## Bart C Weimer

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

82 7,148 149 42 h-index g-index citations papers 8,570 5.58 159 5.5 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
149	Comparative genomics of the lactic acid bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 15611-6	11.5	1053
148	Microbiota-liberated host sugars facilitate post-antibiotic expansion of enteric pathogens. <i>Nature</i> , <b>2013</b> , 502, 96-9	50.4	630
147	Bacteroides in the infant gut consume milk oligosaccharides via mucus-utilization pathways. <i>Cell Host and Microbe</i> , <b>2011</b> , 10, 507-14	23.4	337
146	Cytosporone B is an agonist for nuclear orphan receptor Nur77. Nature Chemical Biology, 2008, 4, 548-5	611.7	232
145	Contribution of impaired myocardial insulin signaling to mitochondrial dysfunction and oxidative stress in the heart. <i>Circulation</i> , <b>2009</b> , 119, 1272-83	16.7	221
144	Gut microbiota-produced succinate promotes C. difficile infection after antibiotic treatment or motility disturbance. <i>Cell Host and Microbe</i> , <b>2014</b> , 16, 770-7	23.4	209
143	Isolation and characterization of acid- and bile-tolerant isolates from strains of Lactobacillus acidophilus. <i>Journal of Dairy Science</i> , <b>1999</b> , 82, 23-31	4	193
142	Proteomic remodelling of mitochondrial oxidative pathways in pressure overload-induced heart failure. <i>Cardiovascular Research</i> , <b>2010</b> , 85, 376-84	9.9	161
141	Discovering lactic acid bacteria by genomics. <i>Antonie Van Leeuwenhoek</i> , <b>2002</b> , 82, 29-58	2.1	149
140	Broad conservation of milk utilization genes in Bifidobacterium longum subsp. infantis as revealed by comparative genomic hybridization. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 7373-81	4.8	147
139	The Bacterial Mobile Resistome Transfer Network Connecting the Animal and Human Microbiomes. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 6672-6681	4.8	145
138	Comparative genomic analysis of the gut bacterium Bifidobacterium longum reveals loci susceptible to deletion during pure culture growth. <i>BMC Genomics</i> , <b>2008</b> , 9, 247	4.5	140
137	Tissue-specific remodeling of the mitochondrial proteome in type 1 diabetic akita mice. <i>Diabetes</i> , <b>2009</b> , 58, 1986-97	0.9	138
136	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , <b>2018</b> , 16, e2006352	9.7	130
135	Conversion of methionine to thiols by lactococci, lactobacilli, and brevibacteria. <i>Applied and Environmental Microbiology</i> , <b>1998</b> , 64, 3320-6	4.8	119
134	Sulfur metabolism in bacteria associated with cheese. <i>Antonie Van Leeuwenhoek</i> , <b>1999</b> , 76, 247-261	2.1	118
133	Glycosylation of human milk lactoferrin exhibits dynamic changes during early lactation enhancing its role in pathogenic bacteria-host interactions. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, M111.0152	248 <sup>6</sup>	113

132	Purification and characterization of L-methionine gamma-lyase from brevibacterium linens BL2. <i>Applied and Environmental Microbiology</i> , <b>1998</b> , 64, 3327-31	4.8	113
131	Optimizing the immobilization of single-stranded DNA onto glass beads. <i>Journal of Proteomics</i> , <b>2001</b> , 47, 221-31		110
130	Study of biochemical pathways and enzymes involved in pyrene degradation by Mycobacterium sp. strain KMS. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 7821-8	4.8	90
129	DNA Macroarray profiling of Lactococcus lactis subsp. lactis IL1403 gene expression during environmental stresses. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 6738-47	4.8	89
128	Insulin receptor substrate signaling suppresses neonatal autophagy in the heart. <i>Journal of Clinical Investigation</i> , <b>2013</b> , 123, 5319-33	15.9	89
127	Carbohydrate starvation causes a metabolically active but nonculturable state in Lactococcus lactis. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 2498-512	4.8	79
126	Influence of carbohydrate starvation and arginine on culturability and amino acid utilization of lactococcus lactis subsp. lactis. <i>Applied and Environmental Microbiology</i> , <b>1999</b> , 65, 665-73	4.8	78
125	Peptide Accumulation and Bitterness in Cheddar Cheese Made Using Single-Strain Lactococcus lactis Starters with Distinct Proteinase Specificities. <i>Journal of Dairy Science</i> , <b>1998</b> , 81, 327-337	4	77
124	Consumption of lysozyme-rich milk can alter microbial fecal populations. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 6153-60	4.8	70
123	Genetic characterization of a cell envelope-associated proteinase from Lactobacillus helveticus CNRZ32. <i>Journal of Bacteriology</i> , <b>1999</b> , 181, 4592-7	3.5	68
122	Discovering lactic acid bacteria by genomics. Antonie Van Leeuwenhoek, 2002, 82, 29-58	2.1	67
121	Genomic epidemiology of Salmonella enterica serotype Enteritidis based on population structure of prevalent lineages. <i>Emerging Infectious Diseases</i> , <b>2014</b> , 20, 1481-9	10.2	62
120	Enhanced cardiac Akt/protein kinase B signaling contributes to pathological cardiac hypertrophy in part by impairing mitochondrial function via transcriptional repression of mitochondrion-targeted nuclear genes. <i>Molecular and Cellular Biology</i> , <b>2015</b> , 35, 831-46	4.8	61
119	Identification of the leucine-to-2-methylbutyric acid catabolic pathway of Lactococcus lactis. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 4264-73	4.8	57
118	Diversity of sulfur compound production in lactic acid bacteria. <i>Journal of Dairy Science</i> , <b>2000</b> , 83, 2740-	-64	53
117	Intraspecies variation in the emergence of hyperinfectious bacterial strains in nature. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002647	7.6	52
116	Genomic Comparison of Campylobacter spp. and Their Potential for Zoonotic Transmission between Birds, Primates, and Livestock. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 7165-7175	4.8	51
115	Preadaptation to cold stress in Salmonella enterica serovar Typhimurium increases survival during subsequent acid stress exposure. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 7281-9	4.8	50

114	Fallacy of the Unique Genome: Sequence Diversity within Single Strains. MBio, 2017, 8,	7.8	49
113	Functional biogeography as evidence of gene transfer in hypersaline microbial communities. <i>PLoS ONE</i> , <b>2010</b> , 5, e12919	3.7	49
112	Mycoepoxydiene, a fungal polyketide, induces cell cycle arrest at the G2/M phase and apoptosis in HeLa cells. <i>Bioorganic and Medicinal Chemistry Letters</i> , <b>2010</b> , 20, 7054-8	2.9	48
111	Use of capillary electrophoresis and laser-induced fluorescence for attomole detection of amino acids. <i>Journal of Chromatography A</i> , <b>2002</b> , 964, 243-53	4.5	48
110	Genetic loss of insulin receptors worsens cardiac efficiency in diabetes. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2012</b> , 52, 1019-26	5.8	45
109	Gastrointestinal microbes interact with canine adipose-derived mesenchymal stem cells in vitro and enhance immunomodulatory functions. <i>Stem Cells and Development</i> , <b>2014</b> , 23, 1831-43	4.4	43
108	Isolation and characterization of a protease from Pseudomonas fluorescens RO98. <i>Journal of Applied Microbiology</i> , <b>2000</b> , 89, 280-8	4.7	42
107	Salmonella Degrades the Host Glycocalyx Leading to Altered Infection and Glycan Remodeling. <i>Scientific Reports</i> , <b>2016</b> , 6, 29525	4.9	42
106	Microarray analysis reveals potential mechanisms of BRMS1-mediated metastasis suppression. <i>Clinical and Experimental Metastasis</i> , <b>2007</b> , 24, 551-65	4.7	40
105	Influence of growth conditions on heat-stable phospholipase activity in Pseudomonas. <i>Journal of Dairy Research</i> , <b>2001</b> , 68, 109-16	1.6	38
104	Capillary electrophoresis of Cheddar cheese. <i>Journal of Chromatography A</i> , <b>1996</b> , 731, 305-313	4.5	38
103	Influence of a poly-ethylene glycol spacer on antigen capture by immobilized antibodies. <i>Journal of Proteomics</i> , <b>2000</b> , 45, 211-9		36
102	Production of volatile sulfur compounds in Cheddar cheese slurries. <i>International Dairy Journal</i> , <b>1999</b> , 9, 605-611	3.5	36
101	Probiotic bacteria survive in Cheddar cheese and modify populations of other lactic acid bacteria. Journal of Applied Microbiology, <b>2014</b> , 116, 1642-56	4.7	34
100	Monocarboxylic acid production by lactococci and lactobacilli. <i>International Dairy Journal</i> , <b>2004</b> , 14, 237	-3,4,6	34
99	Fatty acid production from amino acids and alpha-keto acids by Brevibacterium linens BL2. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 6385-93	4.8	29
98	A Syst-OMICS Approach to Ensuring Food Safety and Reducing the Economic Burden of Salmonellosis. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 996	5.7	28
97	CESA TRAFFICKING INHIBITOR inhibits cellulose deposition and interferes with the trafficking of cellulose synthase complexes and their associated proteins KORRIGAN1 and POM2/CELLULOSE SYNTHASE INTERACTIVE PROTEIN1. <i>Plant Physiology</i> , <b>2015</b> , 167, 381-93	6.6	28

96	Dissecting the role of milk components on gut microbiota composition. <i>Gut Microbes</i> , <b>2013</b> , 4, 136-9	8.8	28	
95	Metabolome searcher: a high throughput tool for metabolite identification and metabolic pathway mapping directly from mass spectrometry and using genome restriction. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 62	3.6	27	
94	Influence of Host Ecology and Behavior on Campylobacter jejuni Prevalence and Environmental Contamination Risk in a Synanthropic Wild Bird Species. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 4811-20	4.8	27	
93	Complete Genome Sequences of a Clinical Isolate and an Environmental Isolate of Vibrio parahaemolyticus. <i>Genome Announcements</i> , <b>2015</b> , 3,		27	
92	100K Pathogen Genome Project. <i>Genome Announcements</i> , <b>2017</b> , 5,		25	
91	Salmonella Typhimurium Enzymatically Landscapes the Host Intestinal Epithelial Cell (IEC) Surface Glycome to Increase Invasion. <i>Molecular and Cellular Proteomics</i> , <b>2016</b> , 15, 3653-3664	7.6	25	
90	Role of aminotransferase IlvE in production of branched-chain fatty acids by Lactococcus lactis subsp. lactis. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 638-41	4.8	25	
89	Relationship of arginine and lactose utilization by Lactococcus lactis ssp. lactis ML3. <i>International Dairy Journal</i> , <b>2001</b> , 11, 253-258	3.5	25	
88	A new method for converting foodwaste into pathogen free soil amendment for enhancing agricultural sustainability. <i>Journal of Cleaner Production</i> , <b>2016</b> , 112, 205-213	10.3	24	
87	Solid-phase capture of proteins, spores, and bacteria. <i>Applied and Environmental Microbiology</i> , <b>2001</b> , 67, 1300-7	4.8	23	
86	Identification of dehydration responsive genes from two non-nodulated alfalfa cultivars using Medicago truncatula microarrays. <i>Acta Physiologiae Plantarum</i> , <b>2008</b> , 30, 183-199	2.6	22	
85	Prolonged drought imparts lasting compositional changes to the rice root microbiome. <i>Nature Plants</i> , <b>2021</b> , 7, 1065-1077	11.5	22	
84	Tryptophan catabolism in Brevibacterium linens as a potential cheese flavor adjunct. <i>Journal of Dairy Science</i> , <b>2001</b> , 84, 1773-82	4	21	
83	Food authentication from shotgun sequencing reads with an application on high protein powders. <i>Npj Science of Food</i> , <b>2019</b> , 3, 24	6.3	21	
82	Exploring bacterial epigenomics in the next-generation sequencing era: a new approach for an emerging frontier. <i>Trends in Microbiology</i> , <b>2014</b> , 22, 292-300	12.4	20	
81	Biodiversity in microbial communities: system scale patterns and mechanisms. <i>Molecular Ecology</i> , <b>2009</b> , 18, 1455-62	5.7	20	
80	Proteolytic Characterization of Lactobacillus delbrueckii ssp. bulgaricus Strains by the o-Phthaldialdehyde Test and Amino Acid Analysis. <i>Journal of Dairy Science</i> , <b>1991</b> , 74, 398-403	4	20	
79	Genetic mechanisms underlying the pathogenicity of cold-stressed Salmonella enterica serovar typhimurium in cultured intestinal epithelial cells. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 694	4 <del>4</del> .8 4 <del>3</del> -53	19	

78	Cross-talk between E. coli strains and a human colorectal adenocarcinoma-derived cell line. <i>Scientific Reports</i> , <b>2013</b> , 3, 3416	4.9	19
77	Analytical methodologies for broad metabolite coverage of exhaled breath condensate. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , <b>2017</b> , 1061-1062, 17-25	3.2	17
76	Automation of PacBio SMRTbell NGS library preparation for bacterial genome sequencing. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 27		16
75	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in Listeria monocytogenes. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	16
74	Species and genotype diversity drive community and ecosystem properties in experimental microcosms. <i>Evolutionary Ecology</i> , <b>2011</b> , 25, 1107-1125	1.8	16
73	Solid-phase capture of pathogenic bacteria by using gangliosides and detection with real-time PCR. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 2254-8	4.8	16
72	A Semiautomated Reflectance Colorimetric Method for the Determination of Lipase Activity in Milk. <i>Journal of Dairy Science</i> , <b>1996</b> , 79, 1164-1171	4	16
71	Prebiotic Oligosaccharides Potentiate Host Protective Responses against L. Monocytogenes Infection. <i>Pathogens</i> , <b>2017</b> , 6,	4.5	15
70	Comparative analysis of Campylobacter isolates from wild birds and chickens using MALDI-TOF MS, biochemical testing, and DNA sequencing. <i>Journal of Veterinary Diagnostic Investigation</i> , <b>2018</b> , 30, 354-	3 <b>6</b> 1 <sup>5</sup>	15
69	Phylogenetic distance in Great Salt Lake microbial communities. <i>Aquatic Microbial Ecology</i> , <b>2011</b> , 64, 267-273	1.1	15
68	Investigation of the ability of a purified protease from Pseudomonas fluorescens RO98 to hydrolyze bitter peptides from cheese. <i>International Dairy Journal</i> , <b>2000</b> , 10, 75-79	3.5	15
67	Defining the food microbiome for authentication, safety, and process management. <i>IBM Journal of Research and Development</i> , <b>2016</b> , 60, 1:1-1:13	2.5	15
66	Large-Scale Release of Campylobacter Draft Genomes: Resources for Food Safety and Public Health from the 100K Pathogen Genome Project. <i>Genome Announcements</i> , <b>2017</b> , 5,		13
65	Human breath metabolomics using an optimized non-invasive exhaled breath condensate sampler. Journal of Breath Research, <b>2016</b> , 11, 016001	3.1	13
64	Development of larval Schistosoma japonicum blocked in Oncomelania hupensis by pre-infection with larval Exorchis sp. <i>Journal of Parasitology</i> , <b>2009</b> , 95, 1321-5	0.9	12
63	Specific integrin subunits in bovine oocytes, including novel sequences for alpha 6 and beta 3 subunits. <i>Molecular Reproduction and Development</i> , <b>2007</b> , 74, 600-7	2.6	11
62	Analysis of SARS-CoV-2 genomic epidemiology reveals disease transmission coupled to variant emergence and allelic variation. <i>Scientific Reports</i> , <b>2021</b> , 11, 7380	4.9	11
61	Enhanced non-invasive respiratory sampling from bottlenose dolphins for breath metabolomics measurements. <i>Journal of Breath Research</i> , <b>2016</b> , 10, 046005	3.1	11

60	Effect of temperature control on the metabolite content in exhaled breath condensate. <i>Analytica Chimica Acta</i> , <b>2018</b> , 1006, 49-60	6.6	10
59	Draft Genome Sequences of Campylobacter jejuni Strains That Cause Abortion in Livestock. <i>Genome Announcements</i> , <b>2016</b> , 4,		10
58	Draft Genome Sequences of 1,183 Strains from the 100K Pathogen Genome Project. <i>Genome Announcements</i> , <b>2017</b> , 5,		9
57	Amino Acid Catabolism and Its Relationship to Cheese Flavor Outcomes <b>2017</b> , 483-516		9
56	A SEMI-AUTOMATED COLORIMETRIC METHOD FOR DETERMINATION OF AMINOPEPTIDASE ACTIVITY IN TURBID SOLUTIONS 1. <i>Journal of Rapid Methods and Automation in Microbiology</i> , <b>1995</b> , 3, 223-235		9
55	Implication of Sialidases in Infection: Genome Release of Sialidase Knockout Strains from Serovar Typhimurium LT2. <i>Genome Announcements</i> , <b>2017</b> , 5,		7
54	Monitoring the microbiome for food safety and quality using deep shotgun sequencing. <i>Npj Science of Food</i> , <b>2021</b> , 5, 3	6.3	7
53	100K Pathogen Genome Project: 306 Draft Genome Sequences for Food Safety and Public Health. <i>Genome Announcements</i> , <b>2017</b> , 5,		6
52	Exhaled breath condensate methods adapted from human studies using longitudinal metabolomics for predicting early health alterations in dolphins. <i>Analytical and Bioanalytical Chemistry</i> , <b>2017</b> , 409, 65	23 <sup>4</sup> 6 <sup>5</sup> 3	6 <sup>6</sup>
51	Differential ruminal degradation of alfalfa proteins. Canadian Journal of Plant Science, <b>2009</b> , 89, 1065-	1074	6
50	Amino acid metabolism in relationship to cheese flavor development 2007, 70-101		6
49	Pandemic dynamics of COVID-19 using epidemic stage, instantaneous reproductive number and pathogen genome identity (GENI) score: modeling molecular epidemiology		6
48	Biological Machine Learning Combined with Population Genomics Reveals Virulence Gene Allelic Variants Cause Disease. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	5
47	Whole Cell Cross-Linking to Discover Host-Microbe Protein Cognate Receptor/Ligand Pairs. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1585	5.7	5
46	: A Microbial Community Analysis Tool to Identify and Visualize Significantly Responsive Branches in a Phylogenetic Tree. <i>Computational and Structural Biotechnology Journal</i> , <b>2017</b> , 15, 372-378	6.8	5
45	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239677	3.7	5
44	Comparison of Classical Ion Exchange Amino Acid Analysis and o-Phthaldialdehyde Methods to Characterize Proteolysis by Lactobacillus bulgaricus. <i>Journal of Dairy Science</i> , <b>1989</b> , 72, 2873-2876	4	4
43	Improving the flavour of cheese <b>2007</b> ,		4

42	Insular Microbiogeography: Three Pathogens as Exemplars. <i>Current Issues in Molecular Biology</i> , <b>2020</b> , 36, 89-108	2.9	4
41	Molecular cloning and expression levels of the monoterpene synthase gene (ZMM1) in Cassumunar ginger (Zingiber montanum (Koenig) Link ex Dietr.). <i>Archives of Biological Sciences</i> , <b>2014</b> , 66, 1321-1331	0.7	4
40	Diazotrophic bacteria from maize exhibit multifaceted plant growth promotion traits in multiple hosts. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239081	3.7	4
39	Design of the MCAW compute service for food safety bioinformatics. <i>IBM Journal of Research and Development</i> , <b>2016</b> , 60, 2:1-2:12	2.5	4
38	Draft Genome Sequence of Multidrug-Resistant Abortive from Northern California. <i>Genome Announcements</i> , <b>2017</b> , 5,		3
37	Improving Biosecurity Procedures to Minimize the Risk of Spreading Pathogenic Infections Agents After Carcass Recycling. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 623	5.7	3
36	Draft Genome Sequences: Resources for Food Safety and Public Health. <i>Genome Announcements</i> , <b>2017</b> , 5,		3
35	A novel approach to identify bovine sperm membrane proteins that interact with receptors on the vitelline membrane of bovine oocytes. <i>Molecular Reproduction and Development</i> , <b>2008</b> , 75, 641-9	2.6	3
34	Producing low fat cheese <b>2007</b> , 520-536		3
33	Metabolomics in food and nutrition 2013,		3
33	Metabolomics in food and nutrition 2013,  Biological machine learning combined with bacterial population genomics reveals common and rare allelic variants of genes to cause disease		3
	Biological machine learning combined with bacterial population genomics reveals common and rare	8.6	
32	Biological machine learning combined with bacterial population genomics reveals common and rare allelic variants of genes to cause disease  Assessment of gaseous ozone treatment on Salmonella Typhimurium and Escherichia coli O157:H7	8.6	3
32	Biological machine learning combined with bacterial population genomics reveals common and rare allelic variants of genes to cause disease  Assessment of gaseous ozone treatment on Salmonella Typhimurium and Escherichia coli O157:H7 reductions in poultry litter. Waste Management, 2020, 117, 42-47  Identification of Nitrogen Fixation Genes in Isolated from Maize Using Population Genomics and		3
32 31 30	Biological machine learning combined with bacterial population genomics reveals common and rare allelic variants of genes to cause disease  Assessment of gaseous ozone treatment on Salmonella Typhimurium and Escherichia coli O157:H7 reductions in poultry litter. Waste Management, 2020, 117, 42-47  Identification of Nitrogen Fixation Genes in Isolated from Maize Using Population Genomics and Machine Learning. Microorganisms, 2020, 8,  Whole Genome Sequencing of Pediatric Strains Reveals Important Insights Into Their	4.9	3 3
32 31 30 29	Biological machine learning combined with bacterial population genomics reveals common and rare allelic variants of genes to cause disease  Assessment of gaseous ozone treatment on Salmonella Typhimurium and Escherichia coli O157:H7 reductions in poultry litter. Waste Management, 2020, 117, 42-47  Identification of Nitrogen Fixation Genes in Isolated from Maize Using Population Genomics and Machine Learning. Microorganisms, 2020, 8,  Whole Genome Sequencing of Pediatric Strains Reveals Important Insights Into Their Virulence-Associated Traits. Frontiers in Microbiology, 2021, 12, 711577	4.9	<ul><li>3</li><li>3</li><li>3</li><li>3</li></ul>
32 31 30 29 28	Biological machine learning combined with bacterial population genomics reveals common and rare allelic variants of genes to cause disease  Assessment of gaseous ozone treatment on Salmonella Typhimurium and Escherichia coli O157:H7 reductions in poultry litter. Waste Management, 2020, 117, 42-47  Identification of Nitrogen Fixation Genes in Isolated from Maize Using Population Genomics and Machine Learning. Microorganisms, 2020, 8,  Whole Genome Sequencing of Pediatric Strains Reveals Important Insights Into Their Virulence-Associated Traits. Frontiers in Microbiology, 2021, 12, 711577  Responses of Lactic Acid Bacteria to Starvation 2011, 129-144	4.9	3 3 3 3

24	Compounds associated with cheese flavor <b>2007</b> , 26-51	2
23	Gene Expression Arrays in Food <b>2005</b> , 333-343	2
22	Volatile Sulfur Detection in Fermented Foods <b>2005</b> , 397-403	2
21	Sulfur metabolism in bacteria associated with cheese <b>1999</b> , 247-261	2
20	Misclassification of a whole genome sequence reference defined by the Human Microbiome Project: a detrimental carryover effect to microbiome studies	2
19	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage	2
18	Monitoring the microbiome for food safety and quality using deep shotgun sequencing	2
17	Novel LC-MS-TOF method to detect and quantify ascorbic and uric acid simultaneously in different biological matrices. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life 3.2 Sciences</i> , <b>2021</b> , 1168, 122588	. 2
16	Phylogenetic and Biogeographic Patterns of Vibrio parahaemolyticus Strains from North America Inferred from Whole-Genome Sequence Data. <i>Applied and Environmental Microbiology</i> , <b>2021</b> , 87,	3 2
15	Analyses of publicly available genomes revealed genetic distances indicating they belong to more than one species. <i>Virulence</i> , <b>2021</b> , 12, 1950-1964	7 2
14	Molecular Epidemiology and Antimicrobial Resistance of in Hospitalized Patients From Mexico  Frontiers in Microbiology, <b>2021</b> , 12, 787451	2
13	Draft Genome Sequences of Serovar Typhimurium LT2 with Deleted Chitinases That Are Emerging Virulence Factors. <i>Genome Announcements</i> , <b>2017</b> , 5,	1
12	Draft Genome Sequence of Bacillus velezensis CE2, Which Genetically Encodes a Novel Multicomponent Lantibiotic. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1
11	Amino Acids as Food Quality Factors in Parmigiano Reggiano Hard Cheese <b>2017</b> , 357-367	1
10	The Family Brevibacteriaceae <b>2014</b> , 141-153	1
9	Quantification of antibiotic resistance genes and mobile genetic in dairy manure <i>PeerJ</i> , <b>2021</b> , 9, e12408 <sub>3.1</sub>	. 1
8	BREVIBACTERIUM <b>1999</b> , 308-314	0
7	Bacterial Epigenomics: Epigenetics in the Age of Population Genomics <b>2020</b> , 233-252	Ο

- Rumen and lower gut microbiomes relationship with feed efficiency and production traits throughout the lactation of Holstein dairy cows.. *Scientific Reports*, **2022**, 12, 4904
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- 5 Biotechnology of flavor formation in fermented dairy products **2016**, 133-164
- Genomics and cheese flavor **2007**, 219-235
- PURIFICATION OF BOVINE SPERM MEMBRANE-PROTEINS INVOLVED IN SPERM-OOCYTE INTERACTIONS: ADHESION, FUSION, AND ACTIVATION. *Biology of Reproduction*, **2007**, 77, 88-88

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- 2 Lactic Acid Bacteria: Physiology and Stress Responses 2022, 238-248
- Biotechnology of Flavor Production in Dairy Products 56-82