

Thomas Clavel

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

102
papers

6,571
citations

45
h-index

80
g-index

110
ext. papers

9,317
ext. citations

7.3
avg, IF

5.73
L-index

#	Paper	IF	Citations
102	Species-targeted sorting and cultivation of commensal bacteria from the gut microbiome using flow cytometry under anaerobic conditions.. <i>Microbiome</i> , 2022 , 10, 24	16.6	2
101	Naturalizing laboratory mice by housing in a farmyard-type habitat confers protection against colorectal carcinogenesis. <i>Gut Microbes</i> , 2021 , 13, 1993581	8.8	1
100	The gut bacterium produces secondary bile acids and influences liver physiology in gnotobiotic mice. <i>Gut Microbes</i> , 2021 , 13, 1-21	8.8	13
99	A diet-specific microbiota drives Salmonella Typhimurium to adapt its in vivo response to plant-derived substrates. <i>Animal Microbiome</i> , 2021 , 3, 24	4.1	1
98	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021 , 311, 151485	3.7	1
97	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. <i>MSystems</i> , 2021 , 6,	7.6	5
96	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. <i>ISME Communications</i> , 2021 , 1,		13
95	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. <i>Microbial Biotechnology</i> , 2021 , 14, 1757-1770	6.3	0
94	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. <i>ISME Communications</i> , 2021 , 1,		7
93	Upregulation of Anti-Oxidative Stress Response Improves Metabolic Changes in L-Selectin-Deficient Mice but Does Not Prevent NAFLD Progression or Fecal Microbiota Shifts. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
92	Gut microbiota and brain alterations in a translational anorexia nervosa rat model. <i>Journal of Psychiatric Research</i> , 2021 , 133, 156-165	5.2	8
91	Associations between habitual diet, metabolic disease, and the gut microbiota using latent Dirichlet allocation. <i>Microbiome</i> , 2021 , 9, 61	16.6	7
90	Allulose in human diet: the knowns and the unknowns. <i>British Journal of Nutrition</i> , 2021 , 1-7	3.6	1
89	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020 , 11, 6389	17.4	26
88	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020 , 30, 2909-2922.e6	10.6	44
87	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020 , 28, 258-272.e6	23.4	68
86	Complementary Use of Cultivation and High-Throughput Amplicon Sequencing Reveals High Biodiversity Within Raw Milk Microbiota. <i>Frontiers in Microbiology</i> , 2020 , 11, 1557	5.7	9

85	Investigation of Adiposity Measures and Operational Taxonomic unit (OTU) Data Transformation Procedures in Stool Samples from a German Cohort Study Using Machine Learning Algorithms. <i>Microorganisms</i> , 2020 , 8,	4.9	1
84	High microbiota reactivity of adult human intestinal IgA requires somatic mutations. <i>Journal of Experimental Medicine</i> , 2020 , 217,	16.6	24
83	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. <i>Molecular Metabolism</i> , 2019 , 22, 96-109	8.8	62
82	Microbiote intestinale, lipides alimentaires et maladies métaboliques. <i>Cahiers De Nutrition Et De Diététique</i> , 2019 , 54, 347-353	0.2	
81	The Compromised Mucosal Immune System of α Integrin-Deficient Mice Has Only Minor Effects on the Fecal Microbiota in Homeostasis. <i>Frontiers in Microbiology</i> , 2019 , 10, 2284	5.7	5
80	A proposed update for the classification and description of bacterial lipolytic enzymes. <i>PeerJ</i> , 2019 , 7, e7249	3.1	19
79	gen. nov., sp. nov., a novel bacterium isolated from the caecum of an obese mouse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019 , 71,	2.2	1
78	Sequence and cultivation study of Muribaculaceae reveals novel species, host preference, and functional potential of this yet undescribed family. <i>Microbiome</i> , 2019 , 7, 28	16.6	202
77	Extibacter 2019 , 1-7		1
76	Muribaculum 2019 , 1-5		1
75	An Open-Labelled Study on Fecal Microbiota Transfer in Irritable Bowel Syndrome Patients Reveals Improvement in Abdominal Pain Associated with the Relative Abundance of Akkermansia Muciniphila. <i>Digestion</i> , 2019 , 100, 127-138	3.6	23
74	Short-Term Overfeeding with Dairy Cream Does Not Modify Gut Permeability, the Fecal Microbiota, or Glucose Metabolism in Young Healthy Men. <i>Journal of Nutrition</i> , 2018 , 148, 77-85	4.1	5
73	Microbiome and Diseases: Metabolic Disorders 2018 , 251-277		
72	The gut microbiota drives the impact of bile acids and fat source in diet on mouse metabolism. <i>Microbiome</i> , 2018 , 6, 134	16.6	98
71	Acetatifactor 2018 , 1-8		
70	Increased Pancreatic Protease Activity in Response to Antibiotics Impairs Gut Barrier and Triggers Colitis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018 , 6, 370-388.e3	7.9	13
69	Nlrp3-dependent IL-1 β inhibits CD103 ⁺ dendritic cell differentiation in the gut. <i>JCI Insight</i> , 2018 , 3,	9.9	16
68	Activated ATF6 Induces Intestinal Dysbiosis and Innate Immune Response to Promote Colorectal Tumorigenesis. <i>Gastroenterology</i> , 2018 , 155, 1539-1552.e12	13.3	51

67	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. <i>Nature Communications</i> , 2018 , 9, 3760	17.4	97
66	Oral versus intravenous iron replacement therapy distinctly alters the gut microbiota and metabolome in patients with IBD. <i>Gut</i> , 2017 , 66, 863-871	19.2	160
65	Performing Skin Microbiome Research: A Method to the Madness. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 561-568	4.3	105
64	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. <i>Gut Microbes</i> , 2017 , 8, 493-503	8.8	57
63	From complex gut communities to minimal microbiomes via cultivation. <i>Current Opinion in Microbiology</i> , 2017 , 38, 148-155	7.9	17
62	Deciphering interactions between the gut microbiota and the immune system via microbial cultivation and minimal microbiomes. <i>Immunological Reviews</i> , 2017 , 279, 8-22	11.3	57
61	Effect of caloric restriction on gut permeability, inflammation markers, and fecal microbiota in obese women. <i>Scientific Reports</i> , 2017 , 7, 11955	4.9	77
60	Randomized controlled trial on the impact of early-life intervention with bifidobacteria on the healthy infant fecal microbiota and metabolome. <i>American Journal of Clinical Nutrition</i> , 2017 , 106, 1274-1286	7.1	66
59	Determinants of postprandial plasma bile acid kinetics in human volunteers. <i>American Journal of Physiology - Renal Physiology</i> , 2017 , 313, G300-G312	5.1	25
58	Rapid analysis of bile acids in different biological matrices using LC-ESI-MS/MS for the investigation of bile acid transformation by mammalian gut bacteria. <i>Analytical and Bioanalytical Chemistry</i> , 2017 , 409, 1231-1245	4.4	57
57	Darmmikrobiom des Menschen: Status quo und Perspektiven. <i>Pädiatrie Up2date</i> , 2017 , 12, 335-349	0.2	
56	Measurements of Intra- and Extra-Cellular 5-Methyltetrahydrofolate Indicate that DSM 20083 and DSM 20438 Do Not Actively Excrete 5-Methyltetrahydrofolate. <i>Frontiers in Microbiology</i> , 2017 , 8, 445	5.7	3
55	Rhea: a transparent and modular R pipeline for microbial profiling based on 16S rRNA gene amplicons. <i>PeerJ</i> , 2017 , 5, e2836	3.1	172
54	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. <i>Gut</i> , 2016 , 65, 225-37	19.2	220
53	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . <i>Environmental Microbiology Reports</i> , 2016 , 8, 1024-1037	3.7	52
52	Dietary fat and gut microbiota interactions determine diet-induced obesity in mice. <i>Molecular Metabolism</i> , 2016 , 5, 1162-1174	8.8	108
51	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <i>Nature Microbiology</i> , 2016 , 1, 16131	26.6	222
50	IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. <i>Scientific Reports</i> , 2016 , 6, 33721	4.9	192

49	Mining gut microbiome oligopeptides by functional metaproteome display. <i>Scientific Reports</i> , 2016 , 6, 34337	4.9	11
48	Exclusive enteral nutrition in active pediatric Crohn disease: Effects on intestinal microbiota and immune regulation. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 138, 592-6	11.5	39
47	Analysis of factors contributing to variation in the C57BL/6J fecal microbiota across German animal facilities. <i>International Journal of Medical Microbiology</i> , 2016 , 306, 343-355	3.7	97
46	The mouse gut microbiome revisited: From complex diversity to model ecosystems. <i>International Journal of Medical Microbiology</i> , 2016 , 306, 316-327	3.7	50
45	Genome-guided design of a defined mouse microbiota that confers colonization resistance against <i>Salmonella enterica</i> serovar Typhimurium. <i>Nature Microbiology</i> , 2016 , 2, 16215	26.6	168
44	Gut barrier impairment by high-fat diet in mice depends on housing conditions. <i>Molecular Nutrition and Food Research</i> , 2016 , 60, 897-908	5.9	40
43	Microbiome sequencing: challenges and opportunities for molecular medicine. <i>Expert Review of Molecular Diagnostics</i> , 2016 , 16, 795-805	3.8	25
42	Development of stable isotope dilution assays for the quantitation of intra- and extracellular folate patterns of <i>Bifidobacterium adolescentis</i> . <i>Journal of Chromatography A</i> , 2016 , 1469, 48-59	4.5	6
41	Dual Role of the Adaptive Immune System in Liver Injury and Hepatocellular Carcinoma Development. <i>Cancer Cell</i> , 2016 , 30, 308-323	24.3	51
40	<i>Murimonas intestini</i> gen. nov., sp. nov., an acetate-producing bacterium of the family Lachnospiraceae isolated from the mouse gut. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 870-878	2.2	14
39	The stool microbiota of insulin resistant women with recent gestational diabetes, a high risk group for type 2 diabetes. <i>Scientific Reports</i> , 2015 , 5, 13212	4.9	75
38	Physiological relevance of food grade microcapsules: Impact of milk protein based microcapsules on inflammation in mouse models for inflammatory bowel diseases. <i>Molecular Nutrition and Food Research</i> , 2015 , 59, 1629-34	5.9	4
37	Gut metabolites and bacterial community networks during a pilot intervention study with flaxseeds in healthy adult men. <i>Molecular Nutrition and Food Research</i> , 2015 , 59, 1614-28	5.9	65
36	Metabolic activation of intrahepatic CD8+ T cells and NKT cells causes nonalcoholic steatohepatitis and liver cancer via cross-talk with hepatocytes. <i>Cancer Cell</i> , 2014 , 26, 549-64	24.3	359
35	Discordance between changes in the gut microbiota and pathogenicity in a mouse model of spontaneous colitis. <i>Gut Microbes</i> , 2014 , 5, 286-95	8.8	34
34	Intestinal microbiota in metabolic diseases: from bacterial community structure and functions to species of pathophysiological relevance. <i>Gut Microbes</i> , 2014 , 5, 544-51	8.8	117
33	High-fat diet alters gut microbiota physiology in mice. <i>ISME Journal</i> , 2014 , 8, 295-308	11.9	393
32	Fetal exposure to maternal inflammation does not affect postnatal development of genetically-driven ileitis and colitis. <i>PLoS ONE</i> , 2014 , 9, e98237	3.7	6

31	The Family Coriobacteriaceae 2014 , 201-238		17
30	<i>Streptococcus danieliae</i> sp. nov., a novel bacterium isolated from the caecum of a mouse. <i>Archives of Microbiology</i> , 2013 , 195, 43-9	3	15
29	<i>Intestinimonas butyriciproducens</i> gen. nov., sp. nov., a butyrate-producing bacterium from the mouse intestine. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 4606-4612	2.2	58
28	Phenolics in Human Nutrition: Importance of the Intestinal Microbiome for Isoflavone and Lignan Bioavailability 2013 , 2433-2463		13
27	<i>Parvibacter caecicola</i> gen. nov., sp. nov., a bacterium of the family Coriobacteriaceae isolated from the caecum of a mouse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 2642-2648	2.2	15
26	Gut matters: microbe-host interactions in allergic diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2012 , 129, 1452-9	11.5	57
25	<i>Acetatifactor muris</i> gen. nov., sp. nov., a novel bacterium isolated from the intestine of an obese mouse. <i>Archives of Microbiology</i> , 2012 , 194, 901-7	3	42
24	Lignan transformation by gut bacteria lowers tumor burden in a gnotobiotic rat model of breast cancer. <i>Carcinogenesis</i> , 2012 , 33, 203-8	4.6	59
23	Catechols in caffeic acid phenethyl ester are essential for inhibition of TNF-mediated IP-10 expression through NF- κ B-dependent but HO-1- and p38-independent mechanisms in mouse intestinal epithelial cells. <i>Molecular Nutrition and Food Research</i> , 2011 , 55, 1850-61	5.9	16
22	Depletion of luminal iron alters the gut microbiota and prevents Crohn's disease-like ileitis. <i>Gut</i> , 2011 , 60, 325-33	19.2	198
21	Bacterial transformation of dietary lignans in gnotobiotic rats. <i>FEMS Microbiology Ecology</i> , 2010 , 72, 507-14	4.4	53
20	<i>Enterorhabdus caecimuris</i> sp. nov., a member of the family Coriobacteriaceae isolated from a mouse model of spontaneous colitis, and emended description of the genus <i>Enterorhabdus</i> Clavel et al. 2009. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010 , 60, 1527-1531	2.2	33
19	Posttranslational inhibition of proinflammatory chemokine secretion in intestinal epithelial cells: implications for specific IBD indications. <i>Journal of Clinical Gastroenterology</i> , 2010 , 44 Suppl 1, S10-5	3	8
18	Isolation of bacteria from mouse caecal samples and description of <i>Bacteroides sartorii</i> sp. nov. <i>Archives of Microbiology</i> , 2010 , 192, 427-35	3	14
17	Isolation of bacteria from the ileal mucosa of TNF Δ ARE mice and description of <i>Enterorhabdus mucosicola</i> gen. nov., sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009 , 59, 1805-12	2.2	64
16	Post-translational inhibition of IP-10 secretion in IEC by probiotic bacteria: impact on chronic inflammation. <i>PLoS ONE</i> , 2009 , 4, e4365	3.7	58
15	Conversion of daidzein and genistein by an anaerobic bacterium newly isolated from the mouse intestine. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 4847-52	4.8	88
14	Bacteria- and host-derived mechanisms to control intestinal epithelial cell homeostasis: implications for chronic inflammation. <i>Inflammatory Bowel Diseases</i> , 2007 , 13, 1153-64	4.5	79

13	Clostridium saccharogumia sp. nov. and Lactonifactor longoviformis gen. nov., sp. nov., two novel human faecal bacteria involved in the conversion of the dietary phytoestrogen secoisolariciresinol diglucoside. <i>Systematic and Applied Microbiology</i> , 2007 , 30, 16-26	4.2	101
12	Metabolic diversity of the intestinal microbiota: implications for health and disease. <i>Journal of Nutrition</i> , 2007 , 137, 751S-5S	4.1	278
11	Molecular interactions between bacteria, the epithelium, and the mucosal immune system in the intestinal tract: implications for chronic inflammation. <i>Current Issues in Intestinal Microbiology</i> , 2007 , 8, 25-43		29
10	Occurrence and activity of human intestinal bacteria involved in the conversion of dietary lignans. <i>Anaerobe</i> , 2006 , 12, 140-7	2.8	123
9	Bioavailability of lignans in human subjects. <i>Nutrition Research Reviews</i> , 2006 , 19, 187-96	7	88
8	Differences in fecal microbiota in different European study populations in relation to age, gender, and country: a cross-sectional study. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 1027-33	4.8	682
7	Phylogeny of human intestinal bacteria that activate the dietary lignan secoisolariciresinol diglucoside. <i>FEMS Microbiology Ecology</i> , 2006 , 55, 471-8	4.3	127
6	Isoflavones and functional foods alter the dominant intestinal microbiota in postmenopausal women. <i>Journal of Nutrition</i> , 2005 , 135, 2786-92	4.1	109
5	Intestinal bacterial communities that produce active estrogen-like compounds enterodiol and enterolactone in humans. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6077-85	4.8	159
4	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling		5
3	Handling of Spurious Sequences Affects the Outcome of High-Throughput 16S rRNA Gene Amplicon Profiling		2
2	Arrhythmic gut microbiome signatures for risk profiling of Type-2 Diabetes		1
1	An integrated metagenome catalog reveals novel insights into the murine gut microbiome		5