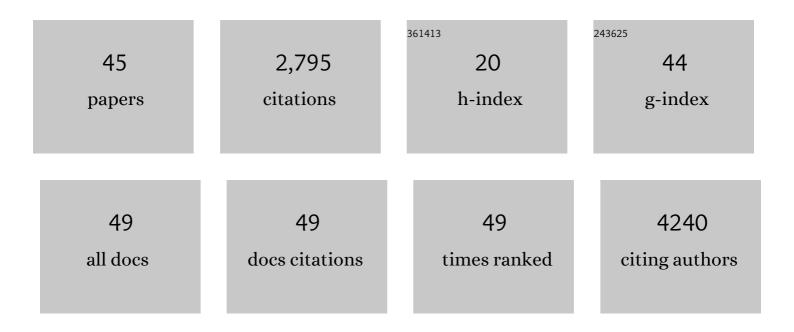
Jarmo Ritari

List of Publications by Year in descending order

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Ιλρμο Ριτλρι

#	Article	IF	CITATIONS
1	KIR gene content imputation from single-nucleotide polymorphisms in the Finnish population. PeerJ, 2022, 10, e12692.	2.0	1
2	HLA-disease association and pleiotropy landscape in over 235,000 Finns. Human Immunology, 2022, 83, 391-398.	2.4	5
3	Sperm Physiological Response to Female Serum—Potential New Insights into the Reproductive Incompatibility Diagnostics. International Journal of Molecular Sciences, 2022, 23, 3428.	4.1	0
4	HLA-DQ and HLA-DRB1 alleles associated with Henoch-Schönlein purpura nephritis in Finnish pediatric population: a genome-wide association study. Pediatric Nephrology, 2021, 36, 2311-2318.	1.7	10
5	Structural dissimilarity of partners' immune genes increases sperm viability in women's reproductive tract. Journal of Evolutionary Biology, 2021, 34, 1125-1132.	1.7	3
6	Selection and characterization of a SpaCBA pilus-secreting food-grade derivative of Lacticaseibacillus rhamnosus GG. Applied Microbiology and Biotechnology, 2021, 105, 1123-1131.	3.6	4
7	Genomic convergence between Akkermansia muciniphila in different mammalian hosts. BMC Microbiology, 2021, 21, 298.	3.3	10
8	Increasing accuracy of HLA imputation by a population-specific reference panel in a FinnGen biobank cohort. NAR Genomics and Bioinformatics, 2020, 2, Iqaa030.	3.2	31
9	Characterization of Highly Mucus-Adherent Non-GMO Derivatives of Lacticaseibacillus rhamnosus GG. Frontiers in Bioengineering and Biotechnology, 2020, 8, 1024.	4.1	9
10	Gamete-level immunogenetic incompatibility in humans–towards deeper understanding of fertilization and infertility?. Heredity, 2020, 125, 281-289.	2.6	9
11	Post-copulatory genetic matchmaking: HLA-dependent effects of cervical mucus on human sperm function. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201682.	2.6	14
12	Colonic Mucosal Microbiota and Association of Bacterial Taxa with the Expression of Host Antimicrobial Peptides in Pediatric Ulcerative Colitis. International Journal of Molecular Sciences, 2020, 21, 6044.	4.1	20
13	Meta-Analysis of Genome-Wide Association and Gene Expression Studies Implicates Donor T Cell Function and Cytokine Pathways in Acute GvHD. Frontiers in Immunology, 2020, 11, 19.	4.8	6
14	Genomic prediction of relapse in recipients of allogeneic haematopoietic stem cell transplantation. Leukemia, 2019, 33, 240-248.	7.2	18
15	Extended HLA Haplotypes and Their Impact on DPB1 Matching of Unrelated Hematologic Stem Cell Transplant Donors. Biology of Blood and Marrow Transplantation, 2019, 25, 1956-1964.	2.0	9
16	Computational Analysis of HLA-presentation of Non-synonymous Recipient Mismatches Indicates Effect on the Risk of Chronic Graft-vsHost Disease After Allogeneic HSCT. Frontiers in Immunology, 2019, 10, 1625.	4.8	20
17	Increased MHC Matching by C4 Gene Compatibility in Unrelated Donor Hematopoietic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2019, 25, 891-898.	2.0	2
18	IL-10 polymorphisms +434T/C, +504G/T, and -2849C/T may predispose to tubulointersititial nephritis and uveitis in pediatric population. PLoS ONE, 2019, 14, e0211915.	2.5	8

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19	Hidden genomic MHC disparity between HLA-matched sibling pairs in hematopoietic stem cell transplantation. Scientific Reports, 2018, 8, 5396.	3.3	11
20	Romboutsia hominis sp. nov., the first human gut-derived representative of the genus Romboutsia, isolated from ileostoma effluent. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3479-3486.	1.7	37
21	Complete Genome Sequence of Akkermansia glycaniphila Strain Pyt ^T , a Mucin-Degrading Specialist of the Reticulated Python Gut. Genome Announcements, 2017, 5, .	0.8	16
22	Complete Genome Sequence of Eubacterium hallii Strain L2-7. Genome Announcements, 2017, 5, .	0.8	17
23	An Inducible Operon Is Involved in Inulin Utilization in Lactobacillus plantarum Strains, as Revealed by Comparative Proteogenomics and Metabolic Profiling. Applied and Environmental Microbiology, 2017, 83, .	3.1	43
24	Genetic polymorphism related to monocyte-macrophage function is associated with graft-versus-host disease. Scientific Reports, 2017, 7, 15666.	3.3	22
25	Feasibility of Metatranscriptome Analysis from Infant Gut Microbiota: Adaptation to Solid Foods Results in Increased Activity of Firmicutes at Six Months. International Journal of Microbiology, 2017, 2017, 1-9.	2.3	11
26	Genotypic and phenotypic diversity of Lactobacillus rhamnosus clinical isolates, their comparison with strain GG and their recognition by complement system. PLoS ONE, 2017, 12, e0176739.	2.5	21
27	Lactobacillus oligofermentans glucose, ribose and xylose transcriptomes show higher similarity between glucose and xylose catabolism-induced responses in the early exponential growth phase. BMC Genomics, 2016, 17, 539.	2.8	27
28	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
29	The Variable Regions of <i>Lactobacillus rhamnosus</i> Genomes Reveal the Dynamic Evolution of Metabolic and Host-Adaptation Repertoires. Genome Biology and Evolution, 2016, 8, 1889-1905.	2.5	53
30	Polymorphisms, Chromosomal Rearrangements, and Mutator Phenotype Development during Experimental Evolution of Lactobacillus rhamnosus GG. Applied and Environmental Microbiology, 2016, 82, 3783-3792.	3.1	27
31	Comparative genomics and physiology of the butyrateâ€producing bacterium <i>Intestinimonas butyriciproducens</i> . Environmental Microbiology Reports, 2016, 8, 1024-1037.	2.4	104
32	Production of butyrate from lysine and the Amadori product fructoselysine by a human gut commensal. Nature Communications, 2015, 6, 10062.	12.8	199
33	Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. BMC Genomics, 2015, 16, 1056.	2.8	127
34	Colonic metaproteomic signatures of active bacteria and the host in obesity. Proteomics, 2015, 15, 3544-3552.	2.2	70
35	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. Nature Communications, 2015, 6, 8322.	12.8	488
36	Effects of bowel cleansing on the intestinal microbiota. Gut, 2015, 64, 1562-1568.	12.1	201

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37	Genomic Characterization of Non-Mucus-Adherent Derivatives of Lactobacillus rhamnosus GG Reveals Genes Affecting Pilus Biogenesis. Applied and Environmental Microbiology, 2014, 80, 7001-7009.	3.1	22
38	Comparative Genomic and Functional Analysis of 100 Lactobacillus rhamnosus Strains and Their Comparison with Strain GG. PLoS Genetics, 2013, 9, e1003683.	3.5	180
39	Comparative genome analysis of <i><scp>L</scp>actobacillus casei</i> strains isolated from <scp>A</scp> ctimel and <scp>Y</scp> akult products reveals marked similarities and points to a common origin. Microbial Biotechnology, 2013, 6, 576-587.	4.2	27
40	Identification and Validation of Human Papillomavirus Encoded microRNAs. PLoS ONE, 2013, 8, e70202.	2.5	61
41	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. BMC Microbiology, 2012, 12, 121.	3.3	30
42	Detection of Human Papillomaviruses by Polymerase Chain Reaction and Ligation Reaction on Universal Microarray. PLoS ONE, 2012, 7, e34211.	2.5	12
43	Application of hybridization control probe to increase accuracy on ligation detection or minisequencing diagnostic microarrays. BMC Research Notes, 2009, 2, 249.	1.4	7
44	Comparative genomic analysis of <i>Lactobacillus rhamnosus</i> GG reveals pili containing a human- mucus binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17193-17198.	7.1	654
45	Universal ligation-detection-reaction microarray applied for compost microbes. BMC Microbiology, 2008, 8, 237.	3.3	29