

Marie Joossens

List of Publications by Year in descending order

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67
papers

11,641
citations

117453

34
h-index

128067

60
g-index

68
all docs

68
docs citations

68
times ranked

15677
citing authors

#	ARTICLE	IF	CITATIONS
1	Executioner caspases 3 and 7 are dispensable for intestinal epithelium turnover and homeostasis at steady state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
2	The Effect of Topical Anesthetics on 16S Ribosomal Ribonucleic Acid Amplicon Sequencing Results in Ocular Surface Microbiome Research. <i>Translational Vision Science and Technology</i> , 2022, 11, 2.	1.1	9
3	In search of viable SARS-CoV-2 in the tear film: a prospective clinical study in hospitalized symptomatic patients.. <i>Clinical Microbiology and Infection</i> , 2022, , .	2.8	0
4	Fecal Microbiota Transplantation Reduces Symptoms in Some Patients With Irritable Bowel Syndrome With Predominant Abdominal Bloating: Short- and Long-term Results From a Placebo-Controlled Randomized Trial. <i>Gastroenterology</i> , 2021, 160, 145-157.e8.	0.6	109
5	Evaluation of microbial contamination of different pork carcass areas through culture-dependent and independent methods in small-scale slaughterhouses. <i>International Journal of Food Microbiology</i> , 2021, 336, 108902.	2.1	20
6	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
7	Bacterial shifts on broiler carcasses at retail upon frozen storage. <i>International Journal of Food Microbiology</i> , 2021, 340, 109051.	2.1	5
8	The bacterial diversity of raw Moroccan camel milk. <i>International Journal of Food Microbiology</i> , 2021, 341, 109050.	2.1	16
9	Isolation, characterization and antibiotic resistance of <i>Proteus mirabilis</i> from Belgian broiler carcasses at retail and human stool. <i>Food Microbiology</i> , 2021, 96, 103724.	2.1	5
10	<i>Treponema peruense</i> sp. nov., a commensal spirochaete isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
11	Gut Microbiome Profiling Uncovers a Lower Abundance of <i>Butyricicoccus</i> in Advanced Stages of Chronic Kidney Disease. <i>Journal of Personalized Medicine</i> , 2021, 11, 1118.	1.1	11
12	Analyses of the Bacterial Contamination on Belgian Broiler Carcasses at Retail Level. <i>Frontiers in Microbiology</i> , 2020, 11, 539540.	1.5	9
13	Unlocking the full potential of probiotics: refocusing on microbial demands. <i>Chinese Medical Journal</i> , 2020, 133, 1765-1767.	0.9	0
14	Effects of Low and High FODMAP Diets on Human Gastrointestinal Microbiota Composition in Adults with Intestinal Diseases: A Systematic Review. <i>Microorganisms</i> , 2020, 8, 1638.	1.6	41
15	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020, 5, 1079-1087.	5.9	144
16	Isolation and Quantification of Uremic Toxin Precursor-Generating Gut Bacteria in Chronic Kidney Disease Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1986.	1.8	67
17	Gut microbiome variation is associated to Multiple Sclerosis phenotypic subtypes. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 406-419.	1.7	59
18	P0703 IDENTIFICATION AND QUANTIFICATION OF UREMIC TOXIN PRECURSORS-GENERATING GUT BACTERIA IN CHRONIC KIDNEY DISEASE. <i>Nephrology Dialysis Transplantation</i> , 2020, 35, .	0.4	0

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19	Comparison of five assays for DNA extraction from bacterial cells in human faecal samples. <i>Journal of Applied Microbiology</i> , 2020, 129, 378-388.	1.4	14
20	Gut microbiota generation of protein-bound uremic toxins and related metabolites is not altered at different stages of chronic kidney disease. <i>Kidney International</i> , 2020, 97, 1230-1242.	2.6	125
21	Influences of Ingredients and Bakers on the Bacteria and Fungi in Sourdough Starters and Bread. <i>MSphere</i> , 2020, 5, .	1.3	47
22	Assessment of food microbiological indicators applied on poultry carcasses by culture combined MALDI-TOF MS identification and 16S rRNA amplicon sequencing. <i>Food Microbiology</i> , 2019, 82, 53-61.	2.1	28
23	Assessment of microbial communities on freshly killed wild boar meat by MALDI-TOF MS and 16S rRNA amplicon sequencing. <i>International Journal of Food Microbiology</i> , 2019, 301, 51-60.	2.1	32
24	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019, 4, 623-632.	5.9	1,206
25	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	6.1	149
26	Lactococci dominate the bacterial communities of fermented maize, sorghum and millet slurries in Zimbabwe. <i>International Journal of Food Microbiology</i> , 2019, 289, 77-87.	2.1	15
27	Gut microbiota dynamics and uremic toxins: one size does not fit all. <i>Gut</i> , 2019, 68, 2257.1-2260.	6.1	37
28	Determination of the microbiological contamination in minced pork by culture dependent and 16S amplicon sequencing analysis. <i>International Journal of Food Microbiology</i> , 2019, 290, 27-35.	2.1	26
29	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559.	6.1	46
30	Specific members of the predominant gut microbiota predict pouchitis following colectomy and IPAA in UC. <i>Gut</i> , 2017, 66, 79-88.	6.1	114
31	Assessment of faecal microbial transfer in irritable bowel syndrome with severe bloating. <i>Gut</i> , 2017, 66, 980-982.	6.1	56
32	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. <i>Gastroenterology</i> , 2017, 152, S1.	0.6	5
33	Brief Report: <i>Dialister</i> as a Microbial Marker of Disease Activity in Spondyloarthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 114-121.	2.9	233
34	P767 The FIT trial: anti-inflammatory dietary intervention effects on the intestinal microbiota. <i>Journal of Crohn's and Colitis</i> , 2017, 11, S473-S473.	0.6	1
35	The Probiotic <i>Butyricoccus pullicaecorum</i> Reduces Feed Conversion and Protects from Potentially Harmful Intestinal Microorganisms and Necrotic Enteritis in Broilers. <i>Frontiers in Microbiology</i> , 2016, 7, 1416.	1.5	99
36	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. <i>Gut</i> , 2016, 65, 1681-1689.	6.1	312

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37	Tu1713 Host-Microbiome Interactions in Primary Sclerosing Cholangitis. <i>Gastroenterology</i> , 2016, 150, S927-S928.	0.6	0
38	Su1909 Genetic Risk for Crohn's Disease has Little Impact on Intestinal Microbiota Composition. <i>Gastroenterology</i> , 2016, 150, S585-S586.	0.6	0
39	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398
40	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	6.0	1,716
41	Concordance in Anti-OmpC and Anti-I2 Indicate the Influence of Genetic Predisposition: Results of a European Study of Twins with Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 695-702.	0.6	13
42	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 735-746.	0.6	37
43	Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 387-394.	0.6	256
44	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , 2016, 65, 57-62.	6.1	737
45	Faecal metabolite profiling identifies medium-chain fatty acids as discriminating compounds in IBD. <i>Gut</i> , 2015, 64, 447-458.	6.1	185
46	A decrease of the butyrate-producing species <i>Roseburia hominis</i> and <i>Faecalibacterium prausnitzii</i> defines dysbiosis in patients with ulcerative colitis. <i>Gut</i> , 2014, 63, 1275-1283.	6.1	1,353
47	A metagenomic insight into our gut's microbiome. <i>Gut</i> , 2013, 62, 146-158.	6.1	302
48	Metabolic Profiling of the Impact of Oligofructose-Enriched Inulin in Crohn's Disease Patients: A Double-Blinded Randomized Controlled Trial. <i>Clinical and Translational Gastroenterology</i> , 2013, 4, e30.	1.3	72
49	Assessment of the Microbiota in Microdissected Tissues of Crohn's Disease Patients. <i>International Journal of Inflammation</i> , 2012, 2012, 1-11.	0.9	9
50	Effect of oligofructose-enriched inulin (OF-IN) on bacterial composition and disease activity of patients with Crohn's disease: results from a double-blinded randomised controlled trial: Table 1. <i>Gut</i> , 2012, 61, 958-958.	6.1	90
51	Association of <i>Faecalibacterium Prausnitzii</i> and Disease Activity in Ulcerative Colitis. <i>Gastroenterology</i> , 2011, 140, S-142.	0.6	4
52	High-throughput method for comparative analysis of denaturing gradient gel electrophoresis profiles from human fecal samples reveals significant increases in two bifidobacterial species after inulin-type prebiotic intake. <i>FEMS Microbiology Ecology</i> , 2011, 75, 343-349.	1.3	37
53	Dysbiosis of the faecal microbiota in patients with Crohn's disease and their unaffected relatives. <i>Gut</i> , 2011, 60, 631-637.	6.1	871
54	Familial aggregation and antimicrobial response dose-dependently affect the risk for Crohn's disease. <i>Inflammatory Bowel Diseases</i> , 2010, 16, 58-67.	0.9	34

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55	Clustering of (auto)immune diseases with early-onset and complicated inflammatory bowel disease. <i>European Journal of Pediatrics</i> , 2009, 168, 575-583.	1.3	8
56	<i>Candida albicans</i> Colonization and ASCA in Familial Crohn's Disease. <i>American Journal of Gastroenterology</i> , 2009, 104, 1745-1753.	0.2	172
57	Coamplification of Eukaryotic DNA with 16S rRNA Gene-Based PCR Primers: Possible Consequences for Population Fingerprinting of Complex Microbial Communities. <i>Current Microbiology</i> , 2008, 56, 553-557.	1.0	50
58	P200 MUCOSAL GENE SIGNATURES TO PREDICT RESPONSE TO INFLIXIMAB IN PATIENTS WITH INFLAMMATORY BOWEL DISEASE. <i>Journal of Crohn S and Colitis Supplements</i> , 2008, 2, 64.	0.0	0
59	Mutations in pattern recognition receptor genes modulate seroreactivity to microbial antigens in patients with inflammatory bowel disease. <i>Gut</i> , 2007, 56, 1536-1542.	6.1	91
60	New serological markers in inflammatory bowel disease are associated with complicated disease behaviour. <i>Gut</i> , 2007, 56, 1394-1403.	6.1	267
61	Familial Crohn's Disease in Belgium. <i>Journal of Clinical Gastroenterology</i> , 2007, 41, 583-590.	1.1	18
62	Contribution of genetic and environmental factors in the pathogenesis of Crohn's disease in a large family with multiple cases. <i>Inflammatory Bowel Diseases</i> , 2007, 13, 580-584.	0.9	24
63	Cluster of Crohn's disease in Hery, France, including 2 cases from a common residence. <i>Inflammatory Bowel Diseases</i> , 2007, 13, 1454-1455.	0.9	4
64	The role of vascular endothelial growth factor (VEGF) in inflammatory bowel disease. <i>Inflammatory Bowel Diseases</i> , 2006, 12, 870-878.	0.9	46
65	Environmental Factors in Familial Crohn's Disease in Belgium. <i>Inflammatory Bowel Diseases</i> , 2005, 11, 360-365.	0.9	69
66	Crohn's Disease and Month of Birth. <i>Inflammatory Bowel Diseases</i> , 2005, 11, 597-599.	0.9	32
67	No association between month of birth and Crohn's disease. <i>Gastroenterology</i> , 2003, 124, A215.	0.6	0