Marc J A Stevens

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7617803/publications.pdf

Version: 2024-02-01

331259 344852 1,623 81 21 36 citations h-index g-index papers 84 84 84 2160 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Unraveling the Genotypic and Phenotypic Diversity of the Psychrophilic Clostridium estertheticum Complex, a Meat Spoilage Agent. Frontiers in Microbiology, 2022, 13, 856810.	1.5	4
2	Identification of Valerate as Carrying Capacity Modulator by Analyzing Lactiplantibacillus plantarum Colonization of Colonic Microbiota in vitro. Frontiers in Microbiology, 2022, 13 , .	1.5	1
3	Listeriosis Caused by Persistence of Listeria monocytogenes Serotype 4b Sequence Type 6 in Cheese Production Environment. Emerging Infectious Diseases, 2021, 27, 284-288.	2.0	2
4	Draft Genome Sequences of 19 Clinical stx -Harboring Escherichia coli O80:H2 Strains. Microbiology Resource Announcements, 2021, 10, .	0.3	1
5	Environmental dissemination of pathogenic Listeria monocytogenes in flowing surface waters in Switzerland. Scientific Reports, 2021, 11, 9066.	1.6	39
6	<i>In Vitro</i> Gut Modeling as a Tool for Adaptive Evolutionary Engineering of <i>Lactiplantibacillus plantarum</i> MSystems, 2021, 6, .	1.7	9
7	Feedborne Salmonella enterica Serovar Jerusalem Outbreak in Different Organic Poultry Flocks in Switzerland and Italy Linked to Soya Expeller. Microorganisms, 2021, 9, 1367.	1.6	2
8	Linezolid-resistant Enterococcus faecalis ST16 harbouring optrA on a Tn6674-like element isolated from surface water. Journal of Global Antimicrobial Resistance, 2021, 25, 89-92.	0.9	5
9	High Occurrence of Shiga Toxin-Producing Escherichia coli in Raw Meat-Based Diets for Companion Animals—A Public Health Issue. Microorganisms, 2021, 9, 1556.	1.6	6
10	Molecular Characterization of Corynebacterium pseudotuberculosis Isolated over a 15-Year Period in Switzerland. Veterinary Sciences, 2021, 8, 151.	0.6	2
11	Draft Genome Sequences of Two Clinical Actinobacillus pleuropneumoniae Serotype 19 Strains from Pigs in Switzerland. Microbiology Resource Announcements, 2021, 10, e0058821.	0.3	2
12	Whole Genome Sequence-Based Identification of Clostridium estertheticum Complex Strains Supports the Need for Taxonomic Reclassification Within the Species Clostridium estertheticum. Frontiers in Microbiology, 2021, 12, 727022.	1.5	10
13	Genetic Context of <i>optrA</i> and <i>poxtA</i> in Florfenicol-Resistant Enterococci Isolated from Flowing Surface Water in Switzerland. Antimicrobial Agents and Chemotherapy, 2021, 65, e0108321.	1.4	13
14	Spread of vancomycin-resistant Enterococcus faecium ST133 in the aquatic environment in Switzerland. Journal of Global Antimicrobial Resistance, 2021, 27, 31-36.	0.9	10
15	Listeriosis Caused by Persistence of <i>Listeria monocytogenes</i> Serotype 4b Sequence Type 6 in Cheese Production Environment. Emerging Infectious Diseases, 2021, 27, 284-288.	2.0	34
16	Bistable auto-aggregation phenotype in Lactiplantibacillus plantarum emerges after cultivation in in vitro colonic microbiota. BMC Microbiology, 2021, 21, 268.	1.3	13
17	Distribution of virulence factors, antimicrobial resistance genes and phylogenetic relatedness among Shiga toxin-producing Escherichia coli serogroup O91 from human infections. International Journal of Medical Microbiology, 2021, 311, 151541.	1.5	8
18	Targeted Genome Mining Reveals the Psychrophilic Clostridium estertheticum Complex as a Potential Source for Novel Bacteriocins, Including Cesin A and Estercticin A. Frontiers in Microbiology, 2021, 12, 801467.	1.5	9

#	Article	IF	Citations
19	Different Shades of Listeria monocytogenes: Strain, Serotype, and Lineage-Based Variability in Virulence and Stress Tolerance Profiles. Frontiers in Microbiology, 2021, 12, 792162.	1.5	24
20	Siblings with typhoid fever: An investigation of intrafamilial transmission, clonality, and antibiotic susceptibility. Travel Medicine and Infectious Disease, 2020, 34, 101498.	1.5	2
21	Draft Genome Sequences of Two Phylogenetically Distinct Clostridium gasigenes Strains, CM001 and CM004, Isolated from Chilled Vacuum-Packed Meat. Microbiology Resource Announcements, 2020, 9, .	0.3	2
22	Environmental dissemination of carbapenemase-producing Enterobacteriaceae in rivers in Switzerland. Environmental Pollution, 2020, 265, 115081.	3.7	51
23	Evolution of Listeria monocytogenes During a Persistent Human Prosthetic Hip Joint Infection. Frontiers in Microbiology, 2020, 11, 1726.	1.5	10
24	The Analysis of Field Strains Isolated From Food, Animal and Clinical Sources Uncovers Natural Mutations in Listeria monocytogenes Nisin Resistance Genes. Frontiers in Microbiology, 2020, 11, 549531.	1.5	9
25	Draft Genome Sequence of Psychrobacter okhotskensis Strain 5179-1A, Isolated from a Raw Cured Ham Storage Crate. Microbiology Resource Announcements, 2020, 9, .	0.3	0
26	Draft Genome Sequences of Two Clostridium algidicarnis Strains Isolated from Meat Juice Samples of Chilled Vacuum-Packed Lamb Meat. Microbiology Resource Announcements, 2020, 9, .	0.3	3
27	Population structure, genetic diversity and pathotypes of Streptococcus suis isolated during the last 13Âyears from diseased pigs in Switzerland. Veterinary Research, 2020, 51, 85.	1.1	22
28	Draft Genome Sequence of Clostridium estertheticum CEST001, Belonging to a Novel Subspecies of C. estertheticum, Isolated from Chilled Vacuum-Packed Lamb Meat Imported to Switzerland. Microbiology Resource Announcements, 2020, 9, .	0.3	4
29	Phenotypic and Genotypic Traits of Vancomycin-Resistant Enterococci from Healthy Food-Producing Animals. Microorganisms, 2020, 8, 261.	1.6	15
30	Draft Genome Sequence of CH_213, a Highly Cytotoxic Bacillus cytotoxicus Strain Isolated from Mashed Potatoes. Microbiology Resource Announcements, 2020, 9, .	0.3	3
31	Draft Genome Sequence of CH_48, a Highly Cytotoxic Bacillus thuringiensis Strain Isolated from Rosemary at the Retail Level. Microbiology Resource Announcements, 2020, 9, .	0.3	0
32	Threeâ€reaction highâ€resolution melting assay for rapid differentiation of <i>Mycobacterium tuberculosis</i> complex members. MicrobiologyOpen, 2019, 8, e919.	1.2	9
33	Global Transcriptional Response of Three Highly Acid-Tolerant Field Strains of Listeria monocytogenes to HCl Stress. Microorganisms, 2019, 7, 455.	1.6	14
34	Full Genome Sequence of pT3, a Multiresistant Plasmid Carrying the mcr-3.5 Colistin Resistance Gene, Recovered from an Extended-Spectrum- \hat{l}^2 -Lactamase-Producing Escherichia coli Isolate from Crickets Sold as Food. Microbiology Resource Announcements, 2019, 8, .	0.3	4
35	Draft Genome Sequence of Salmonella bongori N19-781, a Clinical Strain from a Patient with Diarrhea. Microbiology Resource Announcements, 2019, 8, .	0.3	3
36	Massive Diversity in Whole-Genome Sequences of Streptococcus suis Strains from Infected Pigs in Switzerland. Microbiology Resource Announcements, 2019, 8, .	0.3	5

#	Article	IF	Citations
37	Draft Genome Sequence of Streptococcus parasuis 4253, the First Available for the Species. Microbiology Resource Announcements, 2019, 8, .	0.3	7
38	Variable Carbon Source Utilization, Stress Resistance, and Virulence Profiles Among Listeria monocytogenes Strains Responsible for Listeriosis Outbreaks in Switzerland. Frontiers in Microbiology, 2019, 10, 957.	1.5	30
39	Characteristics of Listeria Monocytogenes Strains Persisting in a Meat Processing Facility over a 4-Year Period. Pathogens, 2019, 8, 32.	1.2	56
40	Shiga toxin-producing Escherichia coli (STEC) isolated from fecal samples of African dromedary camels. One Health, 2019, 7, 100087.	1.5	18
41	Whole-genome-based phylogeny of Bacillus cytotoxicus reveals different clades within the species and provides clues on ecology and evolution. Scientific Reports, 2019, 9, 1984.	1.6	35
42	Screening of lactic acid bacteria and yeast strains to select adapted anti-fungal co-cultures for cocoa bean fermentation. International Journal of Food Microbiology, 2019, 290, 262-272.	2.1	38
43	Vagococcus teuberi sp. nov., isolated from the Malian artisanal sour milk fÃ"nÃ". Systematic and Applied Microbiology, 2018, 41, 65-72.	1.2	19
44	Clustering of Pan- and Core-genome of Lactobacillus provides Novel Evolutionary Insights for Differentiation. BMC Genomics, 2018, 19, 284.	1.2	65
45	The transcriptome response of the ruminal methanogen Methanobrevibacter ruminantium strain M1 to the inhibitor lauric acid. BMC Research Notes, 2018, 11 , 135 .	0.6	6
46	Complete and Assembled Genome Sequences of Pantoea calida DSM 22759 T and Pantoea gaviniae DSM 22758 T. Genome Announcements, $2018, 6, .$	0.8	2
47	Complete and assembled genome sequence of an NDM-9- and CTX-M-15-producing Klebsiella pneumoniae ST147 wastewater isolate from Switzerland. Journal of Global Antimicrobial Resistance, 2018, 13, 53-54.	0.9	16
48	Complete and Assembled Genome Sequence of Salmonella enterica subsp. enterica Serotype Senftenberg N17-509, a Strain Lacking Salmonella Pathogen Island 1. Genome Announcements, 2018, 6, .	0.8	6
49	Draft Genome Sequences of Enterococcus mundtii Strains Isolated from Beef Slaughterhouses in Kenya. Genome Announcements, 2018, 6, .	0.8	1
50	Decontamination of Minimally-Processed Fresh Lettuce Using Reuterin Produced by Lactobacillus reuteri. Frontiers in Microbiology, 2018, 9, 1421.	1.5	30
51	Complete and assembled genome sequence of an NDM-5- and CTX-M-15-producing Escherichia coli sequence type 617 isolated from wastewater in Switzerland. Journal of Global Antimicrobial Resistance, 2018, 15, 105-106.	0.9	15
52	First report of a blaNDM-5-harbouring Escherichia coli ST167 isolated from a wound infection in a dog in Switzerland. Journal of Global Antimicrobial Resistance, 2018, 15, 226-227.	0.9	21
53	An approach to select <i>Lactobacillus</i> isolates as protective cultures for food fermentations. Journal of Food Safety, 2018, 38, e12483.	1.1	3
54	Draft Genome Sequence of Staphylococcus aureus 1608, a Strain That Caused Toxic Mastitis in Twin Cows. Genome Announcements, 2017, 5, .	0.8	3

#	Article	IF	CITATIONS
55	The extracellular proteome of two Bifidobacterium species reveals different adaptation strategies to low iron conditions. BMC Genomics, 2017, 18, 41.	1.2	20
56	Complete and Assembled Genome Sequence of Lactobacillus plantarum RI-113 Isolated from Salami. Genome Announcements, 2017, 5 , .	0.8	6
57	Complete Genome Sequences of Lactobacillus curvatus KG6, <i>L. curvatus </i> MRS6, and Lactobacillus sakei FAM18311, Isolated from Fermented Meat Products. Genome Announcements, 2017, 5,	0.8	9
58	Draft Genome Sequence of Staphylococcus aureus S681, a Tetracycline-Sensitive Livestock-Associated CC398 MRSA Strain. Genome Announcements, 2017, 5, .	0.8	2
59	Enhancing oxidative stress resistance in Bifidobacterium thermophilum using a novel overexpression vector and transformation protocol. Plasmid, 2017, 92, 43-48.	0.4	5
60	Draft Genome Sequences of 43 Lactobacillus Strains from the Species L. curvatus , L. fermentum , L. paracasei , L. plantarum , L. rhamnosus, and L. sakei , Isolated from Food Products. Genome Announcements, 2017, 5, .	0.8	5
61	Complete and Assembled Genome Sequence of Vagococcus teuberi DSM $21459\mathrm{T}$, a Novel Species Isolated from Fermented Cow Milk in Mali. Genome Announcements, $2017,5,.$	0.8	4
62	Bifidobacterium thermophilum RBL67 impacts on growth and virulence gene expression of Salmonella enterica subsp. enterica serovar Typhimurium. BMC Microbiology, 2016, 16, 46.	1.3	33
63	Acrolein contributes strongly to antimicrobial and heterocyclic amine transformation activities of reuterin. Scientific Reports, 2016, 6, 36246.	1.6	90
64	Complete and Assembled Genome Sequence of Staphylococcus aureus RKI4, a Food-Poisoning Strain Exhibiting a Novel S. aureus Pathogenicity Island Carrying seb. Genome Announcements, 2015, 3, .	0.8	3
65	Genomics, evolution, and molecular epidemiology of the Streptococcus bovis / Streptococcus equinus complex (SBSEC). Infection, Genetics and Evolution, 2015, 33, 419-436.	1.0	91
66	High-throughput screening assays for antibacterial and antifungal activities of Lactobacillus species. Journal of Microbiological Methods, 2015, 114, 26-29.	0.7	57
67	Bifidobacterium pseudolongum Strain PV8-2, Isolated from a Stool Sample of an Anemic Kenyan Infant. Genome Announcements, 2015, 3, .	0.8	9
68	Complete and Assembled Genome Sequence of Bifidobacterium kashiwanohense PV20-2, Isolated from the Feces of an Anemic Kenyan Infant. Genome Announcements, 2015, 3, .	0.8	10
69	Bisulfite as scavenger for enhanced biotechnological production of 3-hydroxypropionaldehyde by Lactobacillus reuteri. Biochemical Engineering Journal, 2013, 79, 239-245.	1.8	17
70	pDB2011, a 7.6kb multidrug resistance plasmid from Listeria innocua replicating in Gram-positive and Gram-negative hosts. Plasmid, 2013, 70, 284-287.	0.4	21
71	Comparative genome analysis of Streptococcus infantarius subsp. infantariusCJ18, an African fermented camel milk isolate with adaptations to dairy environment. BMC Genomics, 2013, 14, 200.	1.2	61
72	Complete Genome Sequence of the Probiotic Bifidobacterium thermophilum Strain RBL67. Genome Announcements, 2013, 1 , .	0.8	12

#	ARTICLE	IF	CITATION
73	Complete Genome Sequence of the African Dairy Isolate Streptococcus infantarius subsp. infantarius Strain CJ18. Journal of Bacteriology, 2012, 194, 2105-2106.	1.0	13
74	Monitoring horizontal antibiotic resistance gene transfer in a colonic fermentation model. FEMS Microbiology Ecology, 2011, 78, 210-219.	1.3	39
75	1,3-Propanediol dehydrogenases in Lactobacillus reuteri: impact on central metabolism and 3-hydroxypropionaldehyde production. Microbial Cell Factories, 2011, 10, 61.	1.9	27
76	Construction and characterization of Enterococcus faecalis CG110/gfp/pRE25*, a tool for monitoring horizontal gene transfer in complex microbial ecosystems. FEMS Microbiology Letters, 2010, 313, 111-119.	0.7	14
77	Unexpected consequences of administering bacteriocinogenic probiotic strains for Salmonella populations, revealed by an in vitro colonic model of the child gut. Microbiology (United Kingdom), 2010, 156, 3342-3353.	0.7	40
78	$\ddot{l}f$ 54-mediated control of the mannose phosphotransferase sytem in Lactobacillus plantarum impacts on carbohydrate metabolism. Microbiology (United Kingdom), 2010, 156, 695-707.	0.7	24
79	Involvement of the Mannose Phosphotransferase System of <i>Lactobacillus plantarum</i> WCFS1 in Peroxide Stress Tolerance. Applied and Environmental Microbiology, 2010, 76, 3748-3752.	1.4	37
80	Mixed-Culture Transcriptome Analysis Reveals the Molecular Basis of Mixed-Culture Growth in <i>Streptococcus thermophilus</i> and <i>Lactobacillus bulgaricus</i> Applied and Environmental Microbiology, 2010, 76, 7775-7784.	1.4	194
81	Improvement of <i>Lactobacillus plantarum</i> Aerobic Growth as Directed by Comprehensive Transcriptome Analysis. Applied and Environmental Microbiology, 2008, 74, 4776-4778.	1.4	49