

# Jenni Hultman

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

5,435  
citations

236925

25  
h-index

289244

40  
g-index

48  
all docs

48  
docs citations

48  
times ranked

9109  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early-life formula feeding is associated with infant gut microbiota alterations and an increased antibiotic resistance load. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 407-421.	4.7	29
2	<i>Candidatus</i> Nitrosopolaris, a genus of putative ammonia-oxidizing archaea with a polar/alpine distribution. <i>FEMS Microbes</i> , 2022, 3, .	2.1	10
3	Microbiome assembly in thawing permafrost and its feedbacks to climate. <i>Global Change Biology</i> , 2022, 28, 5007-5026.	9.5	34
4	In-depth characterization of denitrifier communities across different soil ecosystems in the tundra. <i>Environmental Microbiomes</i> , 2022, 17, .	5.0	25
5	The activity and functions of soil microbial communities in the Finnish sub-Arctic vary across vegetation types. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	2.7	8
6	Antibiotic Resistomes and Microbiomes in the Surface Water along the Code River in Indonesia Reflect Drainage Basin Anthropogenic Activities. <i>Environmental Science &amp; Technology</i> , 2022, 56, 14994-15006.	10.0	11
7	Sea-Ice Bacteria <i>Halomonas</i> sp. Strain 363 and <i>Paracoccus</i> sp. Strain 392 Produce Multiple Types of Poly-3-Hydroxyalkanoic Acid (PHA) Storage Polymers at Low Temperature. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0092921.	3.1	9
8	Growth and metabolic characteristics of fastidious meat-derived <i>Lactobacillus algidus</i> strains. <i>International Journal of Food Microbiology</i> , 2020, 313, 108379.	4.7	17
9	Longitudinal Metatranscriptomic Analysis of a Meat Spoilage Microbiome Detects Abundant Continued Fermentation and Environmental Stress Responses during Shelf Life and Beyond. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	11
10	Metabolomics and bacterial diversity of packaged yellowfin tuna ( <i>Thunnus albacares</i> ) and salmon ( <i>Salmo salar</i> ) show fish species-specific spoilage development during chilled storage. <i>International Journal of Food Microbiology</i> , 2019, 293, 44-52.	4.7	80
11	Ecology determines how low antibiotic concentration impacts community composition and horizontal transfer of resistance genes. <i>Communications Biology</i> , 2018, 1, 35.	4.4	80
12	Host range of antibiotic resistance genes in wastewater treatment plant influent and effluent. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	148
13	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. <i>Nature Communications</i> , 2018, 9, 3891.	12.8	313
14	Construction and Characterization of Synthetic Bacterial Community for Experimental Ecology and Evolution. <i>Frontiers in Genetics</i> , 2018, 9, 312.	2.3	28
15	Quantifying uncertainty of taxonomic placement in <i>scp</i> DNA barcoding and metabarcoding. <i>Methods in Ecology and Evolution</i> , 2017, 8, 398-407.	5.2	77
16	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
17	Exploring lot-to-lot variation in spoilage bacterial communities on commercial modified atmosphere packaged beef. <i>Food Microbiology</i> , 2017, 62, 147-152.	4.2	49
18	Evaluating the mobility potential of antibiotic resistance genes in environmental resistomes without metagenomics. <i>Scientific Reports</i> , 2016, 6, 35790.	3.3	46

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19	Complete genome sequence of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1, isolated from vacuum-packaged vegetable sausages. <i>Standards in Genomic Sciences</i> , 2016, 11, 40.	1.5	28
20	Development of spoilage bacterial community and volatile compounds in chilled beef under vacuum or high oxygen atmospheres. <i>International Journal of Food Microbiology</i> , 2016, 223, 25-32.	4.7	76
21	Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes. <i>Nature</i> , 2015, 521, 208-212.	27.8	467
22	Meat Processing Plant Microbiome and Contamination Patterns of Cold-Tolerant Bacteria Causing Food Safety and Spoilage Risks in the Manufacture of Vacuum-Packaged Cooked Sausages. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7088-7097.	3.1	111
23	Preparation and antimicrobial characterization of silver-containing packaging materials for meat. <i>Food Packaging and Shelf Life</i> , 2015, 6, 53-60.	7.5	28
24	Inconsistent Denoising and Clustering Algorithms for Amplicon Sequence Data. <i>Journal of Computational Biology</i> , 2015, 22, 743-751.	1.6	15
25	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 130.	3.5	172
26	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014, 42, e145-e145.	14.5	90
27	Evaluation of Molecular Techniques in Characterization of Deep Terrestrial Biosphere. <i>Open Journal of Ecology</i> , 2014, 04, 468-487.	1.0	13
28	Taxonomically and functionally diverse microbial communities in deep crystalline rocks of the Fennoscandian shield. <i>ISME Journal</i> , 2014, 8, 126-138.	9.8	107
29	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	9.8	547
30	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. <i>BMC Microbiology</i> , 2012, 12, 121.	3.3	30
31	Detection of Human Papillomaviruses by Polymerase Chain Reaction and Ligation Reaction on Universal Microarray. <i>PLoS ONE</i> , 2012, 7, e34211.	2.5	12
32	Comparison of microbial communities in marinated and unmarinated broiler meat by metagenomics. <i>International Journal of Food Microbiology</i> , 2012, 157, 142-149.	4.7	101
33	Spatially differing bacterial communities in water columns of the northern Baltic Sea. <i>FEMS Microbiology Ecology</i> , 2011, 75, 99-110.	2.7	41
34	Bacterial diversity at different stages of the composting process. <i>BMC Microbiology</i> , 2010, 10, 94.	3.3	337
35	Determination of fungal succession during municipal solid waste composting using a cloning-based analysis. <i>Journal of Applied Microbiology</i> , 2010, 108, 472-487.	3.1	62
36	Utility of Molecular Tools in Monitoring Large Scale Composting. , 2010, , 135-151.		7

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37	Application of hybridization control probe to increase accuracy on ligation detection or minisequencing diagnostic microarrays. <i>BMC Research Notes</i> , 2009, 2, 249.	1.4	7
38	Universal ligation-detection-reaction microarray applied for compost microbes. <i>BMC Microbiology</i> , 2008, 8, 237.	3.3	29
39	Probe-based negative selection for underrepresented phlotypes in large environmental clone libraries. <i>Journal of Microbiological Methods</i> , 2008, 75, 457-463.	1.6	6
40	Activity, diversity and population size of ammonia-oxidising bacteria in oil-contaminated landfarming soil. <i>FEMS Microbiology Letters</i> , 2005, 250, 33-38.	1.8	210