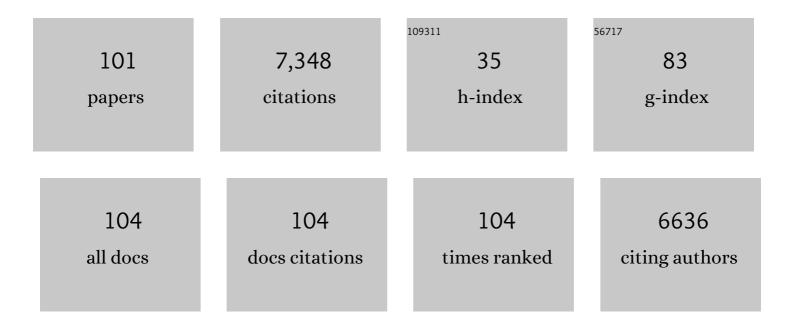
## Eric Altermann

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comparative genomics of the lactic acid bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15611-15616.	7.1	1,303
2	Complete genome sequence of the probiotic lactic acid bacterium <i>Lactobacillus acidophilus</i> NCFM. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3906-3912.	7.1	565
3	S layer protein A of <i>Lactobacillus acidophilus</i> NCFM regulates immature dendritic cell and T cell functions. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19474-19479.	7.1	515
4	The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2512-2517.	7.1	476
5	Functional Analysis of Putative Adhesion Factors in <i>Lactobacillus acidophilus</i> NCFM. Applied and Environmental Microbiology, 2005, 71, 8344-8351.	3.1	350
6	PathwayVoyager: pathway mapping using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. BMC Genomics, 2005, 6, 60.	2.8	286
7	The Genome Sequence of the Rumen Methanogen Methanobrevibacter ruminantium Reveals New Possibilities for Controlling Ruminant Methane Emissions. PLoS ONE, 2010, 5, e8926.	2.5	256
8	Functional and comparative genomic analyses of an operon involved in fructooligosaccharide utilization by Lactobacillus acidophilus. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8957-8962.	7.1	245
9	The Role of Cell Surface Architecture of Lactobacilli in Host-Microbe Interactions in the Gastrointestinal Tract. Mediators of Inflammation, 2013, 2013, 1-16.	3.0	199
10	Genomic features of lactic acid bacteria effecting bioprocessing and health. FEMS Microbiology Reviews, 2005, 29, 393-409.	8.6	176
11	Discovering lactic acid bacteria by genomics. Antonie Van Leeuwenhoek, 2002, 82, 29-58.	1.7	164
12	Isolation and characterization of a Lactobacillus plantarum bacteriophage, ΦJL-1, from a cucumber fermentation. International Journal of Food Microbiology, 2003, 84, 225-235.	4.7	160
13	Analysis of the Genome Sequence of <i>Lactobacillus gasseri </i> ATCC 33323 Reveals the Molecular Basis of an Autochthonous Intestinal Organism. Applied and Environmental Microbiology, 2008, 74, 4610-4625.	3.1	152
14	Identification and Inactivation of Genetic Loci Involved with Lactobacillus acidophilus Acid Tolerance. Applied and Environmental Microbiology, 2004, 70, 5315-5322.	3.1	144
15	Strategies to reduce methane emissions from farmed ruminants grazing on pasture. Veterinary Journal, 2011, 188, 11-17.	1.7	130
16	Specialized adaptation of a lactic acid bacterium to the milk environment: the comparative genomics of Streptococcus thermophilus LMD-9. Microbial Cell Factories, 2011, 10, S22.	4.0	124
17	Microarray Analysis of a Two-Component Regulatory System Involved in Acid Resistance and Proteolytic Activity in Lactobacillus acidophilus. Applied and Environmental Microbiology, 2005, 71, 5794-5804.	3.1	120
18	The Glycobiome of the Rumen Bacterium Butyrivibrio proteoclasticus B316T Highlights Adaptation to a Polysaccharide-Rich Environment. PLoS ONE, 2010, 5, e11942.	2.5	102

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19	Genomic features of lactic acid bacteria effecting bioprocessing and health. FEMS Microbiology Reviews, 2005, 29, 393-409.	8.6	101
20	Genome sequencing of rumen bacteria and archaea and its application to methane mitigation strategies. Animal, 2013, 7, 235-243.	3.3	92
21	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of Lactobacillus gasseri, Lactobacillus salivarius, and Lactobacillus casei. Applied and Environmental Microbiology, 2006, 72, 3130-3146.	3.1	75
22	Discovering lactic acid bacteria by genomics. , 2002, 82, 29-58.		74
23	Genetic Markers Unique to Listeria monocytogenes Serotype 4b Differentiate Epidemic Clone II (Hot) Tj ETQq1 1 2383-2390.	0.784314 3.1	rgBT /Overic 72
24	CAMOLA: A New Local Solution for Sequence Annotation and Analyzing Draft and Finished Prokaryotic Genomes. OMICS A Journal of Integrative Biology, 2003, 7, 161-169.	2.0	68
25	Functional Genomics of Probiotic Lactobacilli. Journal of Clinical Gastroenterology, 2008, 42, S160-S162.	2.2	67
26	Comparative Genomics of Rumen <i>Butyrivibrio</i> spp. Uncovers a Continuum of Polysaccharide-Degrading Capabilities. Applied and Environmental Microbiology, 2019, 86, .	3.1	65
27	Identification and phenotypic characterization of the cell-division protein CdpA. Gene, 2004, 342, 189-197.	2.2	59
28	A comparison of analog and Next-Generation transcriptomic tools for mammalian studies. Briefings in Functional Genomics, 2011, 10, 135-150.	2.7	59
29	Epidemic Clone I-Specific Genetic Markers in Strains of Listeria monocytogenes Serotype 4b from Foods. Applied and Environmental Microbiology, 2004, 70, 4158-4164.	3.1	56
30	Primary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage φadh. Gene, 1999, 236, 333-346.	2.2	49
31	The Complete Genome Sequence of Methanobrevibacter sp. AbM4. Standards in Genomic Sciences, 2013, 8, 215-227.	1.5	42
32	The complete genome sequence of the rumen methanogen Methanosarcina barkeri CM1. Standards in Genomic Sciences, 2015, 10, 57.	1.5	42
33	Sequence Analysis of <i>Leuconostoc mesenteroides</i> Bacteriophage Φ1-A4 Isolated from an Industrial Vegetable Fermentation. Applied and Environmental Microbiology, 2010, 76, 1955-1966.	3.1	41
34	The complete genome sequence of the methanogenic archaeon ISO4-H5 provides insights into the methylotrophic lifestyle of a ruminal representative of the Methanomassiliicoccales. Standards in Genomic Sciences, 2016, 11, 59.	1.5	41
35	Evaluation of Lactococcus lactis Isolates from Nondairy Sources with Potential Dairy Applications Reveals Extensive Phenotype-Genotype Disparity and Implications for a Revised Species. Applied and Environmental Microbiology, 2015, 81, 3961-3972.	3.1	40
36	Tracing Lifestyle Adaptation in Prokaryotic Genomes. Frontiers in Microbiology, 2012, 3, 48.	3.5	39

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37	Exploring rumen methanogen genomes to identify targets for methane mitigation strategies. Animal Feed Science and Technology, 2011, 166-167, 65-75.	2.2	36
38	Interaction between the genomes of Lactococcus lactis and phages of the P335 species. Frontiers in Microbiology, 2013, 4, 257.	3.5	36
39	The complete genome sequence of Eubacterium limosum SA11, a metabolically versatile rumen acetogen. Standards in Genomic Sciences, 2016, 11, 26.	1.5	36
40	Structure of a genome region of the Lactobacillus gasseri temperate phage φadh covering a repressor gene and cognate promoters. Gene, 1998, 210, 61-70.	2.2	31
41	GAMOLA2, a Comprehensive Software Package for the Annotation and Curation of Draft and Complete Microbial Genomes. Frontiers in Microbiology, 2017, 8, 346.	3.5	31
42	Novel plasmid conferring kanamycin and tetracycline resistance in the turkey-derived Campylobacter jejuni strain 11601MD. Plasmid, 2016, 86, 32-37.	1.4	30
43	Influence of the Dairy Environment on Gene Expression and Substrate Utilization in Lactic Acid Bacteria1, ,. Journal of Nutrition, 2007, 137, 748S-750S.	2.9	29
44	The complete genome sequence of the rumen bacterium Butyrivibrio hungatei MB2003. Standards in Genomic Sciences, 2017, 12, 72.	1.5	29
45	Toward Understanding Phage:Host Interactions in the Rumen; Complete Genome Sequences of Lytic Phages Infecting Rumen Bacteria. Frontiers in Microbiology, 2017, 8, 2340.	3.5	28
46	The complete genome sequence of the rumen methanogen Methanobacterium formicicum BRM9. Standards in Genomic Sciences, 2014, 9, 15.	1.5	27
47	Synthesis and Automated Detection of Fluorescently Labeled Primer Extension Products. BioTechniques, 1999, 26, 96-101.	1.8	25
48	Comparative genomics of Clostridium species associated with vacuum-packed meat spoilage. Food Microbiology, 2021, 95, 103687.	4.2	25
49	Sequence analysis of the Lactobacillus plantarum bacteriophage $\hat{I}_{i}^{\dagger}$ JL-1. Gene, 2005, 348, 45-54.	2.2	24
50	Chromosomal <i>tet</i> (O)-Harboring Regions in Campylobacter coli Isolates from Turkeys and Swine. Applied and Environmental Microbiology, 2012, 78, 8488-8491.	3.1	23
51	Inhibition of Rumen Methanogens by a Novel Archaeal Lytic Enzyme Displayed on Tailored Bionanoparticles. Frontiers in Microbiology, 2018, 9, 2378.	3.5	22
52	Complete Genome Sequences of Three Novel Pseudomonas fluorescens SBW25 Bacteriophages, Noxifer, Phabio, and Skulduggery. Genome Announcements, 2017, 5, .	0.8	21
53	Genomic analysis of three Bifidobacterium species isolated from the calf gastrointestinal tract. Scientific Reports, 2016, 6, 30768.	3.3	20
54	Sequence analysis of plasmid pIR52-1 from Lactobacillus helveticus R0052 and investigation of its origin of replication. Plasmid, 2010, 63, 108-117.	1.4	17

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55	The Draft Genome Sequence of the Yersinia entomophaga Entomopathogenic Type Strain MH96T. Toxins, 2016, 8, 143.	3.4	17
56	The complete genome sequence of the rumen methanogen Methanobrevibacter millerae SM9. Standards in Genomic Sciences, 2016, 11, 49.	1.5	15
57	The Effects of Unfermented and Fermented Cow and Sheep Milk on the Gut Microbiota. Frontiers in Microbiology, 2019, 10, 458.	3.5	15
58	Phylogenetic Evidence for Lateral Gene Transfer in the Intestine of Marine Iguanas. PLoS ONE, 2010, 5, e10785.	2.5	15
59	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. BMC Genomics, 2014, 15, 356.	2.8	13
60	Draft Genome Sequence of Clostridium estertheticum subsp. <i>laramiense</i> DSM 14864 <sup>T</sup> , Isolated from Spoiled Uncooked Beef. Microbiology Resource Announcements, 2019, 8, .	0.6	13
61	Live <i>Faecalibacterium prausnitzii</i> induces greater TLR2 and TLR2/6 activation than the dead bacterium in an apical anaerobic co-culture system. Cellular Microbiology, 2018, 20, e12805.	2.1	12
62	Examination of hydrogen cross-feeders using a colonic microbiota model. BMC Bioinformatics, 2021, 22, 3.	2.6	12
63	Draft Genome Sequence of the Rumen Methanogen Methanobrevibacter olleyae YLM1. Genome Announcements, 2016, 4, .	0.8	11
64	Transposition of Tn916â $\in f$ in the four replicons of the Butyrivibrio proteoclasticus B316T genome. FEMS Microbiology Letters, 2011, 316, 144-151.	1.8	10
65	Group-specific comparison of four lactobacilli isolated from human sources using differential blast analysis. Genes and Nutrition, 2011, 6, 319-340.	2.5	10
66	Genetic regulation of antibody responsiveness to immunization in substrains of <scp>BALB</scp> /c mice. Immunology and Cell Biology, 2019, 97, 39-53.	2.3	10
67	Extensive bacteriocin gene shuffling in the Streptococcus bovis/Streptococcus equinus complex reveals gallocin D with activity against vancomycin resistant enterococci. Scientific Reports, 2020, 10, 13431.	3.3	10
68	Complete Genome Sequence of Methanogenic Archaeon ISO4-G1, a Member of the <i>Methanomassiliicoccales</i> , Isolated from a Sheep Rumen. Genome Announcements, 2016, 4, .	0.8	9
69	Genome Sequences of Potential Probiotic Lactobacillus rhamnosus Isolates from Human Infants. Genome Announcements, 2017, 5, .	0.8	9
70	Draft Genome Sequence of Lactococcus lactis subsp. cremoris HP T , the First Defined-Strain Dairy Starter Culture Bacterium. Genome Announcements, 2014, 2, .	0.8	8
71	Structural characterization of a PCP–R didomain from an archaeal nonribosomal peptide synthetase reveals novel interdomain interactions. Journal of Biological Chemistry, 2021, 296, 100432.	3.4	8
72	Whole-Genome Sequences of Agricultural, Host-Associated Campylobacter coli and Campylobacter jejuni Strains. Genome Announcements, 2016, 4, .	0.8	7

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73	Mathematical modelling supports the existence of a threshold hydrogen concentration and media-dependent yields in the growth of a reductive acetogen. Bioprocess and Biosystems Engineering, 2020, 43, 885-894.	3.4	7
74	The large episomes of Butyrivibrio proteoclasticus B316T have arisen through intragenomic gene shuttling from the chromosome to smaller Butyrivibrio-specific plasmids. Plasmid, 2011, 66, 67-78.	1.4	6
75	PLAN-M; Mycobacteriophage Endolysins Fused to Biodegradable Nanobeads Mitigate Mycobacterial Growth in Liquid and on Surfaces. Frontiers in Microbiology, 2021, 12, 562748.	3.5	6
76	Complete Genome Sequence of <i>Paenibacillus</i> sp. Strain E222, a Bacterial Symbiont of an <i>Epichloë</i> Fungal Endophyte of Ryegrass. Microbiology Resource Announcements, 2020, 9, .	0.6	6
77	Invited commentary: lubricating the rusty wheel, new insights into iron oxidizing bacteria through comparative genomics. Frontiers in Microbiology, 2014, 5, 386.	3.5	5
78	Mapping immunogenic epitopes of an adhesin-like protein from Methanobrevibacter ruminantium M1 and comparison of empirical data with in silico prediction methods. Scientific Reports, 2022, 12, .	3.3	5
79	Transcript map of the temperate Lactobacillus gasseri bacteriophage ϕadh. Microbiology (United) Tj ETQq1 1	. 0.784314 rgl 1.8	3T JOverlock
80	Draft Genome Sequence of the Pediocin-Encoding Biopreservative and Biocontrol Strain Pediococcus acidilactici D3. Genome Announcements, 2013, 1, .	0.8	4
81	Draft Genome Sequence of Lactobacillus animalis 381-IL-28. Genome Announcements, 2014, 2, .	0.8	4
82	Lactobacillus fermentum AGR1487 cell surface structures and supernatant increase paracellular permeability through different pathways. MicrobiologyOpen, 2015, 4, 541-552.	3.0	4
83	Competition for Hydrogen Prevents Coexistence of Human Gastrointestinal Hydrogenotrophs in Continuous Culture. Frontiers in Microbiology, 2020, 11, 1073.	3.5	4
84	Draft Genome Sequence of a New Zealand Isolate of Mycoplasma ovipneumoniae. Microbiology Resource Announcements, 2020, 9, .	0.6	4
85	Culture and genome-based analysis of four soil Clostridium isolates reveal their potential for antimicrobial production. BMC Genomics, 2021, 22, 686.	2.8	4
86	Tailored Nanoparticles With the Potential to Reduce Ruminant Methane Emissions. Frontiers in Microbiology, 2022, 13, 816695.	3.5	4
87	Genomic Perspectives on Probiotic Lactic Acid Bacteria. Bioscience and Microflora, 2005, 24, 31-33.	0.5	3
88	Draft Genome Sequence of Clostridium estertheticum-Like Strain FP3, Isolated from Spoiled Uncooked Lamb. Microbiology Resource Announcements, 2020, 9, .	0.6	3
89	Draft Genome Sequence of Psychrotolerant <i>Clostridium</i> sp. Strain M14, Isolated from Spoiled Uncooked Venison. Microbiology Resource Announcements, 2020, 9, .	0.6	3
90	Draft Genome Sequence of Clostridium sp. Strain FP1, with Similarity to Clostridium tagluense , Isolated from Spoiled Lamb. Microbiology Resource Announcements, 2020, 9, .	0.6	3

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91	Inhibition of Listeria monocytogenes by Phage Lytic Enzymes Displayed on Tailored Bionanoparticles. Foods, 2022, 11, 854.	4.3	3
92	Draft Genome Sequences of Two Historical Listeria monocytogenes Strains from Human Listeriosis Cases in 1933. Genome Announcements, 2016, 4, .	0.8	2
93	Genome Sequences of Listeria monocytogenes Strains with Resistance to Arsenic. Genome Announcements, 2017, 5, .	0.8	2
94	Complete Genome Sequence of Lactobacillus fermentum Strain AGR1485, a Human Oral Isolate. Microbiology Resource Announcements, 2020, 9, .	0.6	2
95	Extracellular Polysaccharide Extraction from <i>Streptococcus thermophilus</i> in Fermented Milk. Microbiology Spectrum, 2022, 10, e0228021.	3.0	2
96	Complete Annotated Genome Sequence of Limosilactobacillus fermentum AGR1487. Microbiology Resource Announcements, 2021, 10, .	0.6	1
97	Draft Genome Sequence of Clostridium bowmanii DSM 14206 T , Isolated from an Antarctic Microbial Mat. Microbiology Resource Announcements, 2022, , e0103521.	0.6	1
98	A Return to Microbial Genomes in the Metagenome Age. Journal of Microbial & Biochemical Technology, 2012, 04, .	0.2	0
99	Identification of a <i>Campylobacter coli</i> methyltransferase targeting adenines at GATC sites. FEMS Microbiology Letters, 2017, 364, fnw268.	1.8	0
100	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
101	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		Ο