

Stanislav Dusko Ehrlich

List of Publications by Year in descending order

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170
papers

49,565
citations

14124

69
h-index

5347

170
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176
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176
docs citations

176
times ranked

47621
citing authors

#	ARTICLE	IF	CITATIONS
1	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. <i>Gut</i> , 2022, 71, 2463-2480.	6.1	53
2	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease. <i>Nature Medicine</i> , 2022, 28, 295-302.	15.2	74
3	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	15.2	102
4	Increasing the diversity of dietary fibers in a daily-consumed bread modifies gut microbiota and metabolic profile in subjects at cardiometabolic risk. <i>Gut Microbes</i> , 2022, 14, 2044722.	4.3	28
5	Alterations in Gut Microbiome in Cirrhosis as Assessed by Quantitative Metagenomics: Relationship With Acute-on-Chronic Liver Failure and Prognosis. <i>Gastroenterology</i> , 2021, 160, 206-218.e13.	0.6	89
6	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021, 70, 2105-2114.	6.1	58
7	Conjugated C-6 hydroxylated bile acids in serum relate to human metabolic health and gut Clostridia species. <i>Scientific Reports</i> , 2021, 11, 13252.	1.6	8
8	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	13.7	102
9	Commensal <i>Hafnia alvei</i> strain reduces food intake and fat mass in obese mice—a new potential probiotic for appetite and body weight management. <i>International Journal of Obesity</i> , 2020, 44, 1041-1051.	1.6	55
10	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	5.8	122
11	Compositional and functional differences of the mucosal microbiota along the intestine of healthy individuals. <i>Scientific Reports</i> , 2020, 10, 14977.	1.6	78
12	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
13	Mediterranean diet intervention in overweight and obese subjects lowers plasma cholesterol and causes changes in the gut microbiome and metabolome independently of energy intake. <i>Gut</i> , 2020, 69, 1258-1268.	6.1	279
14	Aberrant gut microbiota alters host metabolome and impacts renal failure in humans and rodents. <i>Gut</i> , 2020, 69, 2131-2142.	6.1	232
15	Major microbiota dysbiosis in severe obesity: fate after bariatric surgery. <i>Gut</i> , 2019, 68, 70-82.	6.1	297
16	<i>Akkermansia muciniphila</i> abundance is lower in severe obesity, but its increased level after bariatric surgery is not associated with metabolic health improvement. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 317, E446-E459.	1.8	67
17	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019, 4, 112-123.	5.9	129
18	MSPminer: abundance-based reconstitution of microbial pan-genomes from shotgun metagenomic data. <i>Bioinformatics</i> , 2019, 35, 1544-1552.	1.8	82

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19	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
20	Microbial ecology perturbation in human IgA deficiency. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	206
21	A computational framework to integrate high-throughput omics datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , 2018, 13, 2781-2800.	5.5	82
22	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , 2018, 6, 11.	4.9	115
23	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
24	Quantitative metagenomics reveals unique gut microbiome biomarkers in ankylosing spondylitis. <i>Genome Biology</i> , 2017, 18, 142.	3.8	268
25	The human gut microbiome impacts health and disease. <i>Comptes Rendus - Biologies</i> , 2016, 339, 319-323.	0.1	28
26	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
27	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , 2016, 1, 16152.	5.9	56
28	Tongue Coating and the Salivary Microbial Communities Vary in Children with Halitosis. <i>Scientific Reports</i> , 2016, 6, 24481.	1.6	51
29	Dissemination of the mcr-1 colistin resistance gene. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 290-291.	4.6	24
30	Dietary modulation of the gut microbiota a randomised controlled trial in obese postmenopausal women. <i>British Journal of Nutrition</i> , 2015, 114, 406-417.	1.2	131
31	Influence of H7N9 virus infection and associated treatment on human gut microbiota. <i>Scientific Reports</i> , 2015, 5, 14771.	1.6	88
32	Effect of Genome and Environment on Metabolic and Inflammatory Profiles. <i>PLoS ONE</i> , 2015, 10, e0120898.	1.1	13
33	Quality control of microbiota metagenomics by k-mer analysis. <i>BMC Genomics</i> , 2015, 16, 183.	1.2	22
34	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	9.4	422
35	Qin et al. reply. <i>Nature</i> , 2015, 525, E2-E3.	13.7	3
36	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627

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37	Dietary Patterns Differently Associate with Inflammation and Gut Microbiota in Overweight and Obese Subjects. PLoS ONE, 2014, 9, e109434.	1.1	111
38	Bacterial protein signals are associated with Crohn's disease. Gut, 2014, 63, 1566-1577.	6.1	80
39	Anti-Inflammatory Properties of Streptococcus salivarius, a Commensal Bacterium of the Oral Cavity and Digestive Tract. Applied and Environmental Microbiology, 2014, 80, 928-934.	1.4	151
40	Alterations of the human gut microbiome in liver cirrhosis. Nature, 2014, 513, 59-64.	13.7	1,782
41	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	9.4	909
42	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	9.4	1,664
43	Changes of the human gut microbiome induced by a fermented milk product. Scientific Reports, 2014, 4, 6328.	1.6	217
44	Human intestinal metagenomics: state of the art and future. Current Opinion in Microbiology, 2013, 16, 232-239.	2.3	62
45	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	13.7	3,641
46	Dietary intervention impact on gut microbial gene richness. Nature, 2013, 500, 585-588.	13.7	1,485
47	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	9.0	442
48	A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature, 2012, 490, 55-60.	13.7	5,345
49	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	13.7	5,800
50	Inhibition of the NF- κ B Pathway in Human Intestinal Epithelial Cells by Commensal Streptococcus salivarius. Applied and Environmental Microbiology, 2011, 77, 4681-4684.	1.4	88
51	MetaHIT: The European Union Project on Metagenomics of the Human Intestinal Tract. , 2011, , 307-316.		65
52	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	13.7	9,342
53	Functional Metagenomics: A High Throughput Screening Method to Decipher Microbiota-Driven NF- κ B Modulation in the Human Gut. PLoS ONE, 2010, 5, e13092.	1.1	72
54	P087, a lactococcal phage with a morphogenesis module similar to an Enterococcus faecalis prophage. Virology, 2009, 388, 49-56.	1.1	31

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55	Activation of mRNA translation by phage protein and low temperature: the case of <i>Lactococcus lactis</i> abortive infection system AbiD1. <i>BMC Molecular Biology</i> , 2009, 10, 4.	3.0	25
56	Probiotics – little evidence for a link to obesity. <i>Nature Reviews Microbiology</i> , 2009, 7, 901-901.	13.6	37
57	DnaB, DnaD and DnaI proteins are components of the <i>Bacillus subtilis</i> replication restart primosome. <i>Molecular Microbiology</i> , 2008, 42, 245-256.	1.2	92
58	The lactococcal abortive infection protein AbiP is membrane-anchored and binds nucleic acids. <i>Virology</i> , 2008, 373, 14-24.	1.1	16
59	The Genetically Remote Pathogenic Strain NVH391-98 of the <i>Bacillus cereus</i> Group Is Representative of a Cluster of Thermophilic Strains. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1276-1280.	1.4	41
60	Development of Software Facilities to Characterize Regulatory Binding Motifs and Application to Streptococcaceae. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2008, 14, 67-73.	1.0	8
61	Extensive horizontal transfer of core genome genes between two <i>Lactobacillus</i> species found in the gastrointestinal tract. <i>BMC Evolutionary Biology</i> , 2007, 7, 141.	3.2	29
62	A distinct single-stranded DNA-binding protein encoded by the <i>Lactococcus lactis</i> bacteriophage bIL67. <i>Virology</i> , 2007, 363, 104-112.	1.1	17
63	KSY1, a lactococcal phage with a T7-like transcription. <i>Virology</i> , 2007, 365, 1-9.	1.1	39
64	Genetic Evidence for a Link Between Glycolysis and DNA Replication. <i>PLoS ONE</i> , 2007, 2, e447.	1.1	64
65	Systematic localisation of proteins fused to the green fluorescent protein in <i>Bacillus subtilis</i> : Identification of new proteins at the DNA replication factory. <i>Proteomics</i> , 2006, 6, 2135-2146.	1.3	84
66	Conservation of key elements of natural competence in <i>Lactococcus lactis</i> spp.. <i>FEMS Microbiology Letters</i> , 2006, 257, 32-42.	0.7	37
67	The replicative polymerases PolC and DnaE are required for theta replication of the <i>Bacillus subtilis</i> plasmid pBS72. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1471-1478.	0.7	12
68	Multiple-Locus Sequence Typing Analysis of <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> Reveals Separate Clustering and a Distinct Population Structure of Psychrotrophic Strains. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1569-1578.	1.4	122
69	Transcriptional analysis of the cyclopropane fatty acid synthase gene of <i>Lactococcus lactis</i> MG1363 at low pH. <i>FEMS Microbiology Letters</i> , 2005, 250, 189-194.	0.7	33
70	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2005, 250, 175-184.	0.7	73
71	DNA polymerase I acts in translesion synthesis mediated by the Y-polymerases in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2005, 57, 678-690.	1.2	44
72	New insights in the molecular biology and physiology of revealed by comparative genomics. <i>FEMS Microbiology Reviews</i> , 2005, 29, 435-463.	3.9	289

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73	Overall control of nitrogen metabolism in <i>Lactococcus lactis</i> by CodY, and possible models for CodY regulation in Firmicutes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3895-3909.	0.7	123
74	Clustered regularly interspaced short palindrome repeats (CRISPRs) have spacers of extrachromosomal origin. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2551-2561.	0.7	1,396
75	The Lactococcal Abortive Phage Infection System AbiP Prevents both Phage DNA Replication and Temporal Transcription Switch. <i>Journal of Bacteriology</i> , 2004, 186, 713-721.	1.0	32
76	Two distinct types of rRNA operons in the <i>Bacillus cereus</i> group. <i>Microbiology (United Kingdom)</i> , 2004, 150, 601-611.	0.7	33
77	A Phage Protein Confers Resistance to the Lactococcal Abortive Infection Mechanism AbiP. <i>Journal of Bacteriology</i> , 2004, 186, 3278-3281.	1.0	13
78	Genes Involved in Formation of Structured Multicellular Communities by <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 3970-3979.	1.0	255
79	Involvement of DnaE, the Second Replicative DNA Polymerase from <i>Bacillus subtilis</i> , in DNA Mutagenesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 1757-1767.	1.6	52
80	PriA Is Essential for Viability of the <i>Escherichia coli</i> Topoisomerase IV parE10 (Ts) Mutant. <i>Journal of Bacteriology</i> , 2004, 186, 1197-1199.	1.0	16
81	The bacterial condensin/cohesin-like protein complex acts in DNA repair and regulation of gene expression. <i>Molecular Microbiology</i> , 2004, 51, 1629-1640.	1.2	53
82	Requirement for RecFOR-mediated recombination in priA mutant. <i>Molecular Microbiology</i> , 2004, 52, 551-562.	1.2	39
83	Distinctive genetic features exhibited by the Y-family DNA polymerases in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2004, 54, 439-451.	1.2	50
84	Functional interplay between the <i>Bacillus subtilis</i> DnaD and DnaB proteins essential for initiation and re-initiation of DNA replication. <i>Molecular Microbiology</i> , 2004, 55, 1138-1150.	1.2	71
85	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 1554-1558.	9.4	485
86	Replication mutations differentially enhance RecA-dependent and RecA-independent recombination between tandem repeats in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2004, 39, 1248-1258.	1.2	16
87	Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species. <i>Genome Biology</i> , 2004, 5, r77.	13.9	319
88	csp-like genes of <i>Lactobacillus delbrueckii</i> ssp. <i>bulgaricus</i> and their response to cold shock. <i>FEMS Microbiology Letters</i> , 2003, 226, 323-330.	0.7	15
89	Replication restart in <i>gyrB</i> <i>Escherichia coli</i> mutants. <i>Molecular Microbiology</i> , 2003, 48, 845-854.	1.2	51
90	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003, 423, 87-91.	13.7	740

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91	Genomics. Current Opinion in Microbiology, 2003, 6, 479-481.	2.3	3
92	A Two-Protein Strategy for the Functional Loading of a Cellular Replicative DNA Helicase. Molecular Cell, 2003, 11, 1009-1020.	4.5	122
93	Transposition in <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> : identification of two thermosensitive replicons and two functional insertion sequences. Microbiology (United Kingdom), 2003, 149, 1503-1511.	0.7	13
94	An expanded view of bacterial DNA replication. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8342-8347.	3.3	176
95	The Peptidyl-Prolyl Isomerase Motif Is Lacking in PmpA, the PrsA-Like Protein Involved in the Secretion Machinery of <i>Lactococcus lactis</i> . Applied and Environmental Microbiology, 2002, 68, 3932-3942.	1.4	34
96	Restart of DNA replication in Gram-positive bacteria: functional characterisation of the <i>Bacillus subtilis</i> PriA initiator. Nucleic Acids Research, 2002, 30, 1593-1605.	6.5	50
97	Mining <i>Bacillus subtilis</i> chromosome heterogeneities using hidden Markov models. Nucleic Acids Research, 2002, 30, 1418-1426.	6.5	69
98	Electrotransformation of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> and <i>L. delbrueckii</i> subsp. <i>lactis</i> with Various Plasmids. Applied and Environmental Microbiology, 2002, 68, 46-52.	1.4	90
99	Filamentous Phage Active on the Gram-Positive Bacterium <i>Propionibacterium freudenreichii</i> . Journal of Bacteriology, 2002, 184, 2030-2033.	1.0	46
100	The beta-propeller protein YxaI increases the processivity of the PcrA helicase. Molecular Genetics and Genomics, 2002, 267, 391-400.	1.0	20
101	Combinational variation of restriction modification specificities in <i>Lactococcus lactis</i> . Molecular Microbiology, 2002, 28, 169-178.	1.2	74
102	<i>Lactococcus lactis</i> phage operon coding for an endonuclease homologous to RuvC. Molecular Microbiology, 2002, 28, 823-834.	1.2	35
103	Acid- and multistress-resistant mutants of <i>Lactococcus lactis</i> : identification of intracellular stress signals. Molecular Microbiology, 2002, 35, 517-528.	1.2	178
104	Primosome assembly requirement for replication restart in the <i>Escherichia coli</i> hsdR10 replication mutant. Molecular Microbiology, 2002, 44, 783-792.	1.2	43
105	Replication fork reversal in DNA polymerase III mutants of <i>Escherichia coli</i> : a role for the β^2 clamp. Molecular Microbiology, 2002, 44, 1331-1339.	1.2	61
106	Discovery of two novel families of proteins that are proposed to interact with prokaryotic SMC proteins, and characterization of the <i>Bacillus subtilis</i> family members ScpA and ScpB. Molecular Microbiology, 2002, 45, 59-71.	1.2	112
107	A new mutation delivery system for genome-scale approaches in <i>Bacillus subtilis</i> . Molecular Microbiology, 2002, 46, 25-36.	1.2	164
108	Co-linear scaffold of the <i>Bacillus licheniformis</i> and <i>Bacillus subtilis</i> genomes and its use to compare their competence genes. FEMS Microbiology Letters, 2002, 209, 23-30.	0.7	23

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109	Lactococcus lactis AbiD1 abortive infection efficiency is drastically increased by a phage protein. FEMS Microbiology Letters, 2002, 214, 283-287.	0.7	16
110	Replication fork collapse at replication terminator sequences. EMBO Journal, 2002, 21, 3898-3907.	3.5	98
111	Studies of genomes of dairy bacteria <i>Lactococcus lactis</i> . Sciences Des Aliments, 2002, 22, 45-53.	0.2	9
112	Effect of a <i>guaA</i> mutation on the acid tolerance of <i>L. lactis</i> . Sciences Des Aliments, 2002, 22, 67-74.	0.2	3
113	Two Essential DNA Polymerases at the Bacterial Replication Fork. Science, 2001, 294, 1716-1719.	6.0	148
114	Transcriptional Pattern of Genes Coding for the Proteolytic System of <i>Lactococcus lactis</i> and Evidence for Coordinated Regulation of Key Enzymes by Peptide Supply. Journal of Bacteriology, 2001, 183, 3614-3622.	1.0	120
115	Pleiotropic transcriptional repressor CodY senses the intracellular pool of branched-chain amino acids in <i>Lactococcus lactis</i> . Molecular Microbiology, 2001, 40, 1227-1239.	1.2	198
116	Early Steps of <i>Bacillus subtilis</i> Primosome Assembly. Journal of Biological Chemistry, 2001, 276, 45818-45825.	1.6	80
117	The RepE Initiator Is a Double-stranded and Single-stranded DNA-binding Protein That Forms an Atypical Open Complex at the Onset of Replication of Plasmid pAM ² 1 from Gram-positive Bacteria. Journal of Biological Chemistry, 2001, 276, 10234-10246.	1.6	27
118	Viability of <i>rep recA</i> Mutants Depends on Their Capacity To Cope with Spontaneous Oxidative Damage and on the DnaK Chaperone Protein. Journal of Bacteriology, 2001, 183, 2165-2171.	1.0	15
119	Identity elements in tRNA-mediated transcription antitermination: implication of tRNA D- and T-arms in mRNA recognition. Microbiology (United Kingdom), 2001, 147, 1223-1233.	0.7	9
120	UvrD-dependent replication of rolling-circle plasmids in <i>Escherichia coli</i> . Molecular Microbiology, 2000, 35, 204-210.	1.2	92
121	Resolution of Holliday junctions by RuvABC prevents dimer formation in <i>rep</i> mutants and UV-irradiated cells. Molecular Microbiology, 2000, 37, 180-191.	1.2	72
122	RuvABC-dependent double-strand breaks in <i>dnaBts</i> mutants require RecA. Molecular Microbiology, 2000, 38, 565-574.	1.2	110
123	Six putative two-component regulatory systems isolated from <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363 The GenBank accession numbers for the sequences of the six 2CSs and surrounding ORFs determined in this work are AF172649, AF176556, AF178425, AF172650, AF176557 and AF176809 for systems A-F, respectively. Microbiology (United Kingdom), 2000, 146, 935-947.	0.7	72
124	Physiological Study of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> Strains in a Novel Chemically Defined Medium. Applied and Environmental Microbiology, 2000, 66, 5306-5311.	1.4	86
125	A Study of the CopF Repressor of Plasmid pAM ² 1 by Phage Display. Journal of Bacteriology, 2000, 182, 2973-2977.	1.0	2
126	Transcriptional and Translational Regulation of β -Acetolactate Decarboxylase of <i>Lactococcus lactis</i> subsp. <i>lactis</i> . Journal of Bacteriology, 2000, 182, 5399-5408.	1.0	20

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127	An Operon for a Putative ATP-Binding Cassette Transport System Involved in Acetoin Utilization of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2000, 182, 5454-5461.	1.0	45
128	Expression of the <i>Staphylococcus hyicus</i> Lipase in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2000, 66, 588-598.	1.4	52
129	Identification of stress-inducible proteins in <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> . , 2000, 21, 2557.		2
130	The 409 bp tandem repeat spanning genes <i>yxaK</i> and <i>yxaL</i> is absent from the <i>Bacillus subtilis</i> chromosome. <i>Microbiology (United Kingdom)</i> , 2000, 146, 2091-2092.	0.7	4
131	Evaluation de la diversité de l'expression génétique chez les lactocoques : développement d'un outil et son application aux peptidases. <i>Sciences Des Aliments</i> , 2000, 20, 55-62.	0.2	2
132	Les lactocoques comme vecteurs pour libérer des protéines dans le duodénum : application au traitement des déficiences pancréatiques en lipase. <i>Sciences Des Aliments</i> , 2000, 20, 127-133.	0.2	0
133	Replication Slippage of Different DNA Polymerases Is Inversely Related to Their Strand Displacement Efficiency. <i>Journal of Biological Chemistry</i> , 1999, 274, 27481-27490.	1.6	84
134	Analysis of the <i>Bacillus subtilis</i> genome sequence reveals nine new T-box leaders. <i>Molecular Microbiology</i> , 1999, 31, 1010-1011.	1.2	0
135	Effects of metabolic flux on stress response pathways in <i>Lactococcus lactis</i> . <i>Molecular Microbiology</i> , 1999, 31, 845-858.	1.2	96
136	<i>sbcB sbcC</i> null mutations allow RecF-mediated repair of arrested replication forks in <i>rep recBC</i> mutants. <i>Molecular Microbiology</i> , 1999, 33, 846-857.	1.2	40
137	Low-redundancy sequencing of the entire <i>Lactococcus lactis</i> IL1403 genome. <i>Antonie Van Leeuwenhoek</i> , 1999, 76, 27-76.	0.7	153
138	Molecular Diversity and Relationship within <i>Lactococcus lactis</i> , as revealed by Randomly Amplified Polymorphic DNA (RAPD). <i>Systematic and Applied Microbiology</i> , 1998, 21, 530-538.	1.2	66
139	Identification of the Chi site of <i>Haemophilus influenzae</i> several sequences related to the <i>Escherichia coli</i> Chi site. <i>Molecular Microbiology</i> , 1998, 27, 1021-1029.	1.2	65
140	<i>tRNA^{Trp}</i> as a key element of antitermination in the <i>Lactococcus lactis</i> <i>trp</i> operon. <i>Molecular Microbiology</i> , 1998, 29, 61-74.	1.2	27
141	Analysis of the <i>Bacillus subtilis</i> genome sequence reveals nine new T-box leaders. <i>Molecular Microbiology</i> , 1998, 29, 662-664.	1.2	23
142	<i>PcrA</i> is an essential DNA helicase of <i>Bacillus subtilis</i> fulfilling functions both in repair and rolling-circle replication. <i>Molecular Microbiology</i> , 1998, 29, 261-273.	1.2	154
143	Inhibition of a naturally occurring rolling-circle replicon in derivatives of the theta-replicating plasmid pIP501. <i>Molecular Microbiology</i> , 1998, 29, 709-718.	1.2	18
144	A five-nucleotide sequence protects DNA from exonucleolytic degradation by AddAB, the RecBCD analogue of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1998, 29, 1369-1377.	1.2	72

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145	Transcription-driven DNA replication of plasmid pAM ²¹ in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1998, 30, 135-145.	1.2	27
146	A vector for systematic gene inactivation in <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 1998, 144, 3097-3104.	0.7	620
147	Transcription of the <i>trp</i> operon in <i>Lactococcus lactis</i> is controlled by antitermination in the leader region. <i>Microbiology (United Kingdom)</i> , 1998, 144, 2103-2111.	0.7	15
148	The <i>kdgRKAT</i> operon of <i>Bacillus subtilis</i> : detection of the transcript and regulation by the <i>kdgR</i> and <i>ccpA</i> genes. <i>Microbiology (United Kingdom)</i> , 1998, 144, 3111-3118.	0.7	32
149	Disruption of the sole <i>IdhL</i> gene in <i>Lactobacillus sakei</i> prevents the production of both L- and D-lactate. <i>Microbiology (United Kingdom)</i> , 1998, 144, 3327-3333.	0.7	43
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