

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	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
2	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
3	Interactions between Medications and the Gut Microbiome in Inflammatory Bowel Disease. <i>Microorganisms</i> , 2022, 10, 1963.	3.6	4
4	The Athlete Gut Microbiome and its Relevance to Health and Performance: A Review. <i>Sports Medicine</i> , 2022, 52, 119-128.	6.7	17
5	Next Generation Sequencing Methods: Pushing the Boundaries. , 2021, , 19-46.		0
6	Ranking microbiome variance in inflammatory bowel disease: a large longitudinal intercontinental study. <i>Gut</i> , 2021, 70, 499-510.	13.7	147
7	Volatility as a Concept to Understand the Impact of Stress on the Microbiome. <i>Psychoneuroendocrinology</i> , 2021, 124, 105047.	2.8	60
8	Bioinformatic Platforms for Metagenomics. , 2021, , 91-112.		0
9	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021, 12, 635781.	3.6	59
10	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
11	Paediatric Inflammatory Bowel Disease and its Relationship with the Microbiome. <i>Microbial Ecology</i> , 2021, 82, 833-844.	3.0	19
12	Esophageal microbiome in active eosinophilic esophagitis and changes induced by different therapies. <i>Scientific Reports</i> , 2021, 11, 7113.	3.4	30
13	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
14	Microbiota from young mice counteracts selective age-associated behavioral deficits. <i>Nature Aging</i> , 2021, 1, 666-676.	8.5	163
15	Biopsy bacterial signature can predict patient tissue malignancy. <i>Scientific Reports</i> , 2021, 11, 18535.	3.4	13
16	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
17	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, 1-17.	3.1	21
18	Gutted! Unraveling the Role of the Microbiome in Major Depressive Disorder. <i>Harvard Review of Psychiatry</i> , 2020, 28, 26-39.	2.2	100

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19	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
20	Fermented-Food Metagenomics Reveals Substrate-Associated Differences in Taxonomy and Health-Associated and Antibiotic Resistance Determinants. <i>MSystems</i> , 2020, 5, .	4.1	90
21	Protoblock - A biological standard for formalin fixed samples. <i>Microbiome</i> , 2020, 8, 122.	11.6	8
22	Recipe for a Healthy Gut: Intake of Unpasteurised Milk Is Associated with Increased Lactobacillus Abundance in the Human Gut Microbiome. <i>Nutrients</i> , 2020, 12, 1468.	4.2	31
23	Sequence-Based Characterization of Intratumoral Bacteria—A Guide to Best Practice. <i>Frontiers in Oncology</i> , 2020, 10, 179.	2.9	42
24	Colonic microbiota is associated with inflammation and host epigenomic alterations in inflammatory bowel disease. <i>Nature Communications</i> , 2020, 11, 1512.	13.2	185
25	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
26	Piphillin predicts metagenomic composition and dynamics from DADA2-corrected 16S rDNA sequences. <i>BMC Genomics</i> , 2020, 21, 56.	2.9	59
27	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
28	Making Sense of the Microbiome in Psychiatry. <i>International Journal of Neuropsychopharmacology</i> , 2019, 22, 37-52.	2.1	156
29	Host Microbiota Regulates Central Nervous System Serotonin Receptor 2C Editing in Rodents. <i>ACS Chemical Neuroscience</i> , 2019, 10, 3953-3960.	3.7	8
30	Microbiome analysis as a platform R&D tool for parasitic nematode disease management. <i>ISME Journal</i> , 2019, 13, 2664-2680.	10.0	19
31	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
32	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
33	Social interaction-induced activation of RNA splicing in the amygdala of microbiome-deficient mice. <i>ELife</i> , 2018, 7, .	5.9	76
34	Species classifier choice is a key consideration when analysing low-complexity food microbiome data. <i>Microbiome</i> , 2018, 6, 50.	11.6	68
35	Translating Omics to Food Microbiology. <i>Annual Review of Food Science and Technology</i> , 2017, 8, 113-134.	10.3	85
36	Tumour-associated and non-tumour-associated microbiota in colorectal cancer. <i>Gut</i> , 2017, 66, 633-643.	13.7	666

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37	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
38	A clinician's guide to microbiome analysis. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2017, 14, 585-595.	18.1	131
39	Phylogenomics and comparative genomics of <i>Lactobacillus salivarius</i> , a mammalian gut commensal. <i>Microbial Genomics</i> , 2017, 3, e000115.	2.1	86
40	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
41	Regulation of prefrontal cortex myelination by the microbiota. <i>Translational Psychiatry</i> , 2016, 6, e774-e774.	4.9	496
42	Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. <i>MSystems</i> , 2016, 1, .	4.1	213
43	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
44	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
45	Comparing Apples and Oranges?: Next Generation Sequencing and Its Impact on Microbiome Analysis. <i>PLoS ONE</i> , 2016, 11, e0148028.	2.5	240
46	SPINGO: a rapid species-classifier for microbial amplicon sequences. <i>BMC Bioinformatics</i> , 2015, 16, 324.	2.7	128
47	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
48	BlastXtract2: Improving early exploration of (meta) genomes. <i>Bioinformatics</i> , 2015, 11, 173-175.	0.5	1
49	Metaphor: Finding Bi-directional Best Hit homology relationships in (meta)genomic datasets. <i>Genomics</i> , 2014, 104, 459-463.	2.9	5
50	Unusual genome complexity in <i>Lactobacillus salivarius</i> JCM1046. <i>BMC Genomics</i> , 2014, 15, 771.	2.9	45
51	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
52	The core faecal bacterial microbiome of Irish Thoroughbred racehorses. <i>Letters in Applied Microbiology</i> , 2013, 57, 492-501.	2.2	92
53	Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 214-221.	3.2	68
54	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

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55	Pro-Inflammatory Flagellin Proteins of Prevalent Motile Commensal Bacteria Are Variably Abundant in the Intestinal Microbiome of Elderly Humans. PLoS ONE, 2013, 8, e68919.	2.5	42
56	An irritable bowel syndrome subtype defined by species-specific alterations in faecal microbiota. Gut, 2012, 61, 997-1006.	13.7	768
57	Categorization of the gut microbiota: enterotypes or gradients?. Nature Reviews Microbiology, 2012, 10, 591-592.	29.2	264
58	Diversity of Bifidobacteria within the Infant Gut Microbiota. PLoS ONE, 2012, 7, e36957.	2.5	538
59	Effect of Lactobacillus salivarius Bacteriocin Abp118 on the Mouse and Pig Intestinal Microbiota. PLoS ONE, 2012, 7, e31113.	2.5	138
60	Characterization of Pro-Inflammatory Flagellin Proteins Produced by Lactobacillus ruminis and Related Motile Lactobacilli. PLoS ONE, 2012, 7, e40592.	2.5	81
61	Gut microbiota composition correlates with diet and health in the elderly. Nature, 2012, 488, 178-184.	36.2	2,718
62	Fibrinogenâ€binding and plateletâ€aggregation activities of a <i>Lactobacillus salivarius</i> septicaemia isolate are mediated by a novel fibrinogenâ€binding protein. Molecular Microbiology, 2012, 85, 862-877.	2.5	46
63	Correlation of rRNA gene amplicon pyrosequencing and bacterial culture for microbial compositional analysis of faecal samples from elderly Irish subjects. Journal of Applied Microbiology, 2011, 111, 467-473.	3.1	21
64	Genome sequences and comparative genomics of two Lactobacillus ruminis strains from the bovine and human intestinal tracts. Microbial Cell Factories, 2011, 10, S13.	4.1	65
65	How Beneficial is the Use of Probiotic Supplements for the Aging Gut?. Aging Health, 2011, 7, 179-186.	0.3	9
66	Functional genome analysis of <i>Bifidobacterium breve</i> UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11217-11222.	7.6	340
67	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, 4586-4591.	7.6	1,467
68	Evaluating the latest high-throughput molecular techniques for the exploration of microbial gut communities. Gut Microbes, 2010, 1, 277-278.	10.6	34
69	Gut microbiota: Changes throughout the lifespan from infancy to elderly. International Dairy Journal, 2010, 20, 281-291.	3.1	226
70	Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. Nucleic Acids Research, 2010, 38, e200-e200.	14.0	828
71	Genome-scale analyses of health-promoting bacteria: probiogenomics. Nature Reviews Microbiology, 2009, 7, 61-71.	29.2	416
72	The Bifidobacterium dentium Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. PLoS Genetics, 2009, 5, e1000785.	3.4	146

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73	Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. PLoS ONE, 2009, 4, e6669.	2.5	734
74	Characterization of Endogenous Plasmids from <i>Lactobacillus salivarius</i> UCC118. Applied and Environmental Microbiology, 2008, 74, 3216-3228.	3.2	47
75	Lactobacillus phylogenomics - towards a reclassification of the genus. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 2945-2954.	1.8	97
76	The genus <i>Lactobacillus</i> as a genomic basis for understanding its diversity. FEMS Microbiology Letters, 2007, 269, 22-28.	1.8	157
77	Genomic island identification in <i>Vibrio vulnificus</i> reveals significant genome plasticity in this human pathogen. Bioinformatics, 2006, 22, 905-910.	4.2	43
78	Comparative and Functional Analysis of Sortase-Dependent Proteins in the Predicted Secretome of <i>Lactobacillus salivarius</i> UCC118. Applied and Environmental Microbiology, 2006, 72, 4143-4153.	3.2	146
79	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6718-6723.	7.6	218
80	Diversity of the genus <i>Lactobacillus</i> revealed by comparative genomics of five species. Microbiology (United Kingdom), 2006, 152, 3185-3196.	1.8	118
81	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> . Applied and Environmental Microbiology, 2006, 72, 3130-3146.	3.2	75
82	GI genomes. Nature Reviews Microbiology, 2005, 3, 368-369.	29.2	2
83	BlastXtract—a new way of exploring translated searches. Bioinformatics, 2005, 21, 3667-3668.	4.2	3