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	Genetic Elements Orchestrating Lactobacillus crispatus Glycogen Metabolism in the Vagina. International Journal of Molecular Sciences, 2022, 23, 5590.	4.1	7
2	Proteome constraints reveal targets for improving microbial fitness in nutrientâ€rich environments. Molecular Systems Biology, 2021, 17, e10093.	7.2	46
3	High biodiversity in a benzene-degrading nitrate-reducing culture is sustained by a few primary consumers. Communications Biology, 2021, 4, 530.	4.4	11
4	Using Functional Annotations to Study Pairwise Interactions in Urinary Tract Infection Communities. Genes, 2021, 12, 1221.	2.4	5
5	Steering microbiomes by organic amendments towards climate-smart agricultural soils. Biology and Fertility of Soils, 2021, 57, 1053-1074.	4.3	13
6	Searching for principles of microbial physiology. FEMS Microbiology Reviews, 2020, 44, 821-844.	8.6	49
7	Macrophage ATP citrate lyase deficiency stabilizes atherosclerotic plaques. Nature Communications, 2020, 11, 6296.	12.8	70
8	Transthyretin-Binding Activity of Complex Mixtures Representing the Composition of Thyroid-Hormone Disrupting Contaminants in House Dust and Human Serum. Environmental Health Perspectives, 2020, 128, 17015.	6.0	36
9	A systematic assessment of current genome-scale metabolic reconstruction tools. Genome Biology, 2019, 20, 158.	8.8	150
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	Vanishing white matter: deregulated integrated stress response as therapy target. Annals of Clinical and Translational Neurology, 2019, 6, 1407-1422.	3.7	60
12	Microbial Communities in Sediments From Four Mildly Acidic Ephemeral Salt Lakes in the Yilgarn Craton (Australia) â€“ Terrestrial Analogs to Ancient Mars. Frontiers in Microbiology, 2019, 10, 779.	3.5	15
13	Taxonomic and Functional Characterization of the Microbial Community During Spontaneous in vitro Fermentation of Riesling Must. Frontiers in Microbiology, 2019, 10, 697.	3.5	30
14	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
15	New Insights Into Cinnamoyl Esterase Activity of Oenococcus oeni. Frontiers in Microbiology, 2019, 10, 2597.	3.5	9
16	Adaption to glucose limitation is modulated by the pleotropic regulator CcpA, independent of selection pressure strength. BMC Evolutionary Biology, 2019, 19, 15.	3.2	19
17	A benzene-degrading nitrate-reducing microbial consortium displays aerobic and anaerobic benzene degradation pathways. Scientific Reports, 2018, 8, 4490.	3.3	74
18	Naturally Fermented Milk From Northern Senegal: Bacterial Community Composition and Probiotic Enrichment With Lactobacillus rhamnosus. Frontiers in Microbiology, 2018, 9, 2218.	3.5	50

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19	Training for translation between disciplines: a philosophy for life and data sciences curricula. Bioinformatics, 2018, 34, i4-i12.	4.1	5
20	Experimental evolution and the adjustment of metabolic strategies in lactic acid bacteria. FEMS Microbiology Reviews, 2017, 41, S201-S219.	8.6	57
21	Nonhierarchical Flux Regulation Exposes the Fitness Burden Associated with Lactate Production in Synechocystis sp. PCC6803. ACS Synthetic Biology, 2017, 6, 395-401.	3.8	26
22	Systems biology of lactic acid bacteria: For food and thought. Current Opinion in Systems Biology, 2017, 6, 7-13.	2.6	60
23	Public goods and metabolic strategies. Current Opinion in Microbiology, 2016, 31, 109-115.	5.1	39
24	Molecular assessment of bacterial vaginosis by Lactobacillus abundance and species diversity. BMC Infectious Diseases, 2016, 16, 180.	2.9	68
25	Binding proteins enhance specific uptake rate by increasing the substrateâ€“transporter encounter rate. FEBS Journal, 2015, 282, 2394-2407.	4.7	23
26	Amino acid analysis using chromatographyâ€“mass spectrometry: An inter platform comparison study. Journal of Pharmaceutical and Biomedical Analysis, 2015, 114, 398-407.	2.8	60
27	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
28	How fastâ€growing bacteria robustly tune their ribosome concentration to approximate growthâ€rate maximization. FEBS Journal, 2015, 282, 2029-2044.	4.7	185
29	Protein costs do not explain evolution of metabolic strategies and regulation of ribosomal content: does protein investment explain an anaerobic bacterial <scp>C</scp>rabtree effect?. Molecular Microbiology, 2015, 97, 77-92.	2.5	57
30	How Biochemical Constraints of Cellular Growth Shape Evolutionary Adaptations in Metabolism. Genetics, 2013, 194, 505-512.	2.9	40
31	Vesicle trafficking via the SpitzenkÃ¶rper during hyphal tip growth in Rhizoctonia solani. Antonie Van Leeuwenhoek, 2013, 103, 921-931.	1.7	9
32	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
33	Genome Instability in Lactobacillus rhamnosus GG. Applied and Environmental Microbiology, 2013, 79, 2233-2239.	3.1	75
34	Bioinformatics and Systems Biology: bridging the gap between heterogeneous student backgrounds. Briefings in Bioinformatics, 2013, 14, 589-598.	6.5	12
35	Microbial domestication signatures of Lactococcus lactis can be reproduced by experimental evolution. Genome Research, 2012, 22, 115-124.	5.5	154
36	Standardized Assay Medium To Measure Lactococcus lactis Enzyme Activities while Mimicking Intracellular Conditions. Applied and Environmental Microbiology, 2012, 78, 134-143.	3.1	66

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37	Metabolic shifts: a fitness perspective for microbial cell factories. Biotechnology Letters, 2012, 34, 2147-2160.	2.2	61
38	PhenoLink - a web-tool for linking phenotype to ~omics data for bacteria: application to gene-trait matching for Lactobacillus plantarum strains. BMC Genomics, 2012, 13, 170.	2.8	46
39	Exploring Metabolic Pathway Reconstruction and Genome-Wide Expression Profiling in Lactobacillus reuteri to Define Functional Probiotic Features. PLoS ONE, 2011, 6, e18783.	2.5	147
40	High local substrate availability stabilizes a cooperative trait. ISME Journal, 2011, 5, 929-932.	9.8	47
41	Functional analysis of the role of CggR (central glycolytic gene regulator) in Lactobacillus plantarum by transcriptome analysis. Microbial Biotechnology, 2011, 4, 345-356.	4.2	9
42	Genomeâ€scale diversity and niche adaptation analysis of Lactococcus lactis by comparative genome hybridization using multiâ€strain arrays. Microbial Biotechnology, 2011, 4, 383-402.	4.2	76
43	AmtB-mediated NH₃transport in prokaryotes must be active and as a consequence regulation of transport by GlnK is mandatory to limit futile cycling of NH4+/NH3. FEBS Letters, 2011, 585, 23-28.	2.8	47
44	Functional identification in Lactobacillus reuteri of a PocR-like transcription factor regulating glycerol utilization and vitamin B12 synthesis. Microbial Cell Factories, 2011, 10, 55.	4.0	38
45	Systems biology of lactic acid bacteria: a critical review. Microbial Cell Factories, 2011, 10, S11.	4.0	64
46	Volatile Compound Fingerprinting of Mixed-Culture Fermentations. Applied and Environmental Microbiology, 2011, 77, 6233-6239.	3.1	41
47	Identification of Lactobacillus plantarum genes modulating the cytokine response of human peripheral blood mononuclear cells. BMC Microbiology, 2010, 10, 293.	3.3	162
48	Convergence in probiotic Lactobacillus gut-adaptive responses in humans and mice. ISME Journal, 2010, 4, 1481-1484.	9.8	95
49	Phenotypic and genomic diversity of Lactobacillus plantarum strains isolated from various environmental niches. Environmental Microbiology, 2010, 12, 758-773.	3.8	262
50	Complete Genome Sequence of Lactococcus lactis subsp. lactis KF147, a Plant-Associated Lactic Acid Bacterium. Journal of Bacteriology, 2010, 192, 2649-2650.	2.2	105
51	The SOS response of Listeria monocytogenes is involved in stress resistance and mutagenesis. Microbiology (United Kingdom), 2010, 156, 374-384.	1.8	84
52	Ïƒ 54-mediated control of the mannose phosphotransferase sytem in Lactobacillus plantarum impacts on carbohydrate metabolism. Microbiology (United Kingdom), 2010, 156, 695-707.	1.8	24
53	Gene Expression Analysis Reveals a Gene Set Discriminatory to Different Metals in Soil. Toxicological Sciences, 2010, 115, 34-40.	3.1	31
54	Involvement of the Mannose Phosphotransferase System of Lactobacillus plantarum WCFS1 in Peroxide Stress Tolerance. Applied and Environmental Microbiology, 2010, 76, 3748-3752.	3.1	37

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55	Physiological responses to folate overproduction in Lactobacillus plantarum WCFS1. Microbial Cell Factories, 2010, 9, 100.	4.0	19
56	Mixed-Culture Transcriptome Analysis Reveals the Molecular Basis of Mixed-Culture Growth in Streptococcus thermophilus and Lactobacillus bulgaricus. Applied and Environmental Microbiology, 2010, 76, 7775-7784.	3.1	194
57	PanCGH: a genotype-calling algorithm for pangenome CGH data. Bioinformatics, 2009, 25, 309-314.	4.1	26
58	Large Intergenic Cruciform-Like Supermotifs in the Lactobacillus plantarum Genome. Journal of Bacteriology, 2009, 191, 3420-3423.	2.2	4
59	Shifts in growth strategies reflect tradeoffs in cellular economics. Molecular Systems Biology, 2009, 5, 323.	7.2	535
60	Effect of Amino Acid Availability on Vitamin B 12 Production in Lactobacillus reuteri. Applied and Environmental Microbiology, 2009, 75, 3930-3936.	3.1	26
61	Regulatory Phenotyping Reveals Important Diversity within the Species Lactococcus lactis. Applied and Environmental Microbiology, 2009, 75, 5687-5694.	3.1	26
62	The pivotal regulator GlnB of Escherichiaâ€ƒcoli is engaged in subtle and contextâ€dependent control. FEBS Journal, 2009, 276, 3324-3340.	4.7	9
63	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
64	Lifestyle of Lactobacillus plantarum in the mouse caecum. Environmental Microbiology, 2009, 11, 2747-2757.	3.8	99
65	A high-throughput cheese manufacturing model for effective cheese starter culture screening. Journal of Dairy Science, 2009, 92, 5868-5882.	3.4	38
66	Crystal ball â€“ 2009. Environmental Microbiology Reports, 2009, 1, 3-26.	2.4	5
67	Two Homologous Agr-Like Quorum-Sensing Systems Cooperatively Control Adherence, Cell Morphology, and Cell Viability Properties in Lactobacillus plantarum WCFS1. Journal of Bacteriology, 2008, 190, 7655-7665.	2.2	34
68	Genome-Scale Genotype-Phenotype Matching of Two Lactococcus lactis Isolates from Plants Identifies Mechanisms of Adaptation to the Plant Niche. Applied and Environmental Microbiology, 2008, 74, 424-436.	3.1	112
69	Improvement of Lactobacillus plantarum Aerobic Growth as Directed by Comprehensive Transcriptome Analysis. Applied and Environmental Microbiology, 2008, 74, 4776-4778.	3.1	49
70	Identification of the Ïƒ B Regulon of Bacillus cereus and Conservation of Ïƒ B -Regulated Genes in Low-GC-Content Gram-Positive Bacteria. Journal of Bacteriology, 2007, 189, 4384-4390.	2.2	53
71	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
72	Identification of Prebiotic Fructooligosaccharide Metabolism in Lactobacillus plantarum WCFS1 through Microarrays. Applied and Environmental Microbiology, 2007, 73, 1753-1765.	3.1	210

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73	Expression of Plant Flavor Genes in Lactococcus lactis. Applied and Environmental Microbiology, 2007, 73, 1544-1552.	3.1	36
74	Thioredoxin reductase is a key factor in the oxidative stress response of Lactobacillus plantarum WCFS1. Microbial Cell Factories, 2007, 6, 29.	4.0	110
75	Dichotomy in post-genomic microbiology. Nature Biotechnology, 2007, 25, 848-849.	17.5	4
76	DNA micro-array-based identification of bile-responsive genes in Lactobacillus plantarum. Journal of Applied Microbiology, 2006, 100, 728-738.	3.1	139
77	Natural diversity and adaptive responses of Lactococcus lactis. Current Opinion in Biotechnology, 2006, 17, 183-190.	6.6	97
78	Introducing glutathione biosynthetic capability into Lactococcus lactis subsp. cremoris NZ9000 improves the oxidative-stress resistance of the host. Metabolic Engineering, 2006, 8, 662-671.	7.0	31
79	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
80	Analysis of Growth of Lactobacillus plantarum WCFS1 on a Complex Medium Using a Genome-scale Metabolic Model. Journal of Biological Chemistry, 2006, 281, 40041-40048.	3.4	261
81	Functional ingredient production: application of global metabolic models. Current Opinion in Biotechnology, 2005, 16, 190-197.	6.6	35
82	Metabolic models for rational improvement of lactic acid bacteria as cell factories. Journal of Applied Microbiology, 2005, 98, 1326-1331.	3.1	33
83	Unity in organisation and regulation of catabolic operons in Lactobacillus plantarum, Lactococcus lactis and Listeria monocytogenes. Systematic and Applied Microbiology, 2005, 28, 187-195.	2.8	34
84	Using Lactococcus lactis for glutathione overproduction. Applied Microbiology and Biotechnology, 2005, 67, 83-90.	3.6	45
85	An agr -Like Two-Component Regulatory System in Lactobacillus plantarum Is Involved in Production of a Novel Cyclic Peptide and Regulation of Adherence. Journal of Bacteriology, 2005, 187, 5224-5235.	2.2	144
86	Exploring Lactobacillus plantarum Genome Diversity by Using Microarrays. Journal of Bacteriology, 2005, 187, 6119-6127.	2.2	229
87	Biodiversity-Based Identification and Functional Characterization of the Mannose-Specific Adhesin ofLactobacillus plantarum. Journal of Bacteriology, 2005, 187, 6128-6136.	2.2	272
88	Visualization for genomics: the Microbial Genome Viewer. Bioinformatics, 2004, 20, 1812-1814.	4.1	67
89	Complete genome sequence of Lactobacillus plantarum WCFS1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1990-1995.	7.1	1,326
90	Glutathione Protects Lactococcus lactis against Oxidative Stress. Applied and Environmental Microbiology, 2003, 69, 5739-5745.	3.1	139

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91	Trehalose degradation and glucose efflux precede cell ejection during germination of heat-resistant ascospores of Talaromyces macrosporus. Archives of Microbiology, 2002, 178, 1-7.	2.2	43
92	Functions of the Membrane-Associated and Cytoplasmic Malate Dehydrogenases in the Citric Acid Cycle of Corynebacterium glutamicum. Journal of Bacteriology, 2000, 182, 6884-6891.	2.2	121
93	Functions of the Membrane-Associated and Cytoplasmic Malate Dehydrogenases in the Citric Acid Cycle of Escherichia coli. Journal of Bacteriology, 2000, 182, 6892-6899.	2.2	97
94	Another Unusual Type of Citric Acid Cycle Enzyme inHelicobacter pylori: the Malate:Quinone Oxidoreductase. Journal of Bacteriology, 2000, 182, 3204-3209.	2.2	86
95	A heat shock following electroporation induces highly efficient transformation of Corynebacterium glutamicum with xenogeneic plasmid DNA. Applied Microbiology and Biotechnology, 1999, 52, 541-545.	3.6	406
96	Biochemical and genetic characterization of the membraneâ€associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum. FEBS Journal, 1998, 254, 395-403.	0.2	101
97	An alternative P_{II} protein in the regulation of glutamine synthetase in Escherichia coli. Molecular Microbiology, 1996, 21, 133-146.	2.5	205
98	DNA supercoiling depends on the phosphorylation potential in Escherichia coli. Molecular Microbiology, 1996, 20, 351-360.	2.5	111
99	Molecular biology for flux control. Biochemical Society Transactions, 1995, 23, 367-370.	3.4	7
100	An additional PIIinEscherichia coli: a new regulatory protein in the glutamine synthetase cascade. FEMS Microbiology Letters, 1995, 132, 153-157.	1.8	57
101	Defining control coefficients in non-ideal metabolic pathways. Biophysical Chemistry, 1995, 56, 215-226.	2.8	47
102	An additional PII in Escherichia coli: a new regulatory protein in the glutamine synthetase cascade. FEMS Microbiology Letters, 1995, 132, 153-157.	1.8	9
103	Nark is a nitrite-extrusion system involved in anaerobic nitrate respiration by Escherichia coli. Molecular Microbiology, 1994, 12, 579-586.	2.5	87
104	Proton motive force-driven and ATP-dependent drug extrusion systems in multidrug-resistant Lactococcus lactis. Journal of Bacteriology, 1994, 176, 6957-6964.	2.2	108
105	Generation of a proton motive force by histidine decarboxylation and electrogenic histidine/histamine antiport in Lactobacillus buchneri. Journal of Bacteriology, 1993, 175, 2864-2870.	2.2	218
106	Characteristics and osmoregulatory roles of uptake systems for proline and glycine betaine in Lactococcus lactis. Journal of Bacteriology, 1993, 175, 5438-5444.	2.2	98
107	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
108	Mechanism of Na(+)-dependent citrate transport in Klebsiella pneumoniae. Journal of Bacteriology, 1992, 174, 4893-4898.	2.2	37

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109	Continuous measurement of the cytoplasmic pH in Lactococcus lactis with a fluorescent pH indicator. Biochimica Et Biophysica Acta - General Subjects, 1991, 1115, 75-83.	2.4	113
110	Malolactic fermentation: electrogenic malate uptake and malate/lactate antiport generate metabolic energy. Journal of Bacteriology, 1991, 173, 6030-6037.	2.2	153
111	Mechanism and energetics of a citrate-transport system of Klebsiella pneumoniae. FEBS Journal, 1991, 195, 71-77.	0.2	37
112	Functional Reconstitution of Photosynthetic Reaction Centre Complexes from Rhodopseudomonas Palustris. , 1989, , 352-361.		0
113	Light Driven Amino Acid Uptake in Membrane Vesicles of Streptococcus Cremoris Fused with Liposomes Containing Bacterial Reaction Centers. , 1989, , 291-295.		0
114	Characterization of protonmotive force generation in liposomes reconstituted from phosphatidylethanolamine, reaction centers with light-harvesting complexes isolated from Rhodopseudomonas palustris. Biochemistry, 1988, 27, 2014-2023.	2.5	33
115	Light-driven amino acid uptake in Streptococcus cremoris or Clostridium acetobutylicum membrane vesicles fused with liposomes containing bacterial reaction centers. Journal of Bacteriology, 1988, 170, 1820-1824.	2.2	27