

Evelyne Mann

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,454
citations

279487

23
h-index

344852

36
g-index

45
all docs

45
docs citations

45
times ranked

1636
citing authors

#	ARTICLE	IF	CITATIONS
1	Biofilms in Water Hoses of a Meat Processing Environment Harbor Complex Microbial Communities. <i>Frontiers in Microbiology</i> , 2022, 13, 832213.	1.5	7
2	Metatranscriptomic Analyses Unravel Dynamic Changes in the Microbial and Metabolic Transcriptional Profiles in Artisanal Austrian Hard-Cheeses During Ripening. <i>Frontiers in Microbiology</i> , 2022, 13, 813480.	1.5	4
3	Co-Occurrence of <i>Listeria</i> spp. and Spoilage Associated Microbiota During Meat Processing Due to Cross-Contamination Events. <i>Frontiers in Microbiology</i> , 2021, 12, 632935.	1.5	26
4	Wolves, dogs and humans in regular contact can mutually impact each other's skin microbiota. <i>Scientific Reports</i> , 2021, 11, 17106.	1.6	10
5	Metaproteomics Reveals Alteration of the Gut Microbiome in Weaned Piglets Due to the Ingestion of the Mycotoxins Deoxynivalenol and Zearalenone. <i>Toxins</i> , 2021, 13, 583.	1.5	9
6	Early Parenteral Administration of Ceftiofur has Gender-Specific Short- and Long-Term Effects on the Fecal Microbiota and Growth in Pigs from the Suckling to Growing Phase. <i>Animals</i> , 2020, 10, 17.	1.0	24
7	The sources and transmission routes of microbial populations throughout a meat processing facility. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 26.	2.9	63
8	Co-infection of Chicken Layers With <i>Histomonas meleagridis</i> and Avian Pathogenic <i>Escherichia coli</i> Is Associated With Dysbiosis, Cecal Colonization and Translocation of the Bacteria From the Gut Lumen. <i>Frontiers in Microbiology</i> , 2020, 11, 586437.	1.5	16
9	Austrian Raw-Milk Hard-Cheese Ripening Involves Successional Dynamics of Non-Inoculated Bacteria and Fungi. <i>Foods</i> , 2020, 9, 1851.	1.9	13
10	Microbiota of newborn calves and their mothers reveals possible transfer routes for newborn calves' gastrointestinal microbiota. <i>PLoS ONE</i> , 2019, 14, e0220554.	1.1	61
11	Reduction potential of steam vacuum and high-pressure water treatment on microbes during beef meat processing. <i>Food Control</i> , 2019, 106, 106728.	2.8	9
12	Culture-Independent Evaluation of Bacterial Contamination Patterns on Pig Carcasses at a Commercial Slaughter Facility. <i>Journal of Food Protection</i> , 2019, 82, 1677-1682.	0.8	4
13	Effects of clay mineral supplementation on particle-associated and epimural microbiota, and gene expression in the rumen of cows fed high-concentrate diet. <i>Anaerobe</i> , 2019, 59, 38-48.	1.0	53
14	<i>Brevibacterium</i> from Austrian hard cheese harbor a putative histamine catabolism pathway and a plasmid for adaptation to the cheese environment. <i>Scientific Reports</i> , 2019, 9, 6164.	1.6	35
15	Microbiota of the Gut-Lymph Node Axis: Depletion of Mucosa-Associated Segmented Filamentous Bacteria and Enrichment of <i>Methanobrevibacter</i> by Colistin Sulfate and Linco-Spectin in Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 599.	1.5	11
16	Microbial shifts in Minas artisanal cheeses from the Serra do Salitre region of Minas Gerais, Brazil throughout ripening time. <i>Food Microbiology</i> , 2019, 82, 349-362.	2.1	32
17	Development of a multi-locus sequence typing system helps reveal the evolution of <i>Cardinium hertigii</i> , a reproductive manipulator symbiont of insects. <i>BMC Microbiology</i> , 2019, 19, 266.	1.3	12
18	Autochthonous facility-specific microbiota dominates washed-rind Austrian hard cheese surfaces and its production environment. <i>International Journal of Food Microbiology</i> , 2018, 267, 54-61.	2.1	31

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19	High-grain diets supplemented with phytogetic compounds or autolyzed yeast modulate ruminal bacterial community and fermentation in dry cows. <i>Journal of Dairy Science</i> , 2018, 101, 2335-2349.	1.4	46
20	Abundance and potential contribution of Gram-negative cheese rind bacteria from Austrian artisanal hard cheeses. <i>International Journal of Food Microbiology</i> , 2018, 266, 95-103.	2.1	17
21	Metatranscriptome Sequencing Reveals Insights into the Gene Expression and Functional Potential of Rumen Wall Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 43.	1.5	54
22	The application of rumen simulation technique (RUSITEC) for studying dynamics of the bacterial community and metabolome in rumen fluid and the effects of a challenge with <i>Clostridium perfringens</i> . <i>PLoS ONE</i> , 2018, 13, e0192256.	1.1	36
23	Biphasic Metabolism and Host Interaction of a Chlamydial Symbiont. <i>MSystems</i> , 2017, 2, .	1.7	32
24	Epimural bacterial community structure in the rumen of Holstein cows with different responses to a long-term subacute ruminal acidosis diet challenge. <i>Journal of Dairy Science</i> , 2017, 100, 1829-1844.	1.4	60
25	Transcriptome Sequencing Reveals Novel Candidate Genes for <i>Cardinium hertigii</i> -Caused Cytoplasmic Incompatibility and Host-Cell Interaction. <i>MSystems</i> , 2017, 2, .	1.7	35
26	Age-Related Differences in the Luminal and Mucosa-Associated Gut Microbiome of Broiler Chickens and Shifts Associated with <i>Campylobacter jejuni</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 154.	1.8	134
27	Epimural Indicator Phylotypes of Transiently-Induced Subacute Ruminal Acidosis in Dairy Cattle. <i>Frontiers in Microbiology</i> , 2016, 7, 274.	1.5	34
28	Psychrophile spoilers dominate the bacterial microbiome in musculature samples of slaughter pigs. <i>Meat Science</i> , 2016, 117, 36-40.	2.7	27
29	High diversity of viable bacteria isolated from lymph nodes of slaughter pigs and its possible impacts for food safety. <i>Journal of Applied Microbiology</i> , 2015, 119, 1420-1432.	1.4	20
30	The Metabolically Active Bacterial Microbiome of Tonsils and Mandibular Lymph Nodes of Slaughter Pigs. <i>Frontiers in Microbiology</i> , 2015, 6, 1362.	1.5	23
31	Pyrosequencing reveals shifts in the bacterial epimural community relative to dietary concentrate amount in goats. <i>Journal of Dairy Science</i> , 2015, 98, 5572-5587.	1.4	46
32	Dietary calcium concentration and cereals differentially affect mineral balance and tight junction proteins expression in jejunum of weaned pigs. <i>British Journal of Nutrition</i> , 2015, 113, 1019-1031.	1.2	13
33	Adaptation of the Cecal Bacterial Microbiome of Growing Pigs in Response to Resistant Starch Type 4. <i>Applied and Environmental Microbiology</i> , 2015, 81, 8489-8499.	1.4	59
34	Mucosa-Associated Bacterial Microbiome of the Gastrointestinal Tract of Weaned Pigs and Dynamics Linked to Dietary Calcium-Phosphorus. <i>PLoS ONE</i> , 2014, 9, e86950.	1.1	106
35	Pyrosequencing reveals diverse fecal microbiota in Simmental calves during early development. <i>Frontiers in Microbiology</i> , 2014, 5, 622.	1.5	78
36	Microbiomes of Unreactive and Pathologically Altered Ileocecal Lymph Nodes of Slaughter Pigs. <i>Applied and Environmental Microbiology</i> , 2014, 80, 193-203.	1.4	27

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37	Cultivation-independent analysis of microbial communities on Austrian raw milk hard cheese rinds. <i>International Journal of Food Microbiology</i> , 2014, 180, 88-97.	2.1	74
38	Rapid testing and quantification of <i>Salmonella</i> in ileocaecal lymph nodes of Austrian pigs slaughtered for consumption. <i>Research in Veterinary Science</i> , 2014, 97, 187-190.	0.9	2
39	Quantification of Gram-positive bacteria: adaptation and evaluation of a preparation strategy using high amounts of clinical tissue. <i>BMC Veterinary Research</i> , 2014, 10, 53.	0.7	25
40	A Robust and Poisson Validated Quantitative 5' Nuclease TaqMan® Real-Time PCR Assay Targeting <i>fimA</i> for the Rapid Detection of <i>Salmonella</i> spp. in Food. <i>Food Analytical Methods</i> , 2013, 6, 991-995.	1.3	12
41	Changing Dietary Calcium-Phosphorus Level and Cereal Source Selectively Alters Abundance of Bacteria and Metabolites in the Upper Gastrointestinal Tracts of Weaned Pigs. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7264-7272.	1.4	64
42	Microbiome Research as an Effective Driver of Success Stories in Agrifood Systems – A Selection of Case Studies. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10