Jan Kok

List of Publications by Year
in descending order

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119

papers

8,502

citations

38742

50

h-index

48315

88

g-index

120

all docs

120

docs citations

120

times ranked

7279

citing authors

#	Article	IF	Citations
1	BAGEL4: a user-friendly web server to thoroughly mine RiPPs and bacteriocins. Nucleic Acids Research, 2018, 46, W278-W281.	14.5	593
2	LysM, a widely distributed protein motif for binding to (peptido)glycans. Molecular Microbiology, 2008, 68, 838-847.	2.5	564
3	Stress Physiology of Lactic Acid Bacteria. Microbiology and Molecular Biology Reviews, 2016, 80, 837-890.	6.6	487
4	Complete Genome Sequence of the Prototype Lactic Acid Bacterium <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363. Journal of Bacteriology, 2007, 189, 3256-3270.	2.2	362
5	A chloride-inducible acid resistance mechanism in Lactococcus lactis and its regulation. Molecular Microbiology, 1998, 27, 299-310.	2.5	245
6	Bet-hedging during bacterial diauxic shift. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7427-7432.	7.1	211
7	Cell Wall Attachment of a Widely Distributed Peptidoglycan Binding Domain Is Hindered by Cell Wall Constituents. Journal of Biological Chemistry, 2003, 278, 23874-23881.	3.4	205
8	Genetics of the proteolytic system of lactic acid bacteria. FEMS Microbiology Letters, 1990, 87, 15-42.	1.8	189
9	Sequence analysis and molecular characterization of the temperate lactococcal bacteriophage r1t. Molecular Microbiology, 1996, 19, 1343-1355.	2.5	182
10	The Lactococcus lactis CodY Regulon. Journal of Biological Chemistry, 2005, 280, 34332-34342.	3.4	176
11	Stability of Integrated Plasmids in the Chromosome of <i>Lactococcus lactis</i>. Applied and Environmental Microbiology, 1990, 56, 2726-2735.	3.1	159
12	Functional analysis of the pediocin operon of Pediococcus acidilactici PAC1.0: PedB is the immunity protein and PedD is the precursor processing enzyme. Molecular Microbiology, 1995, 17, 515-522.	2.5	153
13	Regulation of Glutamine and Glutamate Metabolism by GlnR and GlnA in Streptococcus pneumoniae. Journal of Biological Chemistry, 2006, 281, 25097-25109.	3.4	150
14	Novel Surface Display System for Proteins on Non-Genetically Modified Gram-Positive Bacteria. Applied and Environmental Microbiology, 2006, 72, 880-889.	3.1	146
15	Environmental stress responses inLactococcus lactis. FEMS Microbiology Reviews, 1999, 23, 483-501.	8.6	142
16	Overview on sugar metabolism and its control in â€“ The input from in vivo NMR. FEMS Microbiology Reviews, 2005, 29, 531-554.	8.6	139
17	Gene expression in Lactococcus lactis. FEMS Microbiology Letters, 1992, 88, 73-92.	1.8	138
18	Time-Resolved Determination of the CcpA Regulon of Lactococcus lactis subsp. cremoris MG1363. Journal of Bacteriology, 2007, 189, 1366-1381.	2.2	136

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19	PePPER: a webserver for prediction of prokaryote promoter elements and regulons. BMC Genomics, 2012, 13, 299.	2.8	135
20	AcmA of <i>Lactococcus lactis</i> is an <i>N</i>â€acetylglucosaminidase with an optimal number of LysM domains for proper functioning. FEBS Journal, 2005, 272, 2854-2868.	4.7	122
21	Transcriptome Analysis Reveals Mechanisms by Which Lactococcus lactis Acquires Nisin Resistance. Antimicrobial Agents and Chemotherapy, 2006, 50, 1753-1761.	3.2	118
22	Benchmarking Various Green Fluorescent Protein Variants in Bacillus subtilis, Streptococcus pneumoniae, and Lactococcus lactis for Live Cell Imaging. Applied and Environmental Microbiology, 2013, 79, 6481-6490.	3.1	110
23	Perspectives on the contribution of lactic acid bacteria to cheese flavor development. Current Opinion in Biotechnology, 2013, 24, 135-141.	6.6	109
24	Genome Sequences of <i>Lactococcus lactis</i> MG1363 (Revised) and NZ9000 and Comparative Physiological Studies. Journal of Bacteriology, 2010, 192, 5806-5812.	2.2	108
25	Mucosal vaccine delivery of antigens tightly bound to an adjuvant particle made from food-grade bacteria. Methods, 2006, 38, 144-149.	3.8	101
26	A generally applicable validation scheme for the assessment of factors involved in reproducibility and quality of DNA-microarray data. BMC Genomics, 2005, 6, 77.	2.8	100
27	Inducible gene expression mediated by a repressor-operator system isolated from Lactococcus lactis bacteriophage r1t. Molecular Microbiology, 1996, 19, 1331-1341.	2.5	99
28	Autolysis of Lactococcus lactis Is Increased upon d -Alanine Depletion of Peptidoglycan and Lipoteichoic Acids. Journal of Bacteriology, 2005, 187, 114-124.	2.2	96
29	Cell envelope stress induced by the bacteriocin Lcn972 is sensed by the lactococcal two-component system CesSR. Molecular Microbiology, 2007, 64, 473-486.	2.5	96
30	Specificity and selectivity determinants of peptide transport in Lactococcus lactis and other microorganisms. Molecular Microbiology, 2005, 57, 640-649.	2.5	94
31	To have neighbour's fare: extending the molecular toolbox for Streptococcus pneumoniae. Microbiology (United Kingdom), 2006, 152, 351-359.	1.8	94
32	Genome2D: a visualization tool for the rapid analysis of bacterial transcriptome data. Genome Biology, 2004, 5, R37.	9.6	93
33	SpxB Regulates O-Acetylation-dependent Resistance of Lactococcus lactis Peptidoglycan to Hydrolysis. Journal of Biological Chemistry, 2007, 282, 19342-19354.	3.4	86
34	MicroPreP: a cDNA microarray data pre-processing framework. Applied Bioinformatics, 2003, 2, 241-4.	1.6	82
35	Anchoring of proteins to lactic acid bacteria. Antonie Van Leeuwenhoek, 1999, 76, 367-376.	1.7	78
36	Characterization of the individual glucose uptake systems of <i>Lactococcus lactis</i>: mannoseâ€PTS, cellobioseâ€PTS and the novel GlcU permease. Molecular Microbiology, 2009, 71, 795-806.	2.5	74

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37	Distance-dependent translational coupling and interference inLactococcus lactis. Molecular Genetics and Genomics, 1991, 227, 65-71.	2.4	72
38	The S-layer gene of Lactobacillus helveticus CNRZ 892: cloning, sequence and heterologous expression. Microbiology (United Kingdom), 1998, 144, 719-726.	1.8	71
39	Identification and Functional Characterization of the<i>Lactococcus lactis</i>CodY-Regulated Branched-Chain Amino Acid Permease BcaP (CtrA). Journal of Bacteriology, 2006, 188, 3280-3289.	2.2	70
40	Use of a Genetically Enhanced, Pediocin-Producing Starter Culture, <i>Lactococcus lactis</i> subsp. <i>lactis</i> MM217, To Control <i>Listeria monocytogenes</i> in Cheddar Cheese. Applied and Environmental Microbiology, 1998, 64, 4842-4845.	3.1	70
41	Probing Direct Interactions between CodY and the<i>oppD</i>Promoter of<i>Lactococcus lactis</i>. Journal of Bacteriology, 2005, 187, 512-521.	2.2	68
42	ArgR and AhrC Are Both Required for Regulation of Arginine Metabolism in Lactococcus lactis. Journal of Bacteriology, 2004, 186, 1147-1157.	2.2	67
43	Fructose Utilization in<i>Lactococcus lactis</i>as a Model for Low-GC Gram-Positive Bacteria: Its Regulator, Signal, and DNA-Binding Site. Journal of Bacteriology, 2005, 187, 3752-3761.	2.2	66
44	AcmD, a Homolog of the Major Autolysin AcmA of Lactococcus lactis, Binds to the Cell Wall and Contributes to Cell Separation and Autolysis. PLoS ONE, 2013, 8, e72167.	2.5	66
45	T-REx: Transcriptome analysis webserver for RNA-seq Expression data. BMC Genomics, 2015, 16, 663.	2.8	59
46	Autolysis of Lactococcus lactis Is Influenced by Proteolysis. Journal of Bacteriology, 1998, 180, 5947-5953.	2.2	59
47	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
48	Casein and Peptide Degradation in Lactic Acid Bacteria. Biotechnology and Genetic Engineering Reviews, 1997, 14, 279-302.	6.2	56
49	Increased d-alanylation of lipoteichoic acid and a thickened septum are main determinants in the nisin resistance mechanism of Lactococcus lactis. Microbiology (United Kingdom), 2008, 154, 1755-1762.	1.8	55
50	Exploiting the peptidoglycan-binding motif, LysM, for medical and industrial applications. Applied Microbiology and Biotechnology, 2014, 98, 4331-45.	3.6	55
51	From meadows to milk to mucosa â€“ adaptation of<i>Streptococcus</i>and<i>Lactococcus</i>species to their nutritional environments. FEMS Microbiology Reviews, 2012, 36, 949-971.	8.6	54
52	Transcriptome analysis and related databases of Lactococcus lactis. Antonie Van Leeuwenhoek, 2002, 82, 113-122.	1.7	53
53	Transcriptome landscape of <i>Lactococcus lactis</i> reveals many novel RNAs including a small regulatory RNA involved in carbon uptake and metabolism. RNA Biology, 2016, 13, 353-366.	3.1	53
54	Comparative Analyses of Prophage-Like Elements Present in Two <i>Lactococcus lactis</i> Strains. Applied and Environmental Microbiology, 2007, 73, 7771-7780.	3.1	52

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55	Murein and pseudomurein cell wall binding domains of bacteria and archaeaâ€”a comparative view. Applied Microbiology and Biotechnology, 2011, 92, 921-928.	3.6	46
56	pSEUDO, a Genetic Integration Standard for Lactococcus lactis. Applied and Environmental Microbiology, 2011, 77, 6687-6690.	3.1	46
57	<i><scp>L</scp>actococcus lactis</i>â€...<scp>YfiA</scp> is necessary and sufficient for ribosome dimerization. Molecular Microbiology, 2014, 91, 394-407.	2.5	45
58	High-level heterologous production and functional expression of the sec-dependent enterocin P from Enterococcus faecium P13 in Lactococcus lactis. Applied Microbiology and Biotechnology, 2006, 72, 41-51.	3.6	44
59	A Specific Mutation in the Promoter Region of the Silent <i>cel</i> Cluster Accounts for the Appearance of Lactose-Utilizing Lactococcus lactis MG1363. Applied and Environmental Microbiology, 2012, 78, 5612-5621.	3.1	43
60	Interaction between ArgR and AhrC Controls Regulation of Arginine Metabolism in Lactococcus lactis. Journal of Biological Chemistry, 2005, 280, 19319-19330.	3.4	41
61	The Evolution of gene regulation research in Lactococcus lactis. FEMS Microbiology Reviews, 2017, 41, S220-S243.	8.6	40
62	Stress response of a clinical Enterococcus faecalis isolate subjected to a novel antimicrobial surface coating. Microbiological Research, 2018, 207, 53-64.	5.3	40
63	Design of thermolabile bacteriophage repressor mutants by comparative molecular modeling. Nature Biotechnology, 1997, 15, 980-983.	17.5	39
64	GlnR-Mediated Regulation of Nitrogen Metabolism in Lactococcus lactis. Journal of Bacteriology, 2006, 188, 4978-4982.	2.2	39
65	Different subcellular locations of secretome components of Gram-positive bacteria. Microbiology (United Kingdom), 2006, 152, 2867-2874.	1.8	37
66	Transcriptome Analysis of the Lactococcus lactis ArgR and AhrC Regulons. Applied and Environmental Microbiology, 2008, 74, 4768-4771.	3.1	37
67	A Novel Antimicrobial Coating Represses Biofilm and Virulence-Related Genes in Methicillin-Resistant Staphylococcus aureus. Frontiers in Microbiology, 2018, 9, 221.	3.5	37
68	Inducible gene expression and environmentally regulated genes in lactic acid bacteria. Antonie Van Leeuwenhoek, 1996, 70, 129-145.	1.7	34
69	Plasmid Complement of Lactococcus lactis NCDO712 Reveals a Novel Pilus Gene Cluster. PLoS ONE, 2016, 11, e0167970.	2.5	34
70	The Response of Lactococcus lactis to Membrane Protein Production. PLoS ONE, 2011, 6, e24060.	2.5	33
71	UniFrag and GenomePrimer: selection of primers for genome-wide production of unique amplicons. Bioinformatics, 2003, 19, 1580-1582.	4.1	32
72	Natural sweetening of food products by engineering Lactococcus lactis for glucose production. Metabolic Engineering, 2006, 8, 456-464.	7.0	30

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73	Transcriptional Regulation of Fatty Acid Biosynthesis in Lactococcus lactis. Journal of Bacteriology, 2013, 195, 1081-1089.	2.2	30
74	Efficient Overproduction of Membrane Proteins in Lactococcus lactis Requires the Cell Envelope Stress Sensor/Regulator Couple CesSR. PLoS ONE, 2011, 6, e21873.	2.5	27
75	A lactococcal pWV01-based integration toolbox for bacteria. Cytotechnology, 1998, 20, 35-50.	0.7	23
76	The Transcriptional and Gene Regulatory Network of Lactococcus lactis MG1363 during Growth in Milk. PLoS ONE, 2013, 8, e53085.	2.5	23
77	Comparative and functional genomics of lactococci. FEMS Microbiology Reviews, 2005, 29, 411-433.	8.6	21
78	On the Spatial Organization of mRNA, Plasmids, and Ribosomes in a Bacterial Host Overexpressing Membrane Proteins. PLoS Genetics, 2016, 12, e1006523.	3.5	21
79	Expression of prophage-encoded endolysins contributes to autolysis of Lactococcus lactis. Applied Microbiology and Biotechnology, 2017, 101, 1099-1110.	3.6	20
80	Homologous Expression and Characterization of Gassericin T and Gassericin S, a Novel Class IIb Bacteriocin Produced by Lactobacillus gasseri LA327. Applied and Environmental Microbiology, 2019, 85, .	3.1	19
81	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
82	Characterization of the lyticâ€"lysogenic switch of the lactococcal bacteriophage Tuc2009. Virology, 2006, 347, 434-446.	2.4	18
83	Reduced Lysis upon Growth of <i>Lactococcus lactis</i> on Galactose Is a Consequence of Decreased Binding of the Autolysin AcmA. Applied and Environmental Microbiology, 2008, 74, 4671-4679.	3.1	18
84	Early Transcriptome Response of Lactococcus lactis to Environmental Stresses Reveals Differentially Expressed Small Regulatory RNAs and tRNAs. Frontiers in Microbiology, 2017, 8, 1704.	3.5	18
85	Two Major Archaeal Pseudomurein Endoisopeptidases: PeiW and PeiP. Archaea, 2010, 2010, 1-4.	2.3	17
86	Regulation of Cell Wall Plasticity by Nucleotide Metabolism in Lactococcus lactis. Journal of Biological Chemistry, 2016, 291, 11323-11336.	3.4	17
87	FUNAGE-Pro: comprehensive web server for gene set enrichment analysis of prokaryotes. Nucleic Acids Research, 2022, 50, W330-W336.	14.5	17
88	The Relationship among Tyrosine Decarboxylase and Agmatine Deiminase Pathways in Enterococcus faecalis. Frontiers in Microbiology, 2017, 8, 2107.	3.5	16
89	Lytr, a phage-derived amidase is most effective in induced lysis of Lactococcus lactis compared with other lactococcal amidases and glucosaminidases. International Dairy Journal, 2007, 17, 926-936.	3.0	14
90	Draft Genome Sequences of Three Amino Acid-Secreting Lactococcus lactis Strains. Microbiology Resource Announcements, 2020, 9, .	0.6	13

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91	Human milk oligosaccharides and non-digestible carbohydrates reduce pathogen adhesion to intestinal epithelial cells by decoy effects or by attenuating bacterial virulence. Food Research International, 2022, 151, 110867.	6.2	13
92	DNA-mircoarrays and food-biotechnology. Antonie Van Leeuwenhoek, 1999, 76, 353-355.	1.7	12
93	From DNA sequence to application: possibilities and complications. Antonie Van Leeuwenhoek, 1999, 76, 3-23.	1.7	12
94	The protein regulator ArgR and the sRNA derived from the 3â€™-UTR region of its gene, ArgX, both regulate the arginine deiminase pathway in Lactococcus lactis. PLoS ONE, 2019, 14, e0218508.	2.5	12
95	Disruption of a Transcriptional Repressor by an Insertion Sequence Element Integration Leads to Activation of a Novel Silent Cellobiose Transporter in Lactococcus lactis MG1363. Applied and Environmental Microbiology, 2017, 83, .	3.1	10
96	Further Elucidation of Galactose Utilization in Lactococcus lactis MG1363. Frontiers in Microbiology, 2018, 9, 1803.	3.5	10
97	A genetically engineered protein domain binding to bacterial murein, archaeal pseudomurein, and fungal chitin cell wall material. Applied Microbiology and Biotechnology, 2012, 96, 729-737.	3.6	9
98	A Specific Sugar Moiety in the Lactococcus lactis Cell Wall Pellicle Is Required for Infection by CHPC971, a Member of the Rare 1706 Phage Species. Applied and Environmental Microbiology, 2019, 85, .	3.1	8
99	Transcriptomic analysis of stress response to novel antimicrobial coatings in a clinical MRSA strain. Materials Science and Engineering C, 2021, 119, 111578.	7.3	8
100	Two homologous oligopeptide binding protein genes (oppA) in Lactococcus lactis MG1363. International Journal of Food Microbiology, 2004, 97, 9-15.	4.7	7
101	A Minimum of Three Motifs Is Essential for Optimal Binding of Pseudomurein Cell Wall-Binding Domain of Methanothermobacter thermautotrophicus. PLoS ONE, 2011, 6, e21582.	2.5	7
102	Enterococcus faecalis zinc-responsive proteins mediate bacterial defence against zinc overload, lysozyme and oxidative stress. Microbiology (United Kingdom), 2014, 160, 2755-2762.	1.8	7
103	Transcriptome profiling of TDC cluster deletion mutant of Enterococcus faecalis V583. Genomics Data, 2016, 9, 67-69.	1.3	7
104	Editing of the Proteolytic System of Lactococcus lactis Increases Its Bioactive Potential. Applied and Environmental Microbiology, 2020, 86, .	3.1	7
105	Lysis of a Lactococcus lactis Dipeptidase Mutant and Rescue by Mutation in the Pleiotropic Regulator CodY. Applied and Environmental Microbiology, 2020, 86, .	3.1	7
106	Functional role of surface layer proteins of<i> Lactobacillus acidophilus</i> L-92 in stress tolerance and binding to host cell proteins. Bioscience of Microbiota, Food and Health, 2021, 40, 33-42.	1.8	7
107	Genetics of Proteolysis in Lactococcus lactis. , 2003, , 189-223.		6
108	Reconstruction and inference of the Lactococcus lactis MG1363 gene co-expression network. PLoS ONE, 2019, 14, e0214868.	2.5	5

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109	Another Breaker of the Wall: the Biological Function of the Usp45 Protein of Lactococcus lactis. Applied and Environmental Microbiology, 2020, 86, .	3.1	5
110	Genetics of the proteolytic system of lactic acid bacteria. FEMS Microbiology Letters, 1990, 87, 15-41.	1.8	5
111	Environmental stress responses in Lactococcus lactis. FEMS Microbiology Reviews, 1999, 23, 483-501.	8.6	5
112	Employing lytic phage-mediated horizontal gene transfer in Lactococcus lactis. PLoS ONE, 2020, 15, e0238988.	2.5	4
113	Construction and characterization of a double mutant of Enterococcus faecalis that does not produce biogenic amines. Scientific Reports, 2019, 9, 16881.	3.3	2
114	Complete Genome Sequences of 28 Lactococcal Bacteriophages Isolated from Failed Dairy Fermentation Processes. Microbiology Resource Announcements, 2020, 9, .	0.6	2
115	Riboswitch RS <i> _{thiT} </i> as a Molecular Tool in Lactococcus lactis. Applied and Environmental Microbiology, 2022, 88, AEM0176421.	3.1	1
116	Mutations in Lactococcus lactis, and their Detection. , 2005, , 231-250.		0
117	Mutations in Lactococcus lactis and their Detection. , 2006, , 248-268.		0
118	Editorial: Omics and Systems Approaches to Study the Biology and Applications of Lactic Acid Bacteria. Frontiers in Microbiology, 2020, 11, 1786.	3.5	0
119	High-Resolution Chrono-Transcriptome of Lactococcus lactis Reveals That It Expresses Proteins with Adapted Size and pI upon Acidification and Nutrient Starvation. Applied and Environmental Microbiology, 2022, , e0247621.	3.1	0