

# Thomas Clavel

## List of Publications by Year in descending order

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98  
papers

10,823  
citations

36303

51  
h-index

39675

94  
g-index

110  
all docs

110  
docs citations

110  
times ranked

14824  
citing authors

#	ARTICLE	IF	CITATIONS
1	Allulose in human diet: the knowns and the unknowns. <i>British Journal of Nutrition</i> , 2022, 128, 172-178.	2.3	4
2	Next steps after 15 stimulating years of human gut microbiome research. <i>Microbial Biotechnology</i> , 2022, 15, 164-175.	4.2	11
3	NLRP6 Inflammasome Modulates Disease Progression in a Chronic-Plus-Binge Mouse Model of Alcoholic Liver Disease. <i>Cells</i> , 2022, 11, 182.	4.1	12
4	Species-targeted sorting and cultivation of commensal bacteria from the gut microbiome using flow cytometry under anaerobic conditions. <i>Microbiome</i> , 2022, 10, 24.	11.1	18
5	Anaerobic single-cell dispensing facilitates the cultivation of human gut bacteria. <i>Environmental Microbiology</i> , 2022, 24, 3861-3881.	3.8	15
6	Ring Trial on Quantitative Assessment of Bile Acids Reveals a Method- and Analyte-Specific Accuracy and Reproducibility. <i>Metabolites</i> , 2022, 12, 583.	2.9	5
7	Gut microbiota and brain alterations in a translational anorexia nervosa rat model. <i>Journal of Psychiatric Research</i> , 2021, 133, 156-165.	3.1	21
8	Associations between habitual diet, metabolic disease, and the gut microbiota using latent Dirichlet allocation. <i>Microbiome</i> , 2021, 9, 61.	11.1	47
9	A diet-specific microbiota drives <i>Salmonella Typhimurium</i> to adapt its in vivo response to plant-derived substrates. <i>Animal Microbiome</i> , 2021, 3, 24.	3.8	7
10	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151485.	3.6	15
11	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. <i>MSystems</i> , 2021, 6, .	3.8	68
12	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. <i>ISME Communications</i> , 2021, 1, .	4.2	228
13	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. <i>Microbial Biotechnology</i> , 2021, 14, 1757-1770.	4.2	12
14	Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. <i>ISME Communications</i> , 2021, 1, .	4.2	60
15	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, 7314.	4.1	1
16	The gut bacterium <i>Extribacter muris</i> produces secondary bile acids and influences liver physiology in gnotobiotic mice. <i>Gut Microbes</i> , 2021, 13, 1-21.	9.8	161
17	Naturalizing laboratory mice by housing in a farmyard-type habitat confers protection against colorectal carcinogenesis. <i>Gut Microbes</i> , 2021, 13, 1993581.	9.8	11
18	High microbiota reactivity of adult human intestinal IgA requires somatic mutations. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	53

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19	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	12.8	269
20	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020, 30, 2909-2922.e6.	6.4	85
21	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020, 28, 258-272.e6.	11.0	160
22	Complementary Use of Cultivation and High-Throughput Amplicon Sequencing Reveals High Biodiversity Within Raw Milk Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 1557.	3.5	16
23	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, 547.	3.6	1
24	Microbiote intestinale, lipides alimentaires et maladies métaboliques. <i>Cahiers De Nutrition Et De Diététique</i> , 2019, 54, 347-353.	0.3	0
25	The Compromised Mucosal Immune System of $\beta 2$ Integrin-Deficient Mice Has Only Minor Effects on the Fecal Microbiota in Homeostasis. <i>Frontiers in Microbiology</i> , 2019, 10, 2284.	3.5	6
26	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.	6.5	102
27	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.	11.1	481
28	An Open-Labeled Study on Fecal Microbiota Transfer in Irritable Bowel Syndrome Patients Reveals Improvement in Abdominal Pain Associated with the Relative Abundance of <i>Akkermansia muciniphila</i> . <i>Digestion</i> , 2019, 100, 127-138.	2.3	44
29	<i>Sporofaciens musculi</i> 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, .	1.7	15
30	A proposed update for the classification and description of bacterial lipolytic enzymes. <i>PeerJ</i> , 2019, 7, e7249.	2.0	38
31	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.	2.9	10
32	Activated ATF6 Induces Intestinal Dysbiosis and Innate Immune Response to Promote Colorectal Tumorigenesis. <i>Gastroenterology</i> , 2018, 155, 1539-1552.e12.	1.3	85
33	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. <i>Nature Communications</i> , 2018, 9, 3760.	12.8	200
34	Microbiome and Diseases: Metabolic Disorders. , 2018, , 251-277.		3
35	The gut microbiota drives the impact of bile acids and fat source in diet on mouse metabolism. <i>Microbiome</i> , 2018, 6, 134.	11.1	169
36	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.	4.5	22

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37	Nlrp3-dependent IL-1 $\beta$ inhibits CD103 <sup>+</sup> dendritic cell differentiation in the gut. <i>JCI Insight</i> , 2018, 3, .	5.0	22
38	Oral versus intravenous iron replacement therapy distinctly alters the gut microbiota and metabolome in patients with IBD. <i>Gut</i> , 2017, 66, 863-871.	12.1	237
39	Performing Skin Microbiome Research: A Method to the Madness. <i>Journal of Investigative Dermatology</i> , 2017, 137, 561-568.	0.7	164
40	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. <i>Gut Microbes</i> , 2017, 8, 493-503.	9.8	79
41	From complex gut communities to minimal microbiomes via cultivation. <i>Current Opinion in Microbiology</i> , 2017, 38, 148-155.	5.1	23
42	Deciphering interactions between the gut microbiota and the immune system via microbial cultivation and minimal microbiomes. <i>Immunological Reviews</i> , 2017, 279, 8-22.	6.0	101
43	Effect of caloric restriction on gut permeability, inflammation markers, and fecal microbiota in obese women. <i>Scientific Reports</i> , 2017, 7, 11955.	3.3	119
44	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.	4.7	124
45	Determinants of postprandial plasma bile acid kinetics in human volunteers. <i>American Journal of Physiology - Renal Physiology</i> , 2017, 313, G300-G312.	3.4	38
46	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.	3.7	81
47	Genome-guided design of a defined mouse microbiota that confers colonization resistance against <i>Salmonella enterica</i> serovar Typhimurium. <i>Nature Microbiology</i> , 2017, 2, 16215.	13.3	313
48	Measurements of Intra- and Extra-Cellular 5-Methyltetrahydrofolate Indicate that <i>Bifidobacterium Adolescentis</i> DSM 20083T and <i>Bifidobacterium Pseudocatenulatum</i> DSM 20438T Do Not Actively Excrete 5-Methyltetrahydrofolate In vitro. <i>Frontiers in Microbiology</i> , 2017, 8, 445.	3.5	5
49	Rhea: a transparent and modular R pipeline for microbial profiling based on 16S rRNA gene amplicons. <i>PeerJ</i> , 2017, 5, e2836.	2.0	325
50	Gut barrier impairment by high-fat diet in mice depends on housing conditions. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 897-908.	3.3	49
51	Microbiome sequencing: challenges and opportunities for molecular medicine. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 795-805.	3.1	33
52	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.	3.7	8
53	Dual Role of the Adaptive Immune System in Liver Injury and Hepatocellular Carcinoma Development. <i>Cancer Cell</i> , 2016, 30, 308-323.	16.8	68
54	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . <i>Environmental Microbiology Reports</i> , 2016, 8, 1024-1037.	2.4	104

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55	Dietary fat and gut microbiota interactions determine diet-induced obesity in mice. <i>Molecular Metabolism</i> , 2016, 5, 1162-1174.	6.5	170
56	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.	13.3	465
57	IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. <i>Scientific Reports</i> , 2016, 6, 33721.	3.3	330
58	Mining gut microbiome oligopeptides by functional metaproteome display. <i>Scientific Reports</i> , 2016, 6, 34337.	3.3	19
59	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, 592-596.	2.9	54
60	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.	3.6	196
61	The mouse gut microbiome revisited: From complex diversity to model ecosystems. <i>International Journal of Medical Microbiology</i> , 2016, 306, 316-327.	3.6	70
62	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. <i>Gut</i> , 2016, 65, 225-237.	12.1	317
63	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.	3.3	105
64	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, 1629-1634.	3.3	5
65	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, 1614-1628.	3.3	95
66	<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.	1.7	25
67	Discordance between changes in the gut microbiota and pathogenicity in a mouse model of spontaneous colitis. <i>Gut Microbes</i> , 2014, 5, 286-485.	9.8	44
68	Intestinal microbiota in metabolic diseases. <i>Gut Microbes</i> , 2014, 5, 544-551.	9.8	170
69	High-fat diet alters gut microbiota physiology in mice. <i>ISME Journal</i> , 2014, 8, 295-308.	9.8	583
70	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, 549-564.	16.8	531
71	The Family Coriobacteriaceae. , 2014, , 201-238.		31
72	Fetal Exposure to Maternal Inflammation Does Not Affect Postnatal Development of Genetically-Driven Ileitis and Colitis. <i>PLoS ONE</i> , 2014, 9, e98237.	2.5	6

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73	<i>Streptococcus danieliae</i> sp. nov., a novel bacterium isolated from the caecum of a mouse. <i>Archives of Microbiology</i> , 2013, 195, 43-49.	2.2	20
74	<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.	1.7	95
75	Phenolics in Human Nutrition: Importance of the Intestinal Microbiome for Isoflavone and Lignan Bioavailability. , 2013, , 2433-2463.		20
76	<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.	1.7	32
77	Lignan transformation by gut bacteria lowers tumor burden in a gnotobiotic rat model of breast cancer. <i>Carcinogenesis</i> , 2012, 33, 203-208.	2.8	74
78	Gut matters: Microbe-host interactions in allergic diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 1452-1459.	2.9	68
79	<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, 901-907.	2.2	76
80	Depletion of luminal iron alters the gut microbiota and prevents Crohn's disease-like ileitis. <i>Gut</i> , 2011, 60, 325-333.	12.1	251
81	Catechols in caffeic acid phenethyl ester are essential for inhibition of TNF $\alpha$ -mediated IP $\beta$ 10 expression through NF $\kappa$ B-dependent but HO $1$ and p38 $\alpha$ -independent mechanisms in mouse intestinal epithelial cells. <i>Molecular Nutrition and Food Research</i> , 2011, 55, 1850-1861.		19
82	Posttranslational Inhibition of Proinflammatory Chemokine Secretion in Intestinal Epithelial Cells. <i>Journal of Clinical Gastroenterology</i> , 2010, 44, S10-S15.	2.2	10
83	Isolation of bacteria from mouse caecal samples and description of <i>Bacteroides sartorii</i> sp. nov. <i>Archives of Microbiology</i> , 2010, 192, 427-435.	2.2	25
84	Bacterial transformation of dietary lignans in gnotobiotic rats. <i>FEMS Microbiology Ecology</i> , 2010, 72, 507-514.	2.7	68
85	<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.	1.7	66
86	Isolation of bacteria from the ileal mucosa of TNF $\Delta$ ARE mice and description of <i>Enterorhabdus mucosicola</i> gen. nov., sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 1805-1812.	1.7	97
87	Post-Translational Inhibition of IP-10 Secretion in IEC by Probiotic Bacteria: Impact on Chronic Inflammation. <i>PLoS ONE</i> , 2009, 4, e4365.	2.5	71
88	Conversion of Daidzein and Genistein by an Anaerobic Bacterium Newly Isolated from the Mouse Intestine. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4847-4852.	3.1	110
89	Metabolic Diversity of the Intestinal Microbiota: Implications for Health and Disease <sup>1</sup> . <i>Journal of Nutrition</i> , 2007, 137, 751S-755S.	2.9	329
90	Bacteria- and host-derived mechanisms to control intestinal epithelial cell homeostasis: Implications for chronic inflammation. <i>Inflammatory Bowel Diseases</i> , 2007, 13, 1153-1164.	1.9	91

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91	<i>Clostridium saccharogumia</i> sp. nov. and <i>Lactonifactor longoviformis</i> 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.	2.8	122
92	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.	2.5	29
93	Bioavailability of lignans in human subjects. <i>Nutrition Research Reviews</i> , 2006, 19, 187-196.	4.1	108
94	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, 1027-1033.	3.1	844
95	Phylogeny of human intestinal bacteria that activate the dietary lignan secoisolariciresinol diglucoside. <i>FEMS Microbiology Ecology</i> , 2006, 55, 471-478.	2.7	156
96	Occurrence and activity of human intestinal bacteria involved in the conversion of dietary lignans. <i>Anaerobe</i> , 2006, 12, 140-147.	2.1	143
97	Isoflavones and Functional Foods Alter the Dominant Intestinal Microbiota in Postmenopausal Women. <i>Journal of Nutrition</i> , 2005, 135, 2786-2792.	2.9	129
98	Intestinal Bacterial Communities That Produce Active Estrogen-Like Compounds Enterodiol and Enterolactone in Humans. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6077-6085.	3.1	181