

# Douwe Molenaar

## List of Publications by Year in descending order

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115  
papers

11,040  
citations

30070

54  
h-index

32842

100  
g-index

125  
all docs

125  
docs citations

125  
times ranked

10684  
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genome sequence of <i>Lactobacillus plantarum</i> WCFS1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1990-1995.	7.1	1,326
2	Shifts in growth strategies reflect tradeoffs in cellular economics. Molecular Systems Biology, 2009, 5, 323.	7.2	535
3	Development and application of the human intestinal tract chip, a phylogenetic microarray: analysis of universally conserved phylotypes in the abundant microbiota of young and elderly adults. Environmental Microbiology, 2009, 11, 1736-1751.	3.8	420
4	A heat shock following electroporation induces highly efficient transformation of <i>Corynebacterium glutamicum</i> with xenogeneic plasmid DNA. Applied Microbiology and Biotechnology, 1999, 52, 541-545.	3.6	406
5	Biodiversity-Based Identification and Functional Characterization of the Mannose-Specific Adhesin of <i>Lactobacillus plantarum</i> . Journal of Bacteriology, 2005, 187, 6128-6136.	2.2	272
6	Phenotypic and genomic diversity of <i>Lactobacillus plantarum</i> strains isolated from various environmental niches. Environmental Microbiology, 2010, 12, 758-773.	3.8	262
7	Analysis of Growth of <i>Lactobacillus plantarum</i> WCFS1 on a Complex Medium Using a Genome-scale Metabolic Model. Journal of Biological Chemistry, 2006, 281, 40041-40048.	3.4	261
8	The micro-Petri dish, a million-well growth chip for the culture and high-throughput screening of microorganisms. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18217-18222.	7.1	255
9	Exploring <i>Lactobacillus plantarum</i> Genome Diversity by Using Microarrays. Journal of Bacteriology, 2005, 187, 6119-6127.	2.2	229
10	Finding Functional Differences Between Species in a Microbial Community: Case Studies in Wine Fermentation and Kefir Culture. Frontiers in Microbiology, 2019, 10, 1347.	3.5	229
11	Generation of a proton motive force by histidine decarboxylation and electrogenic histidine/histamine antiport in <i>Lactobacillus buchneri</i> . Journal of Bacteriology, 1993, 175, 2864-2870.	2.2	218
12	Identification of Prebiotic Fructooligosaccharide Metabolism in <i>Lactobacillus plantarum</i> WCFS1 through Microarrays. Applied and Environmental Microbiology, 2007, 73, 1753-1765.	3.1	210
13	An alternative P <sub>II</sub> protein in the regulation of glutamine synthetase in <i>Escherichia coli</i> . Molecular Microbiology, 1996, 21, 133-146.	2.5	205
14	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.	3.1	194
15	How fast-growing bacteria robustly tune their ribosome concentration to approximate growth rate maximization. FEBS Journal, 2015, 282, 2029-2044.	4.7	185
16	Availability of public goods shapes the evolution of competing metabolic strategies. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14302-14307.	7.1	169
17	Identification of <i>Lactobacillus plantarum</i> genes modulating the cytokine response of human peripheral blood mononuclear cells. BMC Microbiology, 2010, 10, 293.	3.3	162
18	Microbial domestication signatures of <i>Lactococcus lactis</i> can be reproduced by experimental evolution. Genome Research, 2012, 22, 115-124.	5.5	154

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19	Malolactic fermentation: electrogenic malate uptake and malate/lactate antiport generate metabolic energy. <i>Journal of Bacteriology</i> , 1991, 173, 6030-6037.	2.2	153
20	A systematic assessment of current genome-scale metabolic reconstruction tools. <i>Genome Biology</i> , 2019, 20, 158.	8.8	150
21	Exploring Metabolic Pathway Reconstruction and Genome-Wide Expression Profiling in <i>Lactobacillus reuteri</i> to Define Functional Probiotic Features. <i>PLoS ONE</i> , 2011, 6, e18783.	2.5	147
22	An agr-Like Two-Component Regulatory System in <i>Lactobacillus plantarum</i> Is Involved in Production of a Novel Cyclic Peptide and Regulation of Adherence. <i>Journal of Bacteriology</i> , 2005, 187, 5224-5235.	2.2	144
23	Glutathione Protects <i>Lactococcus lactis</i> against Oxidative Stress. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5739-5745.	3.1	139
24	DNA micro-array-based identification of bile-responsive genes in <i>Lactobacillus plantarum</i> . <i>Journal of Applied Microbiology</i> , 2006, 100, 728-738.	3.1	139
25	Functions of the Membrane-Associated and Cytoplasmic Malate Dehydrogenases in the Citric Acid Cycle of <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2000, 182, 6884-6891.	2.2	121
26	Continuous measurement of the cytoplasmic pH in <i>Lactococcus lactis</i> with a fluorescent pH indicator. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1991, 1115, 75-83.	2.4	113
27	Genome-Scale Genotype-Phenotype Matching of Two <i>Lactococcus lactis</i> Isolates from Plants Identifies Mechanisms of Adaptation to the Plant Niche. <i>Applied and Environmental Microbiology</i> , 2008, 74, 424-436.	3.1	112
28	DNA supercoiling depends on the phosphorylation potential in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1996, 20, 351-360.	2.5	111
29	Thioredoxin reductase is a key factor in the oxidative stress response of <i>Lactobacillus plantarum</i> WCFS1. <i>Microbial Cell Factories</i> , 2007, 6, 29.	4.0	110
30	Proton motive force-driven and ATP-dependent drug extrusion systems in multidrug-resistant <i>Lactococcus lactis</i> . <i>Journal of Bacteriology</i> , 1994, 176, 6957-6964.	2.2	108
31	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> KF147, a Plant-Associated Lactic Acid Bacterium. <i>Journal of Bacteriology</i> , 2010, 192, 2649-2650.	2.2	105
32	Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> . <i>FEBS Journal</i> , 1998, 254, 395-403.	0.2	101
33	Lifestyle of <i>Lactobacillus plantarum</i> in the mouse caecum. <i>Environmental Microbiology</i> , 2009, 11, 2747-2757.	3.8	99
34	Characteristics and osmoregulatory roles of uptake systems for proline and glycine betaine in <i>Lactococcus lactis</i> . <i>Journal of Bacteriology</i> , 1993, 175, 5438-5444.	2.2	98
35	Functions of the Membrane-Associated and Cytoplasmic Malate Dehydrogenases in the Citric Acid Cycle of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2000, 182, 6892-6899.	2.2	97
36	Natural diversity and adaptive responses of <i>Lactococcus lactis</i> . <i>Current Opinion in Biotechnology</i> , 2006, 17, 183-190.	6.6	97

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37	Lactobacillus plantarum gene clusters encoding putative cell-surface protein complexes for carbohydrate utilization are conserved in specific gram-positive bacteria. BMC Genomics, 2006, 7, 126.	2.8	96
38	Convergence in probiotic <i>Lactobacillus</i> gut-adaptive responses in humans and mice. ISME Journal, 2010, 4, 1481-1484.	9.8	95
39	The efflux of a fluorescent probe is catalyzed by an ATP-driven extrusion system in Lactococcus lactis. Journal of Bacteriology, 1992, 174, 3118-3124.	2.2	87
40	Nark is a nitrite-extrusion system involved in anaerobic nitrate respiration by Escherichia coli. Molecular Microbiology, 1994, 12, 579-586.	2.5	87
41	Another Unusual Type of Citric Acid Cycle Enzyme in Helicobacter pylori: the Malate:Quinone Oxidoreductase. Journal of Bacteriology, 2000, 182, 3204-3209.	2.2	86
42	The SOS response of Listeria monocytogenes is involved in stress resistance and mutagenesis. Microbiology (United Kingdom), 2010, 156, 374-384.	1.8	84
43	Comparative genomics of human Lactobacillus crispatus isolates reveals genes for glycosylation and glycogen degradation: implications for in vivo dominance of the vaginal microbiota. Microbiome, 2019, 7, 49.	11.1	84
44	Genome-scale diversity and niche adaptation analysis of <i>Lactococcus lactis</i> by comparative genome hybridization using multi-strain arrays. Microbial Biotechnology, 2011, 4, 383-402.	4.2	76
45	Genome Instability in Lactobacillus rhamnosus GG. Applied and Environmental Microbiology, 2013, 79, 2233-2239.	3.1	75
46	A benzene-degrading nitrate-reducing microbial consortium displays aerobic and anaerobic benzene degradation pathways. Scientific Reports, 2018, 8, 4490.	3.3	74
47	Genome-Wide Transposon Mutagenesis Indicates that Mycobacterium marinum Customizes Its Virulence Mechanisms for Survival and Replication in Different Hosts. Infection and Immunity, 2015, 83, 1778-1788.	2.2	72
48	Macrophage ATP citrate lyase deficiency stabilizes atherosclerotic plaques. Nature Communications, 2020, 11, 6296.	12.8	70
49	Molecular assessment of bacterial vaginosis by Lactobacillus abundance and species diversity. BMC Infectious Diseases, 2016, 16, 180.	2.9	68
50	Visualization for genomics: the Microbial Genome Viewer. Bioinformatics, 2004, 20, 1812-1814.	4.1	67
51	Standardized Assay Medium To Measure Lactococcus lactis Enzyme Activities while Mimicking Intracellular Conditions. Applied and Environmental Microbiology, 2012, 78, 134-143.	3.1	66
52	Systems biology of lactic acid bacteria: a critical review. Microbial Cell Factories, 2011, 10, S11.	4.0	64
53	Metabolic shifts: a fitness perspective for microbial cell factories. Biotechnology Letters, 2012, 34, 2147-2160.	2.2	61
54	Amino acid analysis using chromatography-mass spectrometry: An inter platform comparison study. Journal of Pharmaceutical and Biomedical Analysis, 2015, 114, 398-407.	2.8	60

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55	Systems biology of lactic acid bacteria: For food and thought. <i>Current Opinion in Systems Biology</i> , 2017, 6, 7-13.	2.6	60
56	Vanishing white matter: deregulated integrated stress response as therapy target. <i>Annals of Clinical and Translational Neurology</i> , 2019, 6, 1407-1422.	3.7	60
57	An additional Pllin <i>Escherichia coli</i> : a new regulatory protein in the glutamine synthetase cascade. <i>FEMS Microbiology Letters</i> , 1995, 132, 153-157.	1.8	57
58	Protein costs do not explain evolution of metabolic strategies and regulation of ribosomal content: does protein investment explain an anaerobic bacterial $\lambda$ -tree effect?. <i>Molecular Microbiology</i> , 2015, 97, 77-92.	2.5	57
59	Experimental evolution and the adjustment of metabolic strategies in lactic acid bacteria. <i>FEMS Microbiology Reviews</i> , 2017, 41, S201-S219.	8.6	57
60	Identification of the $\sigma^B$ Regulon of <i>Bacillus cereus</i> and Conservation of $\sigma^B$ -Regulated Genes in Low-GC-Content Gram-Positive Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 4384-4390.	2.2	53
61	Naturally Fermented Milk From Northern Senegal: Bacterial Community Composition and Probiotic Enrichment With <i>Lactobacillus rhamnosus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2218.	3.5	50
62	Improvement of <i>Lactobacillus plantarum</i> Aerobic Growth as Directed by Comprehensive Transcriptome Analysis. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4776-4778.	3.1	49
63	Searching for principles of microbial physiology. <i>FEMS Microbiology Reviews</i> , 2020, 44, 821-844.	8.6	49
64	Defining control coefficients in non-ideal metabolic pathways. <i>Biophysical Chemistry</i> , 1995, 56, 215-226.	2.8	47
65	High local substrate availability stabilizes a cooperative trait. <i>ISME Journal</i> , 2011, 5, 929-932.	9.8	47
66	AmtB-mediated $\text{NH}_3$ transport in prokaryotes must be active and as a consequence regulation of transport by GlnK is mandatory to limit futile cycling of $\text{NH}_4^+/\text{NH}_3$ . <i>FEBS Letters</i> , 2011, 585, 23-28.	2.8	47
67	PhenoLink - a web-tool for linking phenotype to -omics data for bacteria: application to gene-trait matching for <i>Lactobacillus plantarum</i> strains. <i>BMC Genomics</i> , 2012, 13, 170.	2.8	46
68	Proteome constraints reveal targets for improving microbial fitness in nutrient-rich environments. <i>Molecular Systems Biology</i> , 2021, 17, e10093.	7.2	46
69	Using <i>Lactococcus lactis</i> for glutathione overproduction. <i>Applied Microbiology and Biotechnology</i> , 2005, 67, 83-90.	3.6	45
70	Trehalose degradation and glucose efflux precede cell ejection during germination of heat-resistant ascospores of <i>Talaromyces macrosporus</i> . <i>Archives of Microbiology</i> , 2002, 178, 1-7.	2.2	43
71	Volatile Compound Fingerprinting of Mixed-Culture Fermentations. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6233-6239.	3.1	41
72	How Biochemical Constraints of Cellular Growth Shape Evolutionary Adaptations in Metabolism. <i>Genetics</i> , 2013, 194, 505-512.	2.9	40

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73	Public goods and metabolic strategies. <i>Current Opinion in Microbiology</i> , 2016, 31, 109-115.	5.1	39
74	A high-throughput cheese manufacturing model for effective cheese starter culture screening. <i>Journal of Dairy Science</i> , 2009, 92, 5868-5882.	3.4	38
75	Functional identification in <i>Lactobacillus reuteri</i> of a PocR-like transcription factor regulating glycerol utilization and vitamin B12 synthesis. <i>Microbial Cell Factories</i> , 2011, 10, 55.	4.0	38
76	Mechanism and energetics of a citrate-transport system of <i>Klebsiella pneumoniae</i> . <i>FEBS Journal</i> , 1991, 195, 71-77.	0.2	37
77	Mechanism of Na(+)-dependent citrate transport in <i>Klebsiella pneumoniae</i> . <i>Journal of Bacteriology</i> , 1992, 174, 4893-4898.	2.2	37
78	Involvement of the Mannose Phosphotransferase System of <i>Lactobacillus plantarum</i> WCFS1 in Peroxide Stress Tolerance. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3748-3752.	3.1	37
79	Expression of Plant Flavor Genes in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 1544-1552.	3.1	36
80	Transthyretin-Binding Activity of Complex Mixtures Representing the Composition of Thyroid-Hormone Disrupting Contaminants in House Dust and Human Serum. <i>Environmental Health Perspectives</i> , 2020, 128, 17015.	6.0	36
81	Functional ingredient production: application of global metabolic models. <i>Current Opinion in Biotechnology</i> , 2005, 16, 190-197.	6.6	35
82	Unity in organisation and regulation of catabolic operons in <i>Lactobacillus plantarum</i> , <i>Lactococcus lactis</i> and <i>Listeria monocytogenes</i> . <i>Systematic and Applied Microbiology</i> , 2005, 28, 187-195.	2.8	34
83	Two Homologous Agr-Like Quorum-Sensing Systems Cooperatively Control Adherence, Cell Morphology, and Cell Viability Properties in <i>Lactobacillus plantarum</i> WCFS1. <i>Journal of Bacteriology</i> , 2008, 190, 7655-7665.	2.2	34
84	Characterization of protonmotive force generation in liposomes reconstituted from phosphatidylethanolamine, reaction centers with light-harvesting complexes isolated from <i>Rhodospseudomonas palustris</i> . <i>Biochemistry</i> , 1988, 27, 2014-2023.	2.5	33
85	Metabolic models for rational improvement of lactic acid bacteria as cell factories. <i>Journal of Applied Microbiology</i> , 2005, 98, 1326-1331.	3.1	33
86	Introducing glutathione biosynthetic capability into <i>Lactococcus lactis</i> subsp. <i>cremoris</i> NZ9000 improves the oxidative-stress resistance of the host. <i>Metabolic Engineering</i> , 2006, 8, 662-671.	7.0	31
87	Gene Expression Analysis Reveals a Gene Set Discriminatory to Different Metals in Soil. <i>Toxicological Sciences</i> , 2010, 115, 34-40.	3.1	31
88	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous in vitro Fermentation of Riesling Must. <i>Frontiers in Microbiology</i> , 2019, 10, 697.	3.5	30
89	Light-driven amino acid uptake in <i>Streptococcus cremoris</i> or <i>Clostridium acetobutylicum</i> membrane vesicles fused with liposomes containing bacterial reaction centers. <i>Journal of Bacteriology</i> , 1988, 170, 1820-1824.	2.2	27
90	PanCGH: a genotype-calling algorithm for pangenome CGH data. <i>Bioinformatics</i> , 2009, 25, 309-314.	4.1	26

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91	Effect of Amino Acid Availability on Vitamin B 12 Production in <i>Lactobacillus reuteri</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 3930-3936.	3.1	26
92	Regulatory Phenotyping Reveals Important Diversity within the Species <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 5687-5694.	3.1	26
93	Nonhierarchical Flux Regulation Exposes the Fitness Burden Associated with Lactate Production in <i>Synechocystis</i> sp. PCC6803. <i>ACS Synthetic Biology</i> , 2017, 6, 395-401.	3.8	26
94	Ïf 54-mediated control of the mannose phosphotransferase sytem in <i>Lactobacillus plantarum</i> impacts on carbohydrate metabolism. <i>Microbiology (United Kingdom)</i> , 2010, 156, 695-707.	1.8	24
95	Binding proteins enhance specific uptake rate by increasing the substrateâ€“transporter encounter rate. <i>FEBS Journal</i> , 2015, 282, 2394-2407.	4.7	23
96	Physiological responses to folate overproduction in <i>Lactobacillus plantarum</i> WCFS1. <i>Microbial Cell Factories</i> , 2010, 9, 100.	4.0	19
97	Adaption to glucose limitation is modulated by the pleotropic regulator CcpA, independent of selection pressure strength. <i>BMC Evolutionary Biology</i> , 2019, 19, 15.	3.2	19
98	Microbial Communities in Sediments From Four Mildly Acidic Ephemeral Salt Lakes in the Yilgarn Craton (Australia) â€“ Terrestrial Analogs to Ancient Mars. <i>Frontiers in Microbiology</i> , 2019, 10, 779.	3.5	15
99	Steering microbiomes by organic amendments towards climate-smart agricultural soils. <i>Biology and Fertility of Soils</i> , 2021, 57, 1053-1074.	4.3	13
100	Bioinformatics and Systems Biology: bridging the gap between heterogeneous student backgrounds. <i>Briefings in Bioinformatics</i> , 2013, 14, 589-598.	6.5	12
101	High biodiversity in a benzene-degrading nitrate-reducing culture is sustained by a few primary consumers. <i>Communications Biology</i> , 2021, 4, 530.	4.4	11
102	An additional PII in <i>Escherichia coli</i> : a new regulatory protein in the glutamine synthetase cascade. <i>FEMS Microbiology Letters</i> , 1995, 132, 153-157.	1.8	9
103	The pivotal regulator GlnB of <i>Escherichia coli</i> is engaged in subtle and contextâ€“dependent control. <i>FEBS Journal</i> , 2009, 276, 3324-3340.	4.7	9
104	Functional analysis of the role of CggR (central glycolytic gene regulator) in <i>Lactobacillus plantarum</i> by transcriptome analysis. <i>Microbial Biotechnology</i> , 2011, 4, 345-356.	4.2	9
105	Vesicle trafficking via the SpitzenkÃ“rper during hyphal tip growth in <i>Rhizoctonia solani</i> . <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 921-931.	1.7	9
106	New Insights Into Cinnamoyl Esterase Activity of <i>Oenococcus oeni</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2597.	3.5	9
107	Molecular biology for flux control. <i>Biochemical Society Transactions</i> , 1995, 23, 367-370.	3.4	7
108	Genetic Elements Orchestrating <i>Lactobacillus crispatus</i> Glycogen Metabolism in the Vagina. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5590.	4.1	7

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109	Crystal ball “ 2009. Environmental Microbiology Reports, 2009, 1, 3-26.	2.4	5
110	Training for translation between disciplines: a philosophy for life and data sciences curricula. Bioinformatics, 2018, 34, i4-i12.	4.1	5
111	Using Functional Annotations to Study Pairwise Interactions in Urinary Tract Infection Communities. Genes, 2021, 12, 1221.	2.4	5
112	Dichotomy in post-genomic microbiology. Nature Biotechnology, 2007, 25, 848-849.	17.5	4
113	Large Intergenic Cruciform-Like Supermotifs in the Lactobacillus plantarum Genome. Journal of Bacteriology, 2009, 191, 3420-3423.	2.2	4
114	Functional Reconstitution of Photosynthetic Reaction Centre Complexes from Rhodospseudomonas Palustris. , 1989, , 352-361.		0
115	Light Driven Amino Acid Uptake in Membrane Vesicles of Streptococcus Cremoris Fused with Liposomes Containing Bacterial Reaction Centers. , 1989, , 291-295.		0