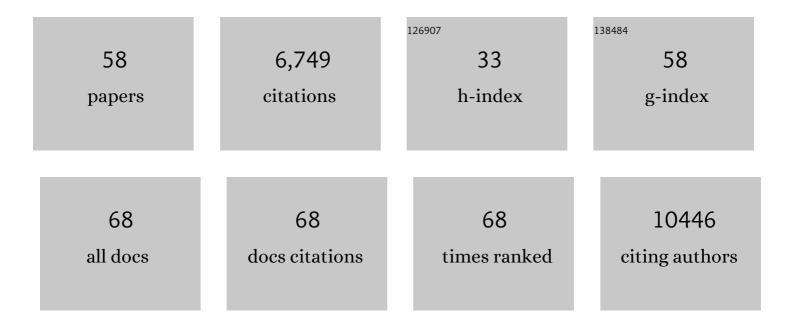
Anne Maarit Salonen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5726989/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Gut microbiota can utilize prebiotic birch glucuronoxylan in production of short-chain fatty acids in rats. Food and Function, 2022, 13, 3746-3759.	4.6	10
2	Potential pathobionts in vaginal microbiota are affected by fish oil and/or probiotics intervention in overweight and obese pregnant women. Biomedicine and Pharmacotherapy, 2022, 149, 112841.	5.6	9
3	In vitro Effects of Bacterial Exposure on Secretion of Zonulin Family Peptides and Their Detection in Human Tissue Samples. Frontiers in Microbiology, 2022, 13, 848128.	3.5	5
4	The gut fungal and bacterial microbiota in pediatric patients with inflammatory bowel disease introduced to treatment with anti-tumor necrosis factor-α. Scientific Reports, 2022, 12, 6654.	3.3	5
5	The Effect of Antibiotics on the Infant Gut Fungal Microbiota. Journal of Fungi (Basel, Switzerland), 2022, 8, 328.	3.5	11
6	Gut microbiota predicts body fat change following a low-energy diet: a PREVIEW intervention study. Genome Medicine, 2022, 14, .	8.2	32
7	Parity and gestational age are associated with vaginal microbiota composition in term and late term pregnancies. EBioMedicine, 2022, 81, 104107.	6.1	18
8	Fecal microbiota in congenital chloride diarrhea and inflammatory bowel disease. PLoS ONE, 2022, 17, e0269561.	2.5	5
9	Bacterial and Fungal Profiles as Markers of Infliximab Drug Response in Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2021, 15, 1019-1031.	1.3	34
10	Impact of short-term overfeeding of saturated or unsaturated fat or sugars on the gut microbiota in relation to liver fat in obese and overweight adults. Clinical Nutrition, 2021, 40, 207-216.	5.0	28
11	Protocol for oral transplantation of maternal fecal microbiota to newborn infants born by cesarean section. STAR Protocols, 2021, 2, 100271.	1.2	7
12	Commentary: How to Count Our Microbes? The Effect of Different Quantitative Microbiome Profiling Approaches. Frontiers in Cellular and Infection Microbiology, 2021, 11, 627910.	3.9	6
13	Does Day-to-Day Variability in Stool Consistency Link to the Fecal Microbiota Composition?. Frontiers in Cellular and Infection Microbiology, 2021, 11, 639667.	3.9	11
14	Early-life gut microbiota and its connection to metabolic health in children: Perspective on ecological drivers and need for quantitative approach. EBioMedicine, 2021, 69, 103475.	6.1	47
15	Fecal Bacteria Implicated in Biofilm Production Are Enriched and Associate to Gastrointestinal Symptoms in Patients With APECED – A Pilot Study. Frontiers in Immunology, 2021, 12, 668219.	4.8	6
16	Personalized approach to childhood obesity: Lessons from gut microbiota and omics studies. Narrative review and insights from the 29th European childhood obesity congress. Pediatric Obesity, 2021, 16, e12835.	2.8	10
17	Gut microbiota develop towards an adult profile in a sex-specific manner during puberty. Scientific Reports, 2021, 11, 23297.	3.3	31
18	Maternal Fecal Microbiota Transplantation in Cesarean-Born Infants Rapidly Restores Normal Gut Microbial Development: A Proof-of-Concept Study. Cell, 2020, 183, 324-334.e5.	28.9	188

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19	Quantitative PCR provides a simple and accessible method for quantitative microbiota profiling. PLoS ONE, 2020, 15, e0227285.	2.5	207
20	Antibiotics in early life associate with specific gut microbiota signatures in a prospective longitudinal infant cohort. Pediatric Research, 2020, 88, 438-443.	2.3	51
21	Considerations for the design and conduct of human gut microbiota intervention studies relating to foods. European Journal of Nutrition, 2020, 59, 3347-3368.	3.9	17
22	Cohort profile: Finnish Health and Early Life Microbiota (HELMi) longitudinal birth cohort. BMJ Open, 2019, 9, e028500.	1.9	25
23	Vaginal microbiota in pregnancy: Role in induction of labor and seeding the neonate's microbiota?. Journal of Biosciences, 2019, 44, 1.	1.1	19
24	Vaginal Microbiota Composition Correlates Between Pap Smear Microscopy and Next Generation Sequencing and Associates to Socioeconomic Status. Scientific Reports, 2019, 9, 7750.	3.3	32
25	Randomised clinical trial: effect of low-FODMAP rye bread versus regular rye bread on the intestinal microbiota of irritable bowel syndrome patients: association with individual symptom variation. BMC Nutrition, 2019, 5, 12.	1.6	15
26	The Effect of Allogenic Versus Autologous Fecal Microbiota Transfer on Symptoms, Visceral Perception and Fecal and Mucosal Microbiota in Irritable Bowel Syndrome: A Randomized Controlled Study. Clinical and Translational Gastroenterology, 2019, 10, e00034.	2.5	70
27	Vaginal microbiota in pregnancy: Role in induction of labor and seeding the neonate''s microbiota?. Journal of Biosciences, 2019, 44, .	1.1	7
28	Intestinal Microbiota in Hirschsprung Disease. Journal of Pediatric Gastroenterology and Nutrition, 2018, 67, 594-600.	1.8	36
29	Probiotic supplementation restores normal microbiota composition and function in antibiotic-treated and in caesarean-born infants. Microbiome, 2018, 6, 182.	11.1	160
30	Fucosylated oligosaccharides in mother's milk alleviate the effects of caesarean birth on infant gut microbiota. Scientific Reports, 2018, 8, 13757.	3.3	86
31	Saturated Fat Is More Metabolically Harmful for the Human Liver Than Unsaturated Fat or Simple Sugars. Diabetes Care, 2018, 41, 1732-1739.	8.6	266
32	Intestinal Microbiota Signatures Associated With Histological Liver Steatosis in Pediatricâ€Onset Intestinal Failure. Journal of Parenteral and Enteral Nutrition, 2017, 41, 238-248.	2.6	75
33	Towards standards for human fecal sample processing in metagenomic studies. Nature Biotechnology, 2017, 35, 1069-1076.	17.5	581
34	Comparative analysis of vaginal microbiota sampling using 16S rRNA gene analysis. PLoS ONE, 2017, 12, e0181477.	2.5	46
35	Science, innovation and society. EFSA Journal, 2016, 14, e00502.	1.8	1
36	Lactobacillus rhamnosus GG Intake Modifies Preschool Children's Intestinal Microbiota, Alleviates Penicillin-Associated Changes, and Reduces Antibiotic Use. PLoS ONE, 2016, 11, e0154012.	2.5	62

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37	Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. PLoS ONE, 2016, 11, e0153294.	2.5	70
38	Association of Early-Life Antibiotic Use and Protective Effects of Breastfeeding. JAMA Pediatrics, 2016, 170, 750.	6.2	76
39	Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. Nature Communications, 2016, 7, 10410.	12.8	557
40	Colonic metaproteomic signatures of active bacteria and the host in obesity. Proteomics, 2015, 15, 3544-3552.	2.2	70
41	Fecal Microbiota in Pediatric Inflammatory Bowel Disease and Its Relation to Inflammation. American Journal of Gastroenterology, 2015, 110, 921-930.	0.4	193
42	Intestinal Microbiota And Diet in IBS: Causes, Consequences, or Epiphenomena?. American Journal of Gastroenterology, 2015, 110, 278-287.	0.4	283
43	Microbial signatures in post-infectious irritable bowel syndrome – toward patient stratification for improved diagnostics and treatment. Gut Microbes, 2015, 6, 364-369.	9.8	51
44	Effects of bowel cleansing on the intestinal microbiota. Gut, 2015, 64, 1562-1568.	12.1	201
45	Gut Microbiota Signatures Predict Host and Microbiota Responses to Dietary Interventions in Obese Individuals. PLoS ONE, 2014, 9, e90702.	2.5	163
46	Tipping elements in the human intestinal ecosystem. Nature Communications, 2014, 5, 4344.	12.8	217
47	Impact of Diet on Human Intestinal Microbiota and Health. Annual Review of Food Science and Technology, 2014, 5, 239-262.	9.9	173
48	Faecal microbiota composition and host–microbe cross-talk following gastroenteritis and in postinfectious irritable bowel syndrome. Gut, 2014, 63, 1737-1745.	12.1	282
49	Impact of diet and individual variation on intestinal microbiota composition and fermentation products in obese men. ISME Journal, 2014, 8, 2218-2230.	9.8	489
50	Intake of Whole-Grain and Fiber-Rich Rye Bread Versus Refined Wheat Bread Does Not Differentiate Intestinal Microbiota Composition in Finnish Adults with Metabolic Syndrome. Journal of Nutrition, 2013, 143, 648-655.	2.9	85
51	Associations between the human intestinal microbiota, <i>Lactobacillus rhamnosus</i> GG and serum lipids indicated by integrated analysis of high-throughput profiling data. PeerJ, 2013, 1, e32.	2.0	166
52	Comparative Metaproteomics and Diversity Analysis of Human Intestinal Microbiota Testifies for Its Temporal Stability and Expression of Core Functions. PLoS ONE, 2012, 7, e29913.	2.5	183
53	Intestinal Microbiota in Healthy Adults: Temporal Analysis Reveals Individual and Common Core and Relation to Intestinal Symptoms. PLoS ONE, 2011, 6, e23035.	2.5	302
54	Comparative analysis of fecal DNA extraction methods with phylogenetic microarray: Effective recovery of bacterial and archaeal DNA using mechanical cell lysis. Journal of Microbiological Methods, 2010, 81, 127-134.	1.6	480

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55	Gastrointestinal microbiota in irritable bowel syndrome: present state and perspectives. Microbiology (United Kingdom), 2010, 156, 3205-3215.	1.8	231
56	Microbial functionality in the human intestinal tract. Frontiers in Bioscience - Landmark, 2009, Volume, 3074.	3.0	17
57	Role of the Amphipathic Peptide of Semliki Forest Virus Replicase Protein nsP1 in Membrane Association and Virus Replication. Journal of Virology, 2007, 81, 872-883.	3.4	98
58	Properly Folded Nonstructural Polyprotein Directs the Semliki Forest Virus Replication Complex to the Endosomal Compartment. Journal of Virology, 2003, 77, 1691-1702.	3.4	120