

Stanislav Dusko Ehrlich

List of Publications by Year in descending order

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171
papers

49,565
citations

12330

69
h-index

4432

172
g-index

176
all docs

176
docs citations

176
times ranked

43821
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	27.8	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
3	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60.	27.8	5,345
4	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	27.8	3,641
5	Alterations of the human gut microbiome in liver cirrhosis. <i>Nature</i> , 2014, 513, 59-64.	27.8	1,782
6	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	17.5	1,664
7	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	27.8	1,627
8	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	27.8	1,506
9	Dietary intervention impact on gut microbial gene richness. <i>Nature</i> , 2013, 500, 585-588.	27.8	1,485
10	Clustered regularly interspaced short palindrome repeats (CRISPRs) have spacers of extrachromosomal origin. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2551-2561.	1.8	1,396
11	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	17.5	909
12	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003, 423, 87-91.	27.8	740
13	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
14	A vector for systematic gene inactivation in <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 1998, 144, 3097-3104.	1.8	620
15	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
16	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 1554-1558.	17.5	485
17	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	19.0	442
18	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	17.5	422

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19	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.	9.6	319
20	Major microbiota dysbiosis in severe obesity: fate after bariatric surgery. <i>Gut</i> , 2019, 68, 70-82.	12.1	297
21	New insights in the molecular biology and physiology of revealed by comparative genomics. <i>FEMS Microbiology Reviews</i> , 2005, 29, 435-463.	8.6	289
22	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	27.8	283
23	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.	12.1	279
24	Quantitative metagenomics reveals unique gut microbiome biomarkers in ankylosing spondylitis. <i>Genome Biology</i> , 2017, 18, 142.	8.8	268
25	Genes Involved in Formation of Structured Multicellular Communities by <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 3970-3979.	2.2	255
26	Aberrant gut microbiota alters host metabolome and impacts renal failure in humans and rodents. <i>Gut</i> , 2020, 69, 2131-2142.	12.1	232
27	Changes of the human gut microbiome induced by a fermented milk product. <i>Scientific Reports</i> , 2014, 4, 6328.	3.3	217
28	Microbial ecology perturbation in human IgA deficiency. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	206
29	Pleiotropic transcriptional repressor CodY senses the intracellular pool of branched-chain amino acids in <i>Lactococcus lactis</i> . <i>Molecular Microbiology</i> , 2001, 40, 1227-1239.	2.5	198
30	Acid- and multistress-resistant mutants of <i>Lactococcus lactis</i> : identification of intracellular stress signals. <i>Molecular Microbiology</i> , 2002, 35, 517-528.	2.5	178
31	An expanded view of bacterial DNA replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8342-8347.	7.1	176
32	A new mutation delivery system for genome-scale approaches in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2002, 46, 25-36.	2.5	164
33	Structurally stable <i>Bacillus subtilis</i> cloning vectors. <i>Gene</i> , 1990, 87, 53-61.	2.2	155
34	PcrA 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.	2.5	154
35	Low-redundancy sequencing of the entire <i>Lactococcus lactis</i> IL1403 genome. <i>Antonie Van Leeuwenhoek</i> , 1999, 76, 27-76.	1.7	153
36	Anti-Inflammatory Properties of <i>Streptococcus salivarius</i> , a Commensal Bacterium of the Oral Cavity and Digestive Tract. <i>Applied and Environmental Microbiology</i> , 2014, 80, 928-934.	3.1	151

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37	Two Essential DNA Polymerases at the Bacterial Replication Fork. <i>Science</i> , 2001, 294, 1716-1719.	12.6	148
38	Dietary modulation of the gut microbiota – a randomised controlled trial in obese postmenopausal women. <i>British Journal of Nutrition</i> , 2015, 114, 406-417.	2.3	131
39	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019, 4, 112-123.	13.3	129
40	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.	1.8	123
41	A Two-Protein Strategy for the Functional Loading of a Cellular Replicative DNA Helicase. <i>Molecular Cell</i> , 2003, 11, 1009-1020.	9.7	122
42	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.	3.1	122
43	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	12.8	122
44	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. <i>Journal of Bacteriology</i> , 2001, 183, 3614-3622.	2.2	120
45	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , 2018, 6, 11.	11.1	115
46	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. <i>Molecular Microbiology</i> , 2002, 45, 59-71.	2.5	112
47	Dietary Patterns Differently Associate with Inflammation and Gut Microbiota in Overweight and Obese Subjects. <i>PLoS ONE</i> , 2014, 9, e109434.	2.5	111
48	RuvABC-dependent double-strand breaks in dnaBts mutants require RecA. <i>Molecular Microbiology</i> , 2000, 38, 565-574.	2.5	110
49	The recA gene of <i>Lactococcus lactis</i> : characterization and involvement in oxidative and thermal stress. <i>Molecular Microbiology</i> , 1995, 17, 1121-1131.	2.5	109
50	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	27.8	102
51	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	30.7	102
52	Replication fork collapse at replication terminator sequences. <i>EMBO Journal</i> , 2002, 21, 3898-3907.	7.8	98
53	An Export-Specific Reporter Designed for Gram-Positive Bacteria: Application to <i>Lactococcus lactis</i> . <i>Journal of Bacteriology</i> , 1998, 180, 1904-1912.	2.2	97
54	Effects of metabolic flux on stress response pathways in <i>Lactococcus lactis</i> . <i>Molecular Microbiology</i> , 1999, 31, 845-858.	2.5	96

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55	UvrD-dependent replication of rolling-circle plasmids in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2000, 35, 204-210.	2.5	92
56	DnaB, DnaD and DnaI proteins are components of the <i>Bacillus subtilis</i> replication restart primosome. <i>Molecular Microbiology</i> , 2008, 42, 245-256.	2.5	92
57	Electrotransformation of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> and <i>L. delbrueckii</i> subsp. <i>lactis</i> with Various Plasmids. <i>Applied and Environmental Microbiology</i> , 2002, 68, 46-52.	3.1	90
58	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.	1.3	89
59	Inhibition of the NF- κ B Pathway in Human Intestinal Epithelial Cells by Commensal <i>Streptococcus salivarius</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 4681-4684.	3.1	88
60	Influence of H7N9 virus infection and associated treatment on human gut microbiota. <i>Scientific Reports</i> , 2015, 5, 14771.	3.3	88
61	Physiological Study of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> Strains in a Novel Chemically Defined Medium. <i>Applied and Environmental Microbiology</i> , 2000, 66, 5306-5311.	3.1	86
62	The organization of the <i>Bacillus subtilis</i> 168 chromosome region between the <i>spoVA</i> and <i>serA</i> genetic loci, based on sequence data. <i>Molecular Microbiology</i> , 1993, 10, 385-395.	2.5	84
63	Replication Slippage of Different DNA Polymerases Is Inversely Related to Their Strand Displacement Efficiency. <i>Journal of Biological Chemistry</i> , 1999, 274, 27481-27490.	3.4	84
64	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.	2.2	84
65	A computational framework to integrate high-throughput \sim -omics datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , 2018, 13, 2781-2800.	12.0	82
66	MSPminer: abundance-based reconstitution of microbial pan-genomes from shotgun metagenomic data. <i>Bioinformatics</i> , 2019, 35, 1544-1552.	4.1	82
67	Antipairing and strand transferase activities of <i>E. coli</i> helicase II (UvrD). <i>Nucleic Acids Research</i> , 1993, 21, 3205-3209.	14.5	80
68	Early Steps of <i>Bacillus subtilis</i> Primosome Assembly. <i>Journal of Biological Chemistry</i> , 2001, 276, 45818-45825.	3.4	80
69	Bacterial protein signals are associated with Crohn's disease. <i>Gut</i> , 2014, 63, 1566-1577.	12.1	80
70	Lethality of <i>rep recB</i> and <i>rep recC</i> double mutants of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1995, 17, 1177-1188.	2.5	79
71	Compositional and functional differences of the mucosal microbiota along the intestine of healthy individuals. <i>Scientific Reports</i> , 2020, 10, 14977.	3.3	78
72	Combinational variation of restriction modification specificities in <i>Lactococcus lactis</i> . <i>Molecular Microbiology</i> , 2002, 28, 169-178.	2.5	74

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73	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease. <i>Nature Medicine</i> , 2022, 28, 295-302.	30.7	74
74	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2005, 250, 175-184.	1.8	73
75	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.	2.5	72
76	Resolution of Holliday junctions by RuvABC prevents dimer formation in rep mutants and UV-irradiated cells. <i>Molecular Microbiology</i> , 2000, 37, 180-191.	2.5	72
77	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-E, respectively. <i>Microbiology (United Kingdom)</i> , 2000, 146, 935-947.	1.8	72
78	Functional Metagenomics: A High Throughput Screening Method to Decipher Microbiota-Driven NF- κ B Modulation in the Human Gut. <i>PLoS ONE</i> , 2010, 5, e13092.	2.5	72
79	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.	2.5	71
80	Mining <i>Bacillus subtilis</i> chromosome heterogeneities using hidden Markov models. <i>Nucleic Acids Research</i> , 2002, 30, 1418-1426.	14.5	69
81	<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.	3.5	67
82	Transcription-induced deletions in <i>Escherichia coli</i> plasmids. <i>Molecular Microbiology</i> , 1995, 17, 493-504.	2.5	66
83	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.	2.8	66
84	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.	2.5	65
85	MetaHIT: The European Union Project on Metagenomics of the Human Intestinal Tract. , 2011, , 307-316.		65
86	Genetic Evidence for a Link Between Glycolysis and DNA Replication. <i>PLoS ONE</i> , 2007, 2, e447.	2.5	64
87	Dramatic decay of phage transcripts in lactococcal cells carrying the abortive infection determinant <i>AbiB</i> . <i>Molecular Microbiology</i> , 1996, 19, 221-230.	2.5	62
88	Human intestinal metagenomics: state of the art and future. <i>Current Opinion in Microbiology</i> , 2013, 16, 232-239.	5.1	62
89	Replication fork reversal in DNA polymerase III mutants of <i>Escherichia coli</i> : a role for the τ^2 clamp. <i>Molecular Microbiology</i> , 2002, 44, 1331-1339.	2.5	61
90	<i>uvrD</i> mutations enhance tandem repeat deletion in the <i>Escherichia coli</i> chromosome via SOS induction of the RecF recombination pathway. <i>Molecular Microbiology</i> , 1997, 26, 557-567.	2.5	60

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91	Bacillus subtilis can modulate its capacity and specificity for protein secretion through temporally controlled expression of the sipS gene for signal peptidase I. <i>Molecular Microbiology</i> , 1996, 22, 605-618.	2.5	59
92	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.	12.1	58
93	Isolation of a dnaE mutation which enhances RecA-independent homologous recombination in the Escherichia coli chromosome. <i>Molecular Microbiology</i> , 1997, 24, 1225-1234.	2.5	57
94	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , 2016, 1, 16152.	13.3	56
95	Commensal Hafnia alvei 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.	3.4	55
96	The bacterial condensin/cohesin-like protein complex acts in DNA repair and regulation of gene expression. <i>Molecular Microbiology</i> , 2004, 51, 1629-1640.	2.5	53
97	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.	12.1	53
98	Expression of the <i>Staphylococcus hyicus</i> Lipase in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2000, 66, 588-598.	3.1	52
99	Involvement of DnaE, the Second Replicative DNA Polymerase from Bacillus subtilis, in DNA Mutagenesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 1757-1767.	3.4	52
100	Replication restart in gyrB Escherichia coli mutants. <i>Molecular Microbiology</i> , 2003, 48, 845-854.	2.5	51
101	Tongue Coating and the Salivary Microbial Communities Vary in Children with Halitosis. <i>Scientific Reports</i> , 2016, 6, 24481.	3.3	51
102	Restart of DNA replication in Gram-positive bacteria: functional characterisation of the Bacillus subtilis PriA initiator. <i>Nucleic Acids Research</i> , 2002, 30, 1593-1605.	14.5	50
103	Distinctive genetic features exhibited by the Y-family DNA polymerases in Bacillus subtilis. <i>Molecular Microbiology</i> , 2004, 54, 439-451.	2.5	50
104	A Type IC Restriction-Modification System in Lactococcus lactis. <i>Journal of Bacteriology</i> , 1998, 180, 407-411.	2.2	50
105	Filamentous Phage Active on the Gram-Positive Bacterium Propionibacterium freudenreichii. <i>Journal of Bacteriology</i> , 2002, 184, 2030-2033.	2.2	46
106	Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region. <i>Microbiology (United Kingdom)</i> , 1997, 143, 3431-3441.	1.8	45
107	An Operon for a Putative ATP-Binding Cassette Transport System Involved in Acetoin Utilization of Bacillus subtilis. <i>Journal of Bacteriology</i> , 2000, 182, 5454-5461.	2.2	45
108	DNA polymerase I acts in translesion synthesis mediated by the Y-polymerases in Bacillus subtilis. <i>Molecular Microbiology</i> , 2005, 57, 678-690.	2.5	44

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109	Disruption of the sole <i>ldhL</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.	1.8	43
110	Primosome assembly requirement for replication restart in the <i>Escherichia coli</i> hsdR10 replication mutant. <i>Molecular Microbiology</i> , 2002, 44, 783-792.	2.5	43
111	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.	3.1	41
112	<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.	2.5	40
113	Requirement for RecFOR-mediated recombination in <i>priA</i> mutant. <i>Molecular Microbiology</i> , 2004, 52, 551-562.	2.5	39
114	KSY1, a lactococcal phage with a T7-like transcription. <i>Virology</i> , 2007, 365, 1-9.	2.4	39
115	Conservation of key elements of natural competence in <i>Lactococcus lactis</i> spp.. <i>FEMS Microbiology Letters</i> , 2006, 257, 32-42.	1.8	37
116	Probiotics – little evidence for a link to obesity. <i>Nature Reviews Microbiology</i> , 2009, 7, 901-901.	28.6	37
117	<i>Lactococcus lactis</i> phage operon coding for an endonuclease homologous to RuvC. <i>Molecular Microbiology</i> , 2002, 28, 823-834.	2.5	35
118	The Peptidyl-Prolyl Isomerase Motif Is Lacking in PmpA, the PrsA-Like Protein Involved in the Secretion Machinery of <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 3932-3942.	3.1	34
119	Two distinct types of rRNA operons in the <i>Bacillus cereus</i> group. <i>Microbiology (United Kingdom)</i> , 2004, 150, 601-611.	1.8	33
120	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.	1.8	33
121	The transcriptional organization of the <i>Bacillus subtilis</i> 168 chromosome region between the <i>spoVAF</i> and <i>serA</i> genetic loci. <i>Molecular Microbiology</i> , 1993, 10, 397-405.	2.5	32
122	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.	1.8	32
123	The Lactococcal Abortive Phage Infection System <i>AbiP</i> Prevents both Phage DNA Replication and Temporal Transcription Switch. <i>Journal of Bacteriology</i> , 2004, 186, 713-721.	2.2	32
124	P087, a lactococcal phage with a morphogenesis module similar to an <i>Enterococcus faecalis</i> prophage. <i>Virology</i> , 2009, 388, 49-56.	2.4	31
125	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
126	The human gut microbiome impacts health and disease. <i>Comptes Rendus - Biologies</i> , 2016, 339, 319-323.	0.2	28

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127	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.	9.8	28
128	tRNA ^{Trp} as a key element of antitermination in the <i>Lactococcus lactis</i> trp operon. <i>Molecular Microbiology</i> , 1998, 29, 61-74.	2.5	27
129	Transcription-driven DNA replication of plasmid pAM ²¹ in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1998, 30, 135-145.	2.5	27
130	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 ²¹ from Gram-positive Bacteria. <i>Journal of Biological Chemistry</i> , 2001, 276, 10234-10246.	3.4	27
131	The <i>Bacillus subtilis</i> dnaL gene is part of the dnaB operon. <i>Microbiology (United Kingdom)</i> , 1995, 141, 1199-1200.	1.8	26
132	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
133	Dissemination of the mcr-1 colistin resistance gene. <i>Lancet Infectious Diseases</i> , 2016, 16, 290-291.	9.1	24
134	Hypersecretion of a Cellulase from <i>Clostridium thermocellum</i> in <i>Bacillus subtilis</i> by Induction of Chromosomal DNA Amplification. <i>Nature Biotechnology</i> , 1990, 8, 559-563.	17.5	23
135	Analysis of the <i>Bacillus subtilis</i> genome sequence reveals nine new σ box leaders. <i>Molecular Microbiology</i> , 1998, 29, 662-664.	2.5	23
136	Co-linear scaffold of the <i>Bacillus licheniformis</i> and <i>Bacillus subtilis</i> genomes and its use to compare their competence genes. <i>FEMS Microbiology Letters</i> , 2002, 209, 23-30.	1.8	23
137	Quality control of microbiota metagenomics by k-mer analysis. <i>BMC Genomics</i> , 2015, 16, 183.	2.8	22
138	Sequence of the <i>Bacillus subtilis</i> genome region in the vicinity of the lev operon reveals two new extracytoplasmic function RNA polymerase sigma factors SigV and SigZ. <i>Microbiology (United Kingdom)</i> , 2007, 151, 1087-1094.	1.8	21
139	Transcriptional and Translational Regulation of α -Acetolactate Decarboxylase of <i>Lactococcus lactis</i> subsp. <i>lactis</i> . <i>Journal of Bacteriology</i> , 2000, 182, 5399-5408.	2.2	20
140	The beta-propeller protein YxaL increases the processivity of the PcrA helicase. <i>Molecular Genetics and Genomics</i> , 2002, 267, 391-400.	2.1	20
141	Inhibition of a naturally occurring rolling-circle replicon in derivatives of the theta-replicating plasmid pIP501. <i>Molecular Microbiology</i> , 1998, 29, 709-718.	2.5	18
142	A distinct single-stranded DNA-binding protein encoded by the <i>Lactococcus lactis</i> bacteriophage bIL67. <i>Virology</i> , 2007, 363, 104-112.	2.4	17
143	<i>Lactococcus lactis</i> AbiD1 abortive infection efficiency is drastically increased by a phage protein. <i>FEMS Microbiology Letters</i> , 2002, 214, 283-287.	1.8	16
144	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.	2.2	16

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