

# Marcus J Claesson

## List of Publications by Year in descending order

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83  
papers

14,964  
citations

46636

47  
h-index

61462

81  
g-index

90  
all docs

90  
docs citations

90  
times ranked

21367  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota composition correlates with diet and health in the elderly. <i>Nature</i> , 2012, 488, 178-184.	36.2	2,718
2	Composition, variability, and temporal stability of the intestinal microbiota of the elderly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4586-4591.	7.6	1,467
3	Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. <i>Nucleic Acids Research</i> , 2010, 38, e200-e200.	14.0	828
4	An irritable bowel syndrome subtype defined by species-specific alterations in faecal microbiota. <i>Gut</i> , 2012, 61, 997-1006.	13.7	768
5	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.	2.5	734
6	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. <i>Gut</i> , 2017, 66, 633-643.	13.7	666
7	Diversity of Bifidobacteria within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	2.5	538
8	Regulation of prefrontal cortex myelination by the microbiota. <i>Translational Psychiatry</i> , 2016, 6, e774-e774.	4.9	496
9	Genome-scale analyses of health-promoting bacteria: probiogenomics. <i>Nature Reviews Microbiology</i> , 2009, 7, 61-71.	29.2	416
10	Functional genome analysis of <i>Bifidobacterium breve</i> UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11217-11222.	7.6	340
11	Categorization of the gut microbiota: enterotypes or gradients?. <i>Nature Reviews Microbiology</i> , 2012, 10, 591-592.	29.2	264
12	16S rRNA gene sequencing of mock microbial populations- impact of DNA extraction method, primer choice and sequencing platform. <i>BMC Microbiology</i> , 2016, 16, 123.	3.4	249
13	Comparing Apples and Oranges?: Next Generation Sequencing and Its Impact on Microbiome Analysis. <i>PLoS ONE</i> , 2016, 11, e0148028.	2.5	240
14	Gut microbiota: Changes throughout the lifespan from infancy to elderly. <i>International Dairy Journal</i> , 2010, 20, 281-291.	3.1	226
15	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.	2.4	226
16	Microbes & neurodevelopment – Absence of microbiota during early life increases activity-related transcriptional pathways in the amygdala. <i>Brain, Behavior, and Immunity</i> , 2015, 50, 209-220.	6.3	219
17	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6718-6723.	7.6	218
18	Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. <i>MSystems</i> , 2016, 1, .	4.1	213

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19	Gut microbiome, big data and machine learning to promote precision medicine for cancer. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020, 17, 635-648.	18.1	194
20	Colonic microbiota is associated with inflammation and host epigenomic alterations in inflammatory bowel disease. <i>Nature Communications</i> , 2020, 11, 1512.	13.2	185
21	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 634511.	3.6	180
22	Microbiota from young mice counteracts selective age-associated behavioral deficits. <i>Nature Aging</i> , 2021, 1, 666-676.	8.5	163
23	The genus <i>Lactobacillus</i> "a genomic basis for understanding its diversity. <i>FEMS Microbiology Letters</i> , 2007, 269, 22-28.	1.8	157
24	Making Sense of the Microbiome in Psychiatry. <i>International Journal of Neuropsychopharmacology</i> , 2019, 22, 37-52.	2.1	156
25	Ranking microbiome variance in inflammatory bowel disease: a large longitudinal intercontinental study. <i>Gut</i> , 2021, 70, 499-510.	13.7	147
26	Comparative and Functional Analysis of Sortase-Dependent Proteins in the Predicted Secretome of <i>Lactobacillus salivarius</i> UCC118. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4143-4153.	3.2	146
27	The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	3.4	146
28	Effect of <i>Lactobacillus salivarius</i> Bacteriocin Abp118 on the Mouse and Pig Intestinal Microbiota. <i>PLoS ONE</i> , 2012, 7, e31113.	2.5	138
29	A comparison of the gut microbiome between long-term users and non-users of proton pump inhibitors. <i>Alimentary Pharmacology and Therapeutics</i> , 2016, 43, 974-984.	3.7	131
30	A clinician's guide to microbiome analysis. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2017, 14, 585-595.	18.1	131
31	SPINGO: a rapid species-classifier for microbial amplicon sequences. <i>BMC Bioinformatics</i> , 2015, 16, 324.	2.7	128
32	Diversity of the genus <i>Lactobacillus</i> revealed by comparative genomics of five species. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3185-3196.	1.8	118
33	Determinants of Reduced Genetic Capacity for Butyrate Synthesis by the Gut Microbiome in Crohn's Disease and Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2018, 12, 204-216.	1.3	100
34	Gutted! Unraveling the Role of the Microbiome in Major Depressive Disorder. <i>Harvard Review of Psychiatry</i> , 2020, 28, 26-39.	2.2	100
35	<i>Lactobacillus</i> phylogenomics - towards a reclassification of the genus. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2945-2954.	1.8	97
36	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. <i>Letters in Applied Microbiology</i> , 2013, 57, 492-501.	2.2	92

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37	Fermented-Food Metagenomics Reveals Substrate-Associated Differences in Taxonomy and Health-Associated and Antibiotic Resistance Determinants. <i>MSystems</i> , 2020, 5, .	4.1	90
38	Phylogenomics and comparative genomics of <i>Lactobacillus salivarius</i> , a mammalian gut commensal. <i>Microbial Genomics</i> , 2017, 3, e000115.	2.1	86
39	Translating Omics to Food Microbiology. <i>Annual Review of Food Science and Technology</i> , 2017, 8, 113-134.	10.3	85
40	Characterization of Pro-Inflammatory Flagellin Proteins Produced by <i>Lactobacillus ruminis</i> and Related Motile <i>Lactobacilli</i> . <i>PLoS ONE</i> , 2012, 7, e40592.	2.5	81
41	Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.2	80
42	Social interaction-induced activation of RNA splicing in the amygdala of microbiome-deficient mice. <i>ELife</i> , 2018, 7, .	5.9	76
43	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of <i>Lactobacillus gasseri</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3130-3146.	3.2	75
44	Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 214-221.	3.2	68
45	Species classifier choice is a key consideration when analysing low-complexity food microbiome data. <i>Microbiome</i> , 2018, 6, 50.	11.6	68
46	Genome sequences and comparative genomics of two <i>Lactobacillus ruminis</i> strains from the bovine and human intestinal tracts. <i>Microbial Cell Factories</i> , 2011, 10, S13.	4.1	65
47	Volatility as a Concept to Understand the Impact of Stress on the Microbiome. <i>Psychoneuroendocrinology</i> , 2021, 124, 105047.	2.8	60
48	Piphillin predicts metagenomic composition and dynamics from DADA2-corrected 16S rDNA sequences. <i>BMC Genomics</i> , 2020, 21, 56.	2.9	59
49	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.6	59
50	Characterization of Endogenous Plasmids from <i>Lactobacillus salivarius</i> UCC118. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3216-3228.	3.2	47
51	Fibrinogen-binding and platelet-aggregation activities of a <i>Lactobacillus salivarius</i> septicemia isolate are mediated by a novel fibrinogen-binding protein. <i>Molecular Microbiology</i> , 2012, 85, 862-877.	2.5	46
52	The Human Gut Chip ‘HuGChip’, an Explorative Phylogenetic Microarray for Determining Gut Microbiome Diversity at Family Level. <i>PLoS ONE</i> , 2013, 8, e62544.	2.5	46
53	Unusual genome complexity in <i>Lactobacillus salivarius</i> JCM1046. <i>BMC Genomics</i> , 2014, 15, 771.	2.9	45
54	Genomic island identification in <i>Vibrio vulnificus</i> reveals significant genome plasticity in this human pathogen. <i>Bioinformatics</i> , 2006, 22, 905-910.	4.2	43

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55	Sequence-Based Characterization of Intratumoral Bacteria—A Guide to Best Practice. <i>Frontiers in Oncology</i> , 2020, 10, 179.	2.9	42
56	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.	2.5	42
57	Non-specific amplification of human DNA is a major challenge for 16S rRNA gene sequence analysis. <i>Scientific Reports</i> , 2020, 10, 16356.	3.4	37
58	Evaluating the latest high-throughput molecular techniques for the exploration of microbial gut communities. <i>Gut Microbes</i> , 2010, 1, 277-278.	10.6	34
59	Recipe for a Healthy Gut: Intake of Unpasteurised Milk Is Associated with Increased <i>Lactobacillus</i> Abundance in the Human Gut Microbiome. <i>Nutrients</i> , 2020, 12, 1468.	4.2	31
60	Diversity of bacteria populations associated with different thallus regions of the brown alga <i>Laminaria digitata</i> . <i>PLoS ONE</i> , 2020, 15, e0242675.	2.5	31
61	Esophageal microbiome in active eosinophilic esophagitis and changes induced by different therapies. <i>Scientific Reports</i> , 2021, 11, 7113.	3.4	30
62	Correlation of rRNA gene amplicon pyrosequencing and bacterial culture for microbial compositional analysis of faecal samples from elderly Irish subjects. <i>Journal of Applied Microbiology</i> , 2011, 111, 467-473.	3.1	21
63	Butyrate Inhibits Osteoclast Activity In Vitro and Regulates Systemic Inflammation and Bone Healing in a Murine Osteotomy Model Compared to Antibiotic-Treated Mice. <i>Mediators of Inflammation</i> , 2021, 2021, 1-17.	3.1	21
64	Microbiome analysis as a platform R&D tool for parasitic nematode disease management. <i>ISME Journal</i> , 2019, 13, 2664-2680.	10.0	19
65	Paediatric Inflammatory Bowel Disease and its Relationship with the Microbiome. <i>Microbial Ecology</i> , 2021, 82, 833-844.	3.0	19
66	The Athlete Gut Microbiome and its Relevance to Health and Performance: A Review. <i>Sports Medicine</i> , 2022, 52, 119-128.	6.7	17
67	Biopsy bacterial signature can predict patient tissue malignancy. <i>Scientific Reports</i> , 2021, 11, 18535.	3.4	13
68	Differential gene expression in the mesocorticolimbic system of innately high- and low-impulsive rats. <i>Behavioural Brain Research</i> , 2019, 364, 193-204.	2.3	10
69	How Beneficial is the Use of Probiotic Supplements for the Aging Gut?. <i>Aging Health</i> , 2011, 7, 179-186.	0.3	9
70	Improved gut microbiome recovery following drug therapy is linked to abundance and replication of probiotic strains. <i>Gut Microbes</i> , 2022, 14, .	10.6	9
71	Host Microbiota Regulates Central Nervous System Serotonin Receptor 2C Editing in Rodents. <i>ACS Chemical Neuroscience</i> , 2019, 10, 3953-3960.	3.7	8
72	Protoblock - A biological standard for formalin fixed samples. <i>Microbiome</i> , 2020, 8, 122.	11.6	8

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73	Dietary-Induced Bacterial Metabolites Reduce Inflammation and Inflammation-Associated Cancer via Vitamin D Pathway. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1864.	4.2	8
74	260 Alterations in the Microbiota in Irritable Bowel Syndrome; A Comparison of Two Geographically Distinct Cohorts. <i>Gastroenterology</i> , 2016, 150, S63.	1.4	6
75	Differential Analysis of Longitudinal Methicillin-Resistant <i>Staphylococcus aureus</i> Colonization in Relation to Microbial Shifts in the Nasal Microbiome of Neonatal Piglets. <i>MSystems</i> , 2021, 6, e0015221.	4.1	6
76	Metaphor: Finding Bi-directional Best Hit homology relationships in (meta)genomic datasets. <i>Genomics</i> , 2014, 104, 459-463.	2.9	5
77	Interactions between Medications and the Gut Microbiome in Inflammatory Bowel Disease. <i>Microorganisms</i> , 2022, 10, 1963.	3.6	4
78	BlastXtract--a new way of exploring translated searches. <i>Bioinformatics</i> , 2005, 21, 3667-3668.	4.2	3
79	GI genomes. <i>Nature Reviews Microbiology</i> , 2005, 3, 368-369.	29.2	2
80	BlastXtract2: Improving early exploration of (meta) genomes. <i>Bioinformatics</i> , 2015, 11, 173-175.	0.5	1
81	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0
82	Bioinformatic Platforms for Metagenomics. , 2021, , 91-112.		0
83	Low-Molecular-Weight Seaweed-Derived Polysaccharides Lead to Increased Faecal Bulk but Do Not Alter Human Gut Health Markers. <i>Foods</i> , 2021, 10, 2988.	4.3	0