aided capture (TRACA) of plasmids resident in the human gut mobile metagenome. <i>Nature Methods</i> , 2007 , 4, 55-61	21.6	90
159	Culture-independent analysis of desulfovibrios in the human distal colon of healthy, colorectal cancer and polypectomized individuals. <i>FEMS Microbiology Ecology</i> , 2009 , 69, 213-21	4.3	87
158	Effects of Fecal Microbiota Transplantation With Oral Capsules in Obese Patients. <i>Clinical Gastroenterology and Hepatology</i> , 2020 , 18, 855-863.e2	6.9	87
157	Mobile genetic elements of the human gastrointestinal tract: potential for spread of antibiotic resistance genes. <i>Gut Microbes</i> , 2013 , 4, 271-80	8.8	86

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The life history of Lactobacillus acidophilus as a probiotic: a tale of revisionary taxonomy, misidentification and commercial success. <i>FEMS Microbiology Letters</i> , 2013 , 349, 77-87	2.9	84
Fecal Microbiota Transplantation in Patients With Primary Sclerosing Cholangitis: A Pilot Clinical Trial. <i>American Journal of Gastroenterology</i> , 2019 , 114, 1071-1079	0.7	82
Metagenomics and novel gene discovery: promise and potential for novel therapeutics. <i>Virulence</i> , 2014 , 5, 399-412	4.7	8o
Investigation of two evolutionarily unrelated halocarboxylic acid dehalogenase gene families. <i>Journal of Bacteriology</i> , 1999 , 181, 2535-47	3.5	80
Diversity of microbes associated with the marine sponge, Haliclona simulans, isolated from Irish waters and identification of polyketide synthase genes from the sponge metagenome. <i>Environmental Microbiology</i> , 2008 , 10, 1888-902	5.2	75
Degradation of 1,2-dibromoethane by Mycobacterium sp. strain GP1. <i>Journal of Bacteriology</i> , 1999 , 181, 2050-8	3.5	74
Prokaryotic and eukaryotic diversity of the human gut. Advances in Applied Microbiology, 2010, 72, 43-62	4.9	73
Inhibiting Growth of Clostridioides difficile by Restoring Valerate, Produced by the Intestinal Microbiota. <i>Gastroenterology</i> , 2018 , 155, 1495-1507.e15	13.3	70
Human distal gut microbiome. <i>Environmental Microbiology</i> , 2011 , 13, 3088-102	5.2	66
Rapid Detection of Emerging Pathogens and Loss of Microbial Diversity Associated with Severe Lung Disease in Cystic Fibrosis. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 2022-9	9.7	60
Phylogenetic diversity and antimicrobial activities of fungi associated with Haliclona simulans isolated from Irish coastal waters. <i>Marine Biotechnology</i> , 2009 , 11, 540-7	3.4	60
Dietary cholesterol directly induces acute inflammasome-dependent intestinal inflammation. <i>Nature Communications</i> , 2014 , 5, 5864	17.4	58
Haloalkane-utilizing Rhodococcus strains isolated from geographically distinct locations possess a highly conserved gene cluster encoding haloalkane catabolism. <i>Journal of Bacteriology</i> , 2000 , 182, 2725	-3:₽	58
Establishment of vaginal microbiota composition in early pregnancy and its association with subsequent preterm prelabor rupture of the fetal membranes. <i>Translational Research</i> , 2019 , 207, 30-43	11	58
Microbiota- and Radiotherapy-Induced Gastrointestinal Side-Effects (MARS) Study: A Large Pilot Study of the Microbiome in Acute and Late-Radiation Enteropathy. <i>Clinical Cancer Research</i> , 2019 , 25, 6487-6500	12.9	56
Experimental bariatric surgery in rats generates a cytotoxic chemical environment in the gut contents. <i>Frontiers in Microbiology</i> , 2011 , 2, 183	5.7	56
The microbiota and autoimmunity: Their role in thyroid autoimmune diseases. <i>Clinical Immunology</i> , 2017 , 183, 63-74	9	54
Comparative metagenomic analysis of plasmid encoded functions in the human gut microbiome. <i>BMC Genomics</i> , 2010 , 11, 46	4.5	49
	misidentification and commercial success. FEMS Microbiology Letters, 2013, 349, 77-87 Fecal Microbiota Transplantation in Patients With Primary Sclerosing Cholangitis: A Pilot Clinical Trial. American Journal of Gastroenterology, 2019, 114, 1071-1079 Metagenomics and novel gene discovery: promise and potential for novel therapeutics. Virulence, 2014, 5, 399-412 Investigation of two evolutionarily unrelated halocarboxylic acid dehalogenase gene families. Journal of Bacteriology, 1999, 181, 2535-47 Journal of Bacteriology, 1999, 181, 2535-47 Journal of Bacteriology, 1999, 181, 2535-47 Diversity of microbes associated with the marine sponge, Haliclona simulans, isolated from Irish waters and identification of polyketide synthase genes from the sponge metagenome. Environmental Microbiology, 2008, 10, 1888-902 Degradation of 1,2-dibromoethane by Mycobacterium sp. strain GP1. Journal of Bacteriology, 1999, 181, 2050-8 Prokaryotic and eukaryotic diversity of the human gut. Advances in Applied Microbiology, 2010, 72, 43-62 Inhibiting Growth of Clostridioides difficile by Restoring Valerate, Produced by the Intestinal Microbiota. Gastroenterology, 2018, 155, 1495-1507.e15 Human distal gut microbiome. Environmental Microbiology, 2011, 13, 3088-102 Rapid Detection of Emerging Pathogens and Loss of Microbial Diversity Associated with Severe Lung Disease in Cystic Fibrosis. Journal of Clinical Microbiology, 2015, 53, 2022-9 Phylogenetic diversity and antimicrobial activities of fungi associated with Haliclona simulans isolated from Irish coastal waters. Marine Biotechnology, 2009, 11, 540-7 Dietary cholesterol directly induces acute inflammasome-dependent intestinal inflammation. Nature Communications, 2014, 5, 5864 Haloalkane-utilizing Rhodococcus strains isolated from geographically distinct locations possess a highly conserved gene cluster encoding haloalkane catabolism. Journal of Bacteriology, 2000, 182, 2725 Establishment of vaginal microbiota composition in early pregnancy and its association with subs	misidentification and commercial success. FEMS Microbiology Letters, 2013, 349, 77-87 Fecal Microbiota Transplantation in Patients With Primary Sclerosing Cholangitis: A Pilot Clinical Trial. American Journal of Gastroenterology, 2019, 114, 1071-1079 Metagenomics and novel gene discovery: promise and potential for novel therapeutics. Virulence, 2014, 5, 399-412 Investigation of two evolutionarily unrelated halocarboxylic acid dehalogenase gene families. Journal of Bacteriology, 1999, 181, 2535-47 Diversity of microbes associated with the marine sponge, Haliclona simulans, isolated from Irish waters and identification of polyketide synthase genes from the sponge metagenome. Environmental Microbiology, 2008, 10, 1888-902 Degradation of 1,2-dibromoethane by Mycobacterium sp. strain GP1. Journal of Bacteriology, 1999, 181, 2050-8 Prokaryotic and eukaryotic diversity of the human gut. Advances in Applied Microbiology, 2010, 72, 43-624-9 Inhibiting Growth of Clostridioides difficile by Restoring Valerate, Produced by the Intestinal Microbiota. Gastroenterology, 2013, 155, 1495-1507.e15 133 Human distal gut microbiome. Environmental Microbiology, 2011, 13, 3088-102 5.2 Rapid Detection of Emerging Pathogens and Loss of Microbial Diversity Associated with Severe Lung Disease in Cystic Fibrosis. Journal of Clinical Microbiology, 2015, 53, 2022-9 Phylogenetic diversity and antimicrobial activities of fungi associated with Haliclona simulans isolated from Irish coastal waters. Marine Biotechnology, 2009, 11, 540-7 Dietary cholesterol directly induces acute inflammasome-dependent intestinal inflammation. Nature Communications, 2014, 5, 5864 Haloalkane-utilizing Rhodococcus strains isolated from geographically distinct locations possess a highly conserved gene cluster encoding haloalkane catabolism. Journal of Bacteriology, 2000, 182, 2725-347 Establishment of vaginal microbiota composition in early pregnancy and its association with subsequent preterm prelabor rupture of the fetal membranes. Translational Res

138	Antibiotic therapy and outcome from immune-checkpoint inhibitors 2019 , 7, 287		48
137	Network analysis of gut microbiota literature: an overview of the research landscape in non-human animal studies. <i>ISME Journal</i> , 2017 , 11, 2644-2651	11.9	47
136	The vaginal microbiota associates with the regression of untreated cervical intraepithelial neoplasia 2 lesions. <i>Nature Communications</i> , 2020 , 11, 1999	17.4	45
135	Functional microbiomics: Evaluation of gut microbiota-bile acid metabolism interactions in health and disease. <i>Methods</i> , 2018 , 149, 49-58	4.6	44
134	Isolation of sulfate-reducing bacteria from deep sediment layers of the pacific ocean. <i>Geomicrobiology Journal</i> , 1998 , 15, 67-83	2.5	44
133	Functional metagenomics reveals novel salt tolerance loci from the human gut microbiome. <i>ISME Journal</i> , 2012 , 6, 1916-25	11.9	43
132	Degradation of 4-fluorophenol by Arthrobacter sp. strain IF1. <i>Applied Microbiology and Biotechnology</i> , 2008 , 78, 709-17	5.7	43
131	The anti-cholesterolaemic effect of a consortium of probiotics: An acute study in C57BL/6J mice. <i>Scientific Reports</i> , 2017 , 7, 2883	4.9	42
130	Gut microbiota, chemotherapy and the host: the influence of the gut microbiota on cancer treatment. <i>Ecancermedicalscience</i> , 2018 , 12, 868	2.7	42
129	Long-term multi-species Lactobacillus and Bifidobacterium dietary supplement enhances memory and changes regional brain metabolites in middle-aged rats. <i>Neurobiology of Learning and Memory</i> , 2017 , 144, 36-47	3.1	41
128	The association between vaginal bacterial composition and miscarriage: a nested case-control study. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2020 , 127, 264-274	3.7	39
127	Effects of surfactant adsorption and biodegradability on the distribution of bacteria between sediments and water in a freshwater microcosm. <i>Applied and Environmental Microbiology</i> , 1991 , 57, 250	7 ⁴ 183	38
126	Segregation of the Anodic Microbial Communities in a Microbial Fuel Cell Cascade. <i>Frontiers in Microbiology</i> , 2016 , 7, 699	5.7	37
125	The application of omics techniques to understand the role of the gut microbiota in inflammatory bowel disease. <i>Therapeutic Advances in Gastroenterology</i> , 2019 , 12, 1756284818822250	4.7	36
124	Using skimmed milk agar to functionally screen a gut metagenomic library for proteases may lead to false positives. <i>Letters in Applied Microbiology</i> , 2007 , 45, 418-20	2.9	34
123	SDS-degrading bacteria attach to riverine sediment in response to the surfactant or its primary biodegradation product dodecan-1-ol. <i>Microbiology (United Kingdom)</i> , 1994 , 140 (Pt 11), 2999-3006	2.9	34
122	A comparative study of the adsorption of linear alkyl sulphates and alkylbenzene sulphonates on river sediments. <i>Colloids and Surfaces</i> , 1991 , 53, 63-78		33
121	Gut microbiota in experimental murine model of GravesRorbitopathy established in different environments may modulate clinical presentation of disease. <i>Microbiome</i> , 2018 , 6, 97	16.6	32

120	Gut microbiome in chronic rheumatic and inflammatory bowel diseases: Similarities and differences. <i>United European Gastroenterology Journal</i> , 2019 , 7, 1008-1032	5.3	32
119	Comparing the dehalogenase gene pool in cultivated alpha-halocarboxylic acid-degrading bacteria with the environmental metagene pool. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 4375-82	4.8	32
118	Age and microenvironment outweigh genetic influence on the Zucker rat microbiome. <i>PLoS ONE</i> , 2014 , 9, e100916	3.7	32
117	Faecal microbiota transplantation for recurrent infection: An updated systematic review and meta-analysis. <i>EClinicalMedicine</i> , 2020 , 29-30, 100642	11.3	31
116	Commensal Bacteroidetes protect against Klebsiella pneumoniae colonization and transmission through IL-36 signalling. <i>Nature Microbiology</i> , 2020 , 5, 304-313	26.6	30
115	Modeling of Bile Acid Processing by the Human Fecal Microbiota. <i>Frontiers in Microbiology</i> , 2018 , 9, 1153	3 5.7	29
114	The urinary microbiome and its contribution to lower urinary tract symptoms; ICI-RS 2015. <i>Neurourology and Urodynamics</i> , 2017 , 36, 850-853	2.3	28
113	A randomised controlled study shows supplementation of overweight and obese adults with lactobacilli and bifidobacteria reduces bodyweight and improves well-being. <i>Scientific Reports</i> , 2020 , 10, 4183	4.9	27
112	Metabonomics and the Gut Microbiome Associated With Primary Response to Anti-TNF Therapy in Crohnß Disease. <i>Journal of Crohnls and Colitis</i> , 2020 , 14, 1090-1102	1.5	27
111	Prospective observational study of vaginal microbiota pre- and post-rescue cervical cerclage. <i>BJOG:</i> an International Journal of Obstetrics and Gynaecology, 2019 , 126, 916-925	3.7	26
110	A prospective analysis of mucosal microbiome-metabonome interactions in colorectal cancer using a combined MAS 1HNMR and metataxonomic strategy. <i>Scientific Reports</i> , 2017 , 7, 8979	4.9	25
109	The gut microbiome: an under-recognised contributor to the COVID-19 pandemic?. <i>Therapeutic Advances in Gastroenterology</i> , 2020 , 13, 1756284820974914	4.7	25
108	Gut Microbiome in BALB/c and C57BL/6J Mice Undergoing Experimental Thyroid Autoimmunity Associate with Differences in Immunological Responses and Thyroid Function. <i>Hormone and Metabolic Research</i> , 2018 , 50, 932-941	3.1	24
107	Functional environmental screening of a metagenomic library identifies stlA; a unique salt tolerance locus from the human gut microbiome. <i>PLoS ONE</i> , 2013 , 8, e82985	3.7	24
106	Effective fecal microbiota transplantation for recurrent Clostridioides difficile infection in humans is associated with increased signalling in the bile acid-farnesoid X receptor-fibroblast growth factor pathway. <i>Gut Microbes</i> , 2019 , 10, 142-148	8.8	24
105	Swallowable capsule technology: current perspectives and future directions. <i>Endoscopy</i> , 2009 , 41, 357-6	3 .4	23
104	Rifaximin in non-alcoholic steatohepatitis: An open-label pilot study. <i>Hepatology Research</i> , 2018 , 48, 69-	757. 1	22
103	Faecal microbiota transplant: a novel biological approach to extensively drug-resistant organism-related non-relapse mortality. <i>Bone Marrow Transplantation</i> , 2017 , 52, 1452-1454	4.4	22

102	The domestication of the probiotic bacterium Lactobacillus acidophilus. <i>Scientific Reports</i> , 2014 , 4, 7202	4.9	22
101	Accessing the mobile metagenome of the human gut microbiota. <i>Molecular BioSystems</i> , 2007 , 3, 749-58		21
100	Metagenomic identification of a novel salt tolerance gene from the human gut microbiome which encodes a membrane protein with homology to a brp/blh-family Etarotene 15,15Rmonooxygenase. <i>PLoS ONE</i> , 2014 , 9, e103318	3.7	20
99	Combined metagenomic and phenomic approaches identify a novel salt tolerance gene from the human gut microbiome. <i>Frontiers in Microbiology</i> , 2014 , 5, 189	5.7	18
98	Microbial profiling of dental plaque from mechanically ventilated patients. <i>Journal of Medical Microbiology</i> , 2016 , 65, 147-159	3.2	18
97	Effect of the chemical composition of filter media on the microbial community in wastewater biofilms at different temperatures. <i>RSC Advances</i> , 2016 , 6, 104345-104353	3.7	18
96	Disease Prevention Not Decolonization: A Model for Fecal Microbiota Transplantation in Patients Colonized With Multidrug-resistant Organisms. <i>Clinical Infectious Diseases</i> , 2021 , 72, 1444-1447	11.6	18
95	Colorectal carcinogenesis: an archetype of gut microbiota-host interaction. <i>Ecancermedicalscience</i> , 2018 , 12, 865	2.7	18
94	Enhanced Microbial Bile Acid Deconjugation and Impaired Ileal Uptake in Pregnancy Repress Intestinal Regulation of Bile Acid Synthesis. <i>Hepatology</i> , 2019 , 70, 276-293	11.2	17
93	A robust plate assay for detection of extracellular microbial protease activity in metagenomic screens and pure cultures. <i>Journal of Microbiological Methods</i> , 2012 , 91, 144-6	2.8	16
92	The Bacteroidales produce an N-acylated derivative of glycine with both cholesterol-solubilising and hemolytic activity. <i>Scientific Reports</i> , 2017 , 7, 13270	4.9	15
91	Mining the human gut microbiome for novel stress resistance genes. <i>Gut Microbes</i> , 2012 , 3, 394-7	8.8	15
90	Bacterial cell hydrophobicity is modified during the biodegradation of anionic surfactants. <i>FEMS Microbiology Letters</i> , 1994 , 124, 387-392	2.9	15
89	A natural mutation in Pisum sativum L. (pea) alters starch assembly and improves glucose homeostasis in humans. <i>Nature Food</i> , 2020 , 1, 693-704	14.4	15
88	Evaluation of Direct from Sample Metabolomics of Human Feces Using Rapid Evaporative Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2019 , 91, 13448-13457	7.8	14
87	Inflammatory Bowel Disease Outcomes Following Fecal Microbiota Transplantation for Recurrent C. difficile Infection. <i>Inflammatory Bowel Diseases</i> , 2021 , 27, 1371-1378	4.5	14
86	Comparison of vaginal microbiota sampling techniques: cytobrush versus swab. <i>Scientific Reports</i> , 2017 , 7, 9802	4.9	14
85	Systemic Characterization of an Obese Phenotype in the Zucker Rat Model Defining Metabolic Axes of Energy Metabolism and Host-Microbial Interactions. <i>Journal of Proteome Research</i> , 2016 , 15, 1897-90	ē.6	14

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84	Autotaxin, bile acid profile and effect of ileal bile acid transporter inhibition in primary biliary cholangitis patients with pruritus. <i>Liver International</i> , 2019 , 39, 967-975	7.9	13
83	Assessing the impact of long term frozen storage of faecal samples on protein concentration and protease activity. <i>Journal of Microbiological Methods</i> , 2016 , 123, 31-8	2.8	13
82	Fecal microbiota transplant from a rational stool donor improves hepatic encephalopathy: A randomized clinical trial. <i>Hepatology</i> , 2017 , 66, 1354-1355	11.2	13
81	Endoglucanase activities and growth of marine-derived fungi isolated from the sponge Haliclona simulans. <i>Journal of Applied Microbiology</i> , 2010 , 108, 1668-75	4.7	13
8o	Metabolic, immune, and gut microbial signals mount a systems response to Leishmania major infection. <i>Journal of Proteome Research</i> , 2015 , 14, 318-29	5.6	12
79	Inhibition of the growth of Bacillus subtilis DSM10 by a newly discovered antibacterial protein from the soil metagenome. <i>Bioengineered</i> , 2015 , 6, 89-98	5.7	12
78	Understanding the mechanisms of efficacy of fecal microbiota transplant in treating recurrent infection and beyond: the contribution of gut microbial-derived metabolites. <i>Gut Microbes</i> , 2020 , 12, 1810531	8.8	12
77	Probiotics reduce self-reported symptoms of upper respiratory tract infection in overweight and obese adults: should we be considering probiotics during viral pandemics?. <i>Gut Microbes</i> , 2021 , 13, 1-9	8.8	12
76	Community analysis of dental plaque and endotracheal tube biofilms from mechanically ventilated patients. <i>Journal of Critical Care</i> , 2017 , 39, 149-155	4	11
75	Microbiome manipulation with faecal microbiome transplantation as a therapeutic strategy in Clostridium difficile infection. <i>QJM - Monthly Journal of the Association of Physicians</i> , 2015 , 108, 355-9	2.7	11
74	Ursodeoxycholic acid enriches intestinal bile salt hydrolase-expressing Bacteroidetes in cholestatic pregnancy. <i>Scientific Reports</i> , 2020 , 10, 3895	4.9	11
73	Assessment of microbiota:host interactions at the vaginal mucosa interface. <i>Methods</i> , 2018 , 149, 74-84	4.6	11
72	Gaps in knowledge and future directions for the use of faecal microbiota transplant in the treatment of inflammatory bowel disease. <i>Therapeutic Advances in Gastroenterology</i> , 2019 , 12, 1756284	817989	1038
71	Monocyte-macrophage activation is associated with nonalcoholic fatty liver disease and liver fibrosis in HIV monoinfection independently of the gut microbiome and bacterial translocation. <i>Aids</i> , 2019 , 33, 805-814	3.5	11
7°	Current functional metagenomic approaches only expand the existing protease sequence space, but does not presently add any novelty to it. <i>Current Microbiology</i> , 2015 , 70, 19-26	2.4	10
69	Diversity of alpha-halocarboxylic acid dehalogenases in bacteria isolated from a pristine soil after enrichment and selection on the herbicide 2,2-dichloropropionic acid (Dalapon). <i>Environmental Microbiology</i> , 2003 , 5, 48-54	5.2	10
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67	Mechanisms underpinning the efficacy of faecal microbiota transplantation in treating gastrointestinal disease. <i>Therapeutic Advances in Gastroenterology</i> , 2020 , 13, 1756284820946904	4.7	10

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LIST OF PUBLICATIONS

12	Longitudinal profiling of the gut microbiome in patients with psoriatic arthritis and ankylosing spondylitis: a multicentre, prospective, observational study. <i>BMC Rheumatology</i> , 2020 , 4, 60	2.9	1
11	Multiomics Profiling Reveals Signatures of Dysmetabolism in Urban Populations in Central India. <i>Microorganisms</i> , 2021 , 9,	4.9	1
10	Effects of bowel preparation on intestinal bacterial associated urine and faecal metabolites and the associated faecal microbiome <i>BMC Gastroenterology</i> , 2022 , 22, 240	3	1
9	Risk Factors for Ovarian Cancer: An Umbrella Review of the Literature. <i>Cancers</i> , 2022 , 14, 2708	6.6	1
8	Vaginal Microbiota, Genital Inflammation and Extracellular Matrix Remodelling Collagenase: MMP-9 in Pregnant Women With HIV, a Potential Preterm Birth Mechanism Warranting Further Exploration <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 750103	5.9	0
7	Evidence for infection in intervertebral disc degeneration: a systematic review. <i>European Spine Journal</i> , 2021 , 31, 414	2.7	Ο
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5	Functional Metagenomics: Procedures and Progress 2015 , 2.4.3-1-2.4.3-11		
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