

Eric Altermann

List of Publications by Year in Descending Order

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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.

94
papers

5,893
citations

32
h-index

76
g-index

104
ext. papers

6,877
ext. citations

4.6
avg. IF

5.15
L-index

#	Paper	IF	Citations
94	Draft Genome Sequence of <i>Clostridium bowmanii</i> DSM 14206, Isolated from an Antarctic Microbial Mat.. <i>Microbiology Resource Announcements</i> , 2022 , e0103521	1.3	0
93	Tailored Nanoparticles With the Potential to Reduce Ruminant Methane Emissions.. <i>Frontiers in Microbiology</i> , 2022 , 13, 816695	5.7	0
92	Extracellular Polysaccharide Extraction from in Fermented Milk.. <i>Microbiology Spectrum</i> , 2022 , e02280218.9		
91	PLAN-M; Mycobacteriophage Endolysins Fused to Biodegradable Nanobeads Mitigate Mycobacterial Growth in Liquid and on Surfaces. <i>Frontiers in Microbiology</i> , 2021 , 12, 562748	5.7	0
90	Comparative genomics of <i>Clostridium</i> species associated with vacuum-packed meat spoilage. <i>Food Microbiology</i> , 2021 , 95, 103687	6	11
89	Examination of hydrogen cross-feeders using a colonic microbiota model. <i>BMC Bioinformatics</i> , 2021 , 22, 3	3.6	3
88	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis 2021 , 47-90		
87	Culture and genome-based analysis of four soil <i>Clostridium</i> isolates reveal their potential for antimicrobial production. <i>BMC Genomics</i> , 2021 , 22, 686	4.5	1
86	Structural characterization of a PCP-R didomain from an archaeal nonribosomal peptide synthetase reveals novel interdomain interactions. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100432	5.4	3
85	Draft Genome Sequence of Psychrotolerant sp. Strain M14, Isolated from Spoiled Uncooked Venison. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
84	Competition for Hydrogen Prevents Coexistence of Human Gastrointestinal Hydrogenotrophs in Continuous Culture. <i>Frontiers in Microbiology</i> , 2020 , 11, 1073	5.7	2
83	Mathematical modelling supports the existence of a threshold hydrogen concentration and media-dependent yields in the growth of a reductive acetogen. <i>Bioprocess and Biosystems Engineering</i> , 2020 , 43, 885-894	3.7	4
82	Draft Genome Sequence of a New Zealand Isolate of <i>Mycoplasma ovipneumoniae</i> . <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
81	Complete Genome Sequence of sp. Strain E222, a Bacterial Symbiont of a Fungal Endophyte of Ryegrass. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	3
80	Draft Genome Sequence of <i>Clostridium estertheticum</i> -Like Strain FP3, Isolated from Spoiled Uncooked Lamb. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
79	Extensive bacteriocin gene shuffling in the <i>Streptococcus bovis</i> / <i>Streptococcus equinus</i> complex reveals gallocin D with activity against vancomycin resistant enterococci. <i>Scientific Reports</i> , 2020 , 10, 13431	4.9	5
78	The Effects of Unfermented and Fermented Cow and Sheep Milk on the Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019 , 10, 458	5.7	9

77	Comparative Genomics of Rumen spp. Uncovers a Continuum of Polysaccharide-Degrading Capabilities. <i>Applied and Environmental Microbiology</i> , 2019 , 86,	4.8	25
76	Draft Genome Sequence of <i>Clostridium estertheticum</i> subsp. DSM 14864, Isolated from Spoiled Uncooked Beef. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	7
75	Genetic regulation of antibody responsiveness to immunization in substrains of BALB/c mice. <i>Immunology and Cell Biology</i> , 2019 , 97, 39-53	5	4
74	Live <i>Faecalibacterium prausnitzii</i> induces greater TLR2 and TLR2/6 activation than the dead bacterium in an apical anaerobic co-culture system. <i>Cellular Microbiology</i> , 2018 , 20, e12805	3.9	10
73	Inhibition of Rumen Methanogens by a Novel Archaeal Lytic Enzyme Displayed on Tailored Bionanoparticles. <i>Frontiers in Microbiology</i> , 2018 , 9, 2378	5.7	10
72	Genome Sequences of Potential Probiotic Isolates from Human Infants. <i>Genome Announcements</i> , 2017 , 5,		3
71	Genome Sequences of Strains with Resistance to Arsenic. <i>Genome Announcements</i> , 2017 , 5,		2
70	Complete Genome Sequences of Three Novel SBW25 Bacteriophages, Noxifer, Phabio, and Skulduggery. <i>Genome Announcements</i> , 2017 , 5,		9
69	The complete genome sequence of the rumen bacterium MB2003. <i>Standards in Genomic Sciences</i> , 2017 , 12, 72		15
68	GAMOLA2, a Comprehensive Software Package for the Annotation and Curation of Draft and Complete Microbial Genomes. <i>Frontiers in Microbiology</i> , 2017 , 8, 346	5.7	18
67	Toward Understanding Phage:Host Interactions in the Rumen; Complete Genome Sequences of Lytic Phages Infecting Rumen Bacteria. <i>Frontiers in Microbiology</i> , 2017 , 8, 2340	5.7	16
66	Whole-Genome Sequences of Agricultural, Host-Associated <i>Campylobacter coli</i> and <i>Campylobacter jejuni</i> Strains. <i>Genome Announcements</i> , 2016 , 4,		7
65	Genomic analysis of three <i>Bifidobacterium</i> species isolated from the calf gastrointestinal tract. <i>Scientific Reports</i> , 2016 , 6, 30768	4.9	17
64	The complete genome sequence of the methanogenic archaeon ISO4-H5 provides insights into the methylotrophic lifestyle of a ruminal representative of the Methanomassiliicoccales. <i>Standards in Genomic Sciences</i> , 2016 , 11, 59		26
63	The complete genome sequence of the rumen methanogen <i>Methanobrevibacter millerae</i> SM9. <i>Standards in Genomic Sciences</i> , 2016 , 11, 49		5
62	Novel plasmid conferring kanamycin and tetracycline resistance in the turkey-derived <i>Campylobacter jejuni</i> strain 11601MD. <i>Plasmid</i> , 2016 , 86, 32-37	3.3	16
61	The complete genome sequence of <i>Eubacterium limosum</i> SA11, a metabolically versatile rumen acetogen. <i>Standards in Genomic Sciences</i> , 2016 , 11, 26		15
60	The Draft Genome Sequence of the <i>Yersinia entomophaga</i> Entomopathogenic Type Strain MH96T. <i>Toxins</i> , 2016 , 8,	4.9	14

59	Draft Genome Sequence of the Rumen Methanogen <i>Methanobrevibacter olleyae</i> YLM1. <i>Genome Announcements</i> , 2016 , 4,		8
58	Draft Genome Sequences of Two Historical <i>Listeria monocytogenes</i> Strains from Human Listeriosis Cases in 1933. <i>Genome Announcements</i> , 2016 , 4,		1
57	Complete Genome Sequence of Methanogenic Archaeon ISO4-G1, a Member of the Methanomassiliicoccales, Isolated from a Sheep Rumen. <i>Genome Announcements</i> , 2016 , 4,		8
56	Evaluation of <i>Lactococcus lactis</i> Isolates from Nondairy Sources with Potential Dairy Applications Reveals Extensive Phenotype-Genotype Disparity and Implications for a Revised Species. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 3961-72	4.8	27
55	<i>Lactobacillus fermentum</i> AGR1487 cell surface structures and supernatant increase paracellular permeability through different pathways. <i>MicrobiologyOpen</i> , 2015 , 4, 541-52	3-4	2
54	The complete genome sequence of the rumen methanogen <i>Methanosarcina barkeri</i> CM1. <i>Standards in Genomic Sciences</i> , 2015 , 10, 57		29
53	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. <i>BMC Genomics</i> , 2014 , 15, 356	4-5	11
52	The complete genome sequence of the rumen methanogen <i>Methanobacterium formicicum</i> BRM9. <i>Standards in Genomic Sciences</i> , 2014 , 9, 15		23
51	Draft Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> HPT, the First Defined-Strain Dairy Starter Culture Bacterium. <i>Genome Announcements</i> , 2014 , 2,		8
50	Invited commentary: lubricating the rusty wheel, new insights into iron oxidizing bacteria through comparative genomics. <i>Frontiers in Microbiology</i> , 2014 , 5, 386	5-7	3
49	Draft Genome Sequence of <i>Lactobacillus animalis</i> 381-IL-28. <i>Genome Announcements</i> , 2014 , 2,		4
48	Draft Genome Sequence of the Pediocin-Encoding Biopreservative and Biocontrol Strain <i>Pediococcus acidilactici</i> D3. <i>Genome Announcements</i> , 2013 , 1,		4
47	The role of cell surface architecture of lactobacilli in host-microbe interactions in the gastrointestinal tract. <i>Mediators of Inflammation</i> , 2013 , 2013, 237921	4-3	142
46	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013 , 8, 215-27		36
45	Genome sequencing of rumen bacteria and archaea and its application to methane mitigation strategies. <i>Animal</i> , 2013 , 7 Suppl 2, 235-43	3-1	68
44	Interaction between the genomes of <i>Lactococcus lactis</i> and phages of the P335 species. <i>Frontiers in Microbiology</i> , 2013 , 4, 257	5-7	32
43	Tracing lifestyle adaptation in prokaryotic genomes. <i>Frontiers in Microbiology</i> , 2012 , 3, 48	5-7	24
42	Chromosomal tet(O)-harboring regions in <i>Campylobacter coli</i> isolates from turkeys and swine. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8488-91	4.8	9

41	Exploring rumen methanogen genomes to identify targets for methane mitigation strategies. <i>Animal Feed Science and Technology</i> , 2011 , 166-167, 65-75	3	31
40	Transposition of Tn916 in the four replicons of the <i>Butyrivibrio proteoclasticus</i> B316(T) genome. <i>FEMS Microbiology Letters</i> , 2011 , 316, 144-51	2.9	7
39	Strategies to reduce methane emissions from farmed ruminants grazing on pasture. <i>Veterinary Journal</i> , 2011 , 188, 11-7	2.5	100
38	The large episomes of <i>Butyrivibrio proteoclasticus</i> B316T have arisen through intragenomic gene shuttling from the chromosome to smaller <i>Butyrivibrio</i> -specific plasmids. <i>Plasmid</i> , 2011 , 66, 67-78	3.3	5
37	Group-specific comparison of four lactobacilli isolated from human sources using differential blast analysis. <i>Genes and Nutrition</i> , 2011 , 6, 319-40	4.3	9
36	Specialized adaptation of a lactic acid bacterium to the milk environment: the comparative genomics of <i>Streptococcus thermophilus</i> LMD-9. <i>Microbial Cell Factories</i> , 2011 , 10 Suppl 1, S22	6.4	75
35	A comparison of analog and Next-Generation transcriptomic tools for mammalian studies. <i>Briefings in Functional Genomics</i> , 2011 , 10, 135-50	4.9	48
34	The glyco biome of the rumen bacterium <i>Butyrivibrio proteoclasticus</i> B316(T) highlights adaptation to a polysaccharide-rich environment. <i>PLoS ONE</i> , 2010 , 5, e11942	3.7	70
33	The genome sequence of the rumen methanogen <i>Methanobrevibacter ruminantium</i> reveals new possibilities for controlling ruminant methane emissions. <i>PLoS ONE</i> , 2010 , 5, e8926	3.7	202
32	Sequence analysis of <i>Leuconostoc mesenteroides</i> bacteriophage Phi1-A4 isolated from an industrial vegetable fermentation. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 1955-66	4.8	36
31	Sequence analysis of plasmid pIR52-1 from <i>Lactobacillus helveticus</i> R0052 and investigation of its origin of replication. <i>Plasmid</i> , 2010 , 63, 108-17	3.3	16
30	Phylogenetic evidence for lateral gene transfer in the intestine of marine iguanas. <i>PLoS ONE</i> , 2010 , 5, e10785	3.7	11
29	Analysis of the genome sequence of <i>Lactobacillus gasseri</i> ATCC 33323 reveals the molecular basis of an autochthonous intestinal organism. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 4610-25	4.8	132
28	S layer protein A of <i>Lactobacillus acidophilus</i> NCFM regulates immature dendritic cell and T cell functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 19474-9	11.5	429
27	Functional genomics of probiotic <i>Lactobacilli</i> . <i>Journal of Clinical Gastroenterology</i> , 2008 , 42 Suppl 3 Pt 2, S160-2	3	56
26	Influence of the dairy environment on gene expression and substrate utilization in lactic acid bacteria. <i>Journal of Nutrition</i> , 2007 , 137, 748S-50S	4.1	26
25	Comparative genomics and transcriptional analysis of prophages identified in the genomes of <i>Lactobacillus gasseri</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 3130-46	4.8	57
24	Comparative genomics of the lactic acid bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15611-6	11.5	1053

23	Sequence analysis of the Lactobacillus plantarum bacteriophage PhiJL-1. <i>Gene</i> , 2005 , 348, 45-54	3.8	21
22	Genomic features of lactic acid bacteria effecting bioprocessing and health. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 393-409	15.1	152
21	PathwayVoyager: pathway mapping using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. <i>BMC Genomics</i> , 2005 , 6, 60	4.5	222
20	Genomic Perspectives on Probiotic Lactic Acid Bacteria. <i>Bioscience and Microflora</i> , 2005 , 24, 31-33		3
19	Functional analysis of putative adhesion factors in Lactobacillus acidophilus NCFM. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8344-51	4.8	295
18	Microarray analysis of a two-component regulatory system involved in acid resistance and proteolytic activity in Lactobacillus acidophilus. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 5794-804	4.8	106
17	Complete genome sequence of the probiotic lactic acid bacterium Lactobacillus acidophilus NCFM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 3906-12	11.5	472
16	Genomic features of lactic acid bacteria effecting bioprocessing and health. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 393-409	15.1	70
15	Genetic markers unique to Listeria monocytogenes serotype 4b differentiate epidemic clone II (hot dog outbreak strains) from other lineages. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 2383-90	4.8	63
14	Epidemic Clone I-Specific Genetic Markers in Strains of Listeria monocytogenes Serotype 4b from Foods. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 7581-7581	4.8	78
13	Epidemic clone I-specific genetic markers in strains of Listeria monocytogenes serotype 4b from foods. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 4158-64	4.8	52
12	The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 2512-7	11.5	402
11	Identification and inactivation of genetic loci involved with Lactobacillus acidophilus acid tolerance. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 5315-22	4.8	119
10	Identification and phenotypic characterization of the cell-division protein CdpA. <i>Gene</i> , 2004 , 342, 189-97	3.8	41
9	GAMOLA: a new local solution for sequence annotation and analyzing draft and finished prokaryotic genomes. <i>OMICS A Journal of Integrative Biology</i> , 2003 , 7, 161-9	3.8	66
8	Isolation and characterization of a Lactobacillus plantarum bacteriophage, phiJL-1, from a cucumber fermentation. <i>International Journal of Food Microbiology</i> , 2003 , 84, 225-35	5.8	129
7	Functional and comparative genomic analyses of an operon involved in fructooligosaccharide utilization by Lactobacillus acidophilus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8957-62	11.5	218
6	Transcript map of the temperate Lactobacillus gasseri bacteriophage phiadh. <i>Microbiology (United Kingdom)</i> , 2003 , 149, 2987-2999	2.9	4

5	Discovering lactic acid bacteria by genomics. <i>Antonie Van Leeuwenhoek</i> , 2002 , 82, 29-58	2.1	149
4	Discovering lactic acid bacteria by genomics. <i>Antonie Van Leeuwenhoek</i> , 2002 , 82, 29-58	2.1	67
3	Synthesis and automated detection of fluorescently labeled primer extension products. <i>BioTechniques</i> , 1999 , 26, 96-8, 101	2.5	22
2	Primary structure and features of the genome of the <i>Lactobacillus gasseri</i> temperate bacteriophage (phi)adh. <i>Gene</i> , 1999 , 236, 333-46	3.8	47
1	Structure of a genome region of the <i>Lactobacillus gasseri</i> temperate phage phiadh covering a repressor gene and cognate promoters. <i>Gene</i> , 1998 , 210, 61-70	3.8	30