

Petri Auvinen

List of Publications by Year in descending order

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Version: 2024-02-01

195
papers

13,795
citations

22153

59
h-index

24982

109
g-index

217
all docs

217
docs citations

217
times ranked

20183
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 variant with mutations in N gene affecting detection by widely used PCR primers. <i>Journal of Medical Virology</i> , 2022, 94, 1227-1231.	5.0	18
2	Improved chromosome-level genome assembly of the Glanville fritillary butterfly (<i>Melitaea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 11, .	6.4	8
3	Multimics implicate gut microbiota in altered lipid and energy metabolism in Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2022, 8, 39.	5.3	12
4	Bacterial Butyrate in Parkinson's Disease Is Linked to Epigenetic Changes and Depressive Symptoms. <i>Movement Disorders</i> , 2022, 37, 1644-1653.	3.9	44
5	Transcriptomic time-series analysis of cold- and heat-shock response in psychrotrophic lactic acid bacteria. <i>BMC Genomics</i> , 2021, 22, 28.	2.8	16
6	Subgingival microbiota in a population with and without cognitive dysfunction. <i>Journal of Oral Microbiology</i> , 2021, 13, 1854552.	2.7	24
7	A transcriptomic view to wounding response in young Scots pine stems. <i>Scientific Reports</i> , 2021, 11, 3778.	3.3	9
8	High-pressure processing-induced transcriptome response during recovery of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2021, 22, 117.	2.8	18
9	Relationships of gut microbiota, short-chain fatty acids, inflammation, and the gut barrier in Parkinson's disease. <i>Molecular Neurodegeneration</i> , 2021, 16, 6.	10.8	197
10	Analysis of temporal gene regulation of <i>Listeria monocytogenes</i> revealed distinct regulatory response modes after exposure to high pressure processing. <i>BMC Genomics</i> , 2021, 22, 266.	2.8	5
11	The complete genome sequence of <i>Listeria monocytogenes</i> strain S2542 and expression of selected genes under high-pressure processing. <i>BMC Research Notes</i> , 2021, 14, 137.	1.4	1
12	Indocyanine Green-Assisted and LED-Light-Activated Antibacterial Photodynamic Therapy Reduces Dental Plaque. <i>Dentistry Journal</i> , 2021, 9, 52.	2.3	9
13	Microbial Communities of <i>Cladonia</i> Lichens and Their Biosynthetic Gene Clusters Potentially Encoding Natural Products. <i>Microorganisms</i> , 2021, 9, 1347.	3.6	10
14	Gut Microbiome Signatures of Risk and Prodromal Markers of Parkinson Disease. <i>Annals of Neurology</i> , 2021, 90, E1-E12.	5.3	41
15	Gut bacterial tyrosine decarboxylase associates with clinical variables in a longitudinal cohort study of Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2021, 7, 115.	5.3	17
16	Alu element in the RNA binding motif protein, X-linked 2 (RBMX2) gene found to be linked to bipolar disorder. <i>PLoS ONE</i> , 2021, 16, e0261170.	2.5	2
17	Gut microbiota composition is associated with narcolepsy type 1. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2020, 7, .	6.0	20
18	Survey of microbes in industrial-scale second-generation bioethanol production for better process knowledge and operation. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 8049-8064.	3.6	0

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19	Immune-microbiota interaction in Finnish and Russian Karelia young people with high and low allergy prevalence. <i>Clinical and Experimental Allergy</i> , 2020, 50, 1148-1158.	2.9	19
20	Complete Genome Sequences and Methylome Analyses of <i>Cutibacterium acnes</i> subsp. <i>acnes</i> Strains DSM 16379 and DSM 1897. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
21	Skin Microbiome in Cutaneous T-Cell Lymphoma by 16S and Whole-Genome Shotgun Sequencing. <i>Journal of Investigative Dermatology</i> , 2020, 140, 2304-2308.e7.	0.7	22
22	Dual-light photodynamic therapy administered daily provides a sustained antibacterial effect on biofilm and prevents <i>Streptococcus mutans</i> adaptation. <i>PLoS ONE</i> , 2020, 15, e0232775.	2.5	23
23	Identification and Characterization of Splicing Defects by Single-Molecule Real-Time Sequencing Technology (PacBio). <i>Journal of Neuromuscular Diseases</i> , 2020, 7, 477-481.	2.6	7
24	Genomic characterization of the most barotolerant <i>Listeria monocytogenes</i> RO15 strain compared to reference strains used to evaluate food high pressure processing. <i>BMC Genomics</i> , 2020, 21, 455.	2.8	14
25	Microbiome of the Healthy External Auditory Canal. <i>Otology and Neurotology</i> , 2020, Publish Ahead of Print, e609-e614.	1.3	9
26	Title is missing!. , 2020, 15, e0232775.		0
27	Title is missing!. , 2020, 15, e0232775.		0
28	Title is missing!. , 2020, 15, e0232775.		0
29	Title is missing!. , 2020, 15, e0232775.		0
30	Title is missing!. , 2020, 15, e0232775.		0
31	Title is missing!. , 2020, 15, e0232775.		0
32	Notum produced by Paneth cells attenuates regeneration of aged intestinal epithelium. <i>Nature</i> , 2019, 571, 398-402.	27.8	166
33	Red-Brown Pigmentation of <i>Acidipropionibacterium jensenii</i> Is Tied to Haemolytic Activity and <i>cyl</i> -Like Gene Cluster. <i>Microorganisms</i> , 2019, 7, 512.	3.6	10
34	Phenotypic effects of dietary stress in combination with a respiratory chain bypass in mice. <i>Physiological Reports</i> , 2019, 7, e14159.	1.7	8
35	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffolder output. <i>PLoS ONE</i> , 2019, 14, e0216885.	2.5	14
36	Multi-omics analysis identifies mitochondrial pathways associated with anxiety-related behavior. <i>PLoS Genetics</i> , 2019, 15, e1008358.	3.5	43

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37	Gut microbiota in Parkinson's disease: Temporal stability and relations to disease progression. <i>EBioMedicine</i> , 2019, 44, 691-707.	6.1	236
38	Genome description of <i>Phlebia radiata</i> 79 with comparative genomics analysis on lignocellulose decomposition machinery of phlebioid fungi. <i>BMC Genomics</i> , 2019, 20, 430.	2.8	16
39	Alternative oxidase-mediated respiration prevents lethal mitochondrial cardiomyopathy. <i>EMBO Molecular Medicine</i> , 2019, 11, .	6.9	53
40	Serotonin and tryptophan metabolites, autoantibodies and gut microbiome in APECED. <i>Endocrine Connections</i> , 2019, 8, 69-77.	1.9	3
41	BK polyomavirus microRNA expression and sequence variation in polyomavirus-associated nephropathy. <i>Journal of Clinical Virology</i> , 2018, 102, 70-76.	3.1	16
42	Secretome profiling of <i>Propionibacterium freudenreichii</i> reveals highly variable responses even among the closely related strains. <i>Microbial Biotechnology</i> , 2018, 11, 510-526.	4.2	15
43	Food Spoilage-Associated <i>Leuconostoc</i> , <i>Lactococcus</i> , and <i>Lactobacillus</i> Species Display Different Survival Strategies in Response to Competition. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	50
44	The complexity of titin splicing pattern in human adult skeletal muscles. <i>Skeletal Muscle</i> , 2018, 8, 11.	4.2	65
45	Isotretinoin and lymecycline treatments modify the skin microbiota in acne. <i>Experimental Dermatology</i> , 2018, 27, 30-36.	2.9	48
46	Gut microbiome in gestational diabetes: a cross-sectional study of mothers and offspring 5 years postpartum. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2018, 97, 38-46.	2.8	51
47	Bracketing phenogenotypic limits of mammalian hybridization. <i>Royal Society Open Science</i> , 2018, 5, 180903.	2.4	24
48	The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. <i>Plant Cell</i> , 2018, 30, 2813-2837.	6.6	95
49	Metagenomic and metatranscriptomic analysis of the microbial community in Swiss-type Maasdam cheese during ripening. <i>International Journal of Food Microbiology</i> , 2018, 281, 10-22.	4.7	63
50	BARCOSEL: a tool for selecting an optimal barcode set for high-throughput sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 257.	2.6	35
51	<i>Acidipropionibacterium virtanenii</i> sp. nov., isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3175-3183.	1.7	9
52	Genetic Control of Myelin Plasticity after Chronic Psychosocial Stress. <i>ENeuro</i> , 2018, 5, ENEURO.0166-18.2018.	1.9	48
53	Oral and nasal microbiota in Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2017, 38, 61-67.	2.2	159
54	Loss of cutaneous microbial diversity during first 3 weeks of life in very low birthweight infants. <i>Experimental Dermatology</i> , 2017, 26, 861-867.	2.9	21

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55	Significant disparities in allergy prevalence and microbiota between the young people in Finnish and Russian Karelia. <i>Clinical and Experimental Allergy</i> , 2017, 47, 665-674.	2.9	97
56	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. <i>Nature Genetics</i> , 2017, 49, 904-912.	21.4	221
57	Network Analysis Reveals Similar Transcriptomic Responses to Intrinsic Properties of Carbon Nanomaterials <i>in Vitro</i> and <i>in Vivo</i> . <i>ACS Nano</i> , 2017, 11, 3786-3796.	14.6	35
58	More than constipation – bowel symptoms in Parkinson's disease and their connection to gut microbiota. <i>European Journal of Neurology</i> , 2017, 24, 1375-1383.	3.3	112
59	Functional genomics provides insights into the role of <i>Propionibacterium freudenreichii</i> ssp. <i>shermanii</i> JS in cheese ripening. <i>International Journal of Food Microbiology</i> , 2017, 241, 39-48.	4.7	19
60	Skin Microbiome in Small- and Large-plaque Parapsoriasis. <i>Acta Dermato-Venereologica</i> , 2017, 97, 685-691.	1.3	9
61	Bile microbiota in primary sclerosing cholangitis: Impact on disease progression and development of biliary dysplasia. <i>PLoS ONE</i> , 2017, 12, e0182924.	2.5	71
62	Genome sequence of the model plant pathogen <i>Pectobacterium carotovorum</i> SCC1. <i>Standards in Genomic Sciences</i> , 2017, 12, 87.	1.5	16
63	De novo assembly of genomes from long sequence reads reveals uncharted territories of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2017, 18, 790.	2.8	16
64	<i>Lactobacillus oligofermentans</i> glucose, ribose and xylose transcriptomes show higher similarity between glucose and xylose catabolism-induced responses in the early exponential growth phase. <i>BMC Genomics</i> , 2016, 17, 539.	2.8	27
65	Skin microbiome in melanomas and melanocytic nevi. <i>European Journal of Dermatology</i> , 2016, 26, 49-55.	0.6	26
66	Time-scale dynamics of proteome and transcriptome of the white-rot fungus <i>Phlebia radiata</i> : growth on spruce wood and decay effect on lignocellulose. <i>Biotechnology for Biofuels</i> , 2016, 9, 192.	6.2	95
67	Developmental Changes in Scots Pine Transcriptome during Heartwood Formation. <i>Plant Physiology</i> , 2016, 172, 1403-1417.	4.8	46
68	Brief commentary for brain, behavior, and immunity. <i>Brain, Behavior, and Immunity</i> , 2016, 57, 8-9.	4.1	1
69	Single-Molecule Sequencing Revealing the Presence of Distinct JC Polyomavirus Populations in Patients With Progressive Multifocal Leukoencephalopathy. <i>Journal of Infectious Diseases</i> , 2016, 215, jiw399.	4.0	13
70	Cytokinin and Auxin Display Distinct but Interconnected Distribution and Signaling Profiles to Stimulate Cambial Activity. <i>Current Biology</i> , 2016, 26, 1990-1997.	3.9	170
71	Genome-scale study reveals reduced metabolic adaptability in patients with non-alcoholic fatty liver disease. <i>Nature Communications</i> , 2016, 7, 8994.	12.8	103
72	HMGB4 is expressed by neuronal cells and affects the expression of genes involved in neural differentiation. <i>Scientific Reports</i> , 2016, 6, 32960.	3.3	14

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73	NOGO-A/RTN4A and NOGO-B/RTN4B are simultaneously expressed in epithelial, fibroblast and neuronal cells and maintain ER morphology. <i>Scientific Reports</i> , 2016, 6, 35969.	3.3	28
74	Complete genome sequence of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1, isolated from vacuum-packaged vegetable sausages. <i>Standards in Genomic Sciences</i> , 2016, 11, 40.	1.5	28
75	Divergent genes in potential inoculant <i>Sinorhizobium</i> strains are related to DNA replication, recombination, and repair. <i>Journal of Basic Microbiology</i> , 2016, 56, 680-685.	3.3	2
76	Linking Smoking, Coffee, Urate, and Parkinson's Disease – A Role for Gut Microbiota?. <i>Journal of Parkinson's Disease</i> , 2015, 5, 255-262.	2.8	59
77	The microbiome of the human lower airways: a next generation sequencing perspective. <i>World Allergy Organization Journal</i> , 2015, 8, 23.	3.5	36
78	Expression of BKV and JCV encoded microRNA in human cerebrospinal fluid, plasma and urine. <i>Journal of Clinical Virology</i> , 2015, 65, 1-5.	3.1	27
79	Increased transcriptome sequencing efficiency with modified Mint-2 digestion–ligation protocol. <i>Analytical Biochemistry</i> , 2015, 477, 38-40.	2.4	2
80	Multilocus Sequence Typing of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> , a Psychrotrophic Lactic Acid Bacterium Causing Spoilage of Packaged Perishable Foods. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2474-2480.	3.1	13
81	Green areas around homes reduce atopic sensitization in children. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 195-202.	5.7	208
82	Genome Sequence and Transcriptome Analysis of Meat-Spoilage-Associated Lactic Acid Bacterium <i>Lactococcus piscium</i> MKFS47. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3800-3811.	3.1	32
83	Hunt for the origin of allergy – comparing the Finnish and Russian Karelia. <i>Clinical and Experimental Allergy</i> , 2015, 45, 891-901.	2.9	131
84	Seasonal patterns of bacterial communities in the coastal brackish sediments of the Gulf of Finland, Baltic Sea. <i>Estuarine, Coastal and Shelf Science</i> , 2015, 165, 86-96.	2.1	22
85	Flight-induced changes in gene expression in the <i>Glanville</i> fritillary butterfly. <i>Molecular Ecology</i> , 2015, 24, 4886-4900.	3.9	28
86	Differential Isoform Expression and Selective Muscle Involvement in Muscular Dystrophies. <i>American Journal of Pathology</i> , 2015, 185, 2833-2842.	3.8	12
87	Complete genome sequence of <i>Propionibacterium freudenreichii</i> DSM 20271T. <i>Standards in Genomic Sciences</i> , 2015, 10, 83.	1.5	23
88	Inconsistent Denoising and Clustering Algorithms for Amplicon Sequence Data. <i>Journal of Computational Biology</i> , 2015, 22, 743-751.	1.6	15
89	Gut microbiota are related to Parkinson's disease and clinical phenotype. <i>Movement Disorders</i> , 2015, 30, 350-358.	3.9	1,457
90	Comparative Genomics and Characterization of Hybrid Shigatoxigenic and Enterotoxigenic <i>Escherichia coli</i> (STEC/ETEC) Strains. <i>PLoS ONE</i> , 2015, 10, e0135936.	2.5	50

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91	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. PLoS ONE, 2014, 9, e101467.	2.5	24
92	Evaluation of Molecular Techniques in Characterization of Deep Terrestrial Biosphere. Open Journal of Ecology, 2014, 04, 468-487.	1.0	13
93	Taxonomically and functionally diverse microbial communities in deep crystalline rocks of the Fennoscandian shield. ISME Journal, 2014, 8, 126-138.	9.8	107
94	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	12.8	196
95	Transcriptome dynamics-based operon prediction in prokaryotes. BMC Bioinformatics, 2014, 15, 145.	2.6	24
96	Acinetobacter species in the skin microbiota protect against allergic sensitization and inflammation. Journal of Allergy and Clinical Immunology, 2014, 134, 1301-1309.e11.	2.9	163
97	Comparative genomics of <i>Lactobacillus crispatus</i> suggests novel mechanisms for the competitive exclusion of <i>Gardnerella vaginalis</i> . BMC Genomics, 2014, 15, 1070.	2.8	101
98	Comparative proteome profiling of bovine and human <i>Staphylococcus epidermidis</i> strains for screening specifically expressed virulence and adaptation proteins. Proteomics, 2014, 14, 1890-1894.	2.2	7
99	<i>Arabidopsis</i> NAC45/86 direct sieve element morphogenesis culminating in enucleation. Science, 2014, 345, 933-937.	12.6	173
100	Genomics and Proteomics Provide New Insight into the Commensal and Pathogenic Lifestyles of Bovine- and Human-Associated <i>Staphylococcus epidermidis</i> Strains. Journal of Proteome Research, 2014, 13, 3748-3762.	3.7	16
101	High sequence diversity and structural conservation in the human <i>T</i> cell receptor β^2 junctional region during thymic development. European Journal of Immunology, 2013, 43, 2185-2193.	2.9	6
102	Lep-MAP: fast and accurate linkage map construction for large SNP datasets. Bioinformatics, 2013, 29, 3128-3134.	4.1	114
103	Combining high-throughput sequencing with fruit body surveys reveals contrasting life-history strategies in fungi. ISME Journal, 2013, 7, 1696-1709.	9.8	144
104	Mondo/ChREBP-Mlx-Regulated Transcriptional Network Is Essential for Dietary Sugar Tolerance in <i>Drosophila</i> . PLoS Genetics, 2013, 9, e1003438.	3.5	93
105	Significance of Heme-Based Respiration in Meat Spoilage Caused by <i>Leuconostoc gasicomitatum</i> . Applied and Environmental Microbiology, 2013, 79, 1078-1085.	3.1	59
106	Genome Sequence of <i>Dickeya solani</i> , a New soft Rot Pathogen of Potato, Suggests its Emergence May Be Related to a Novel Combination of Non-Ribosomal Peptide/Polyketide Synthetase Clusters. Diversity, 2013, 5, 824-842.	1.7	54
107	Identification and Validation of Human Papillomavirus Encoded microRNAs. PLoS ONE, 2013, 8, e70202.	2.5	61
108	Gene Expression Profiles in Human and Mouse Primary Cells Provide New Insights into the Differential Actions of Vitamin D3 Metabolites. PLoS ONE, 2013, 8, e75338.	2.5	16

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109	Gene Expression Patterns Underlying the Reinstatement of Plasticity in the Adult Visual System. <i>Neural Plasticity</i> , 2013, 2013, 1-8.	2.2	17
110	Lack of RsmA-Mediated Control Results in Constant Hypervirulence, Cell Elongation, and Hyperflagellation in <i>Pectobacterium wasabiae</i> . <i>PLoS ONE</i> , 2013, 8, e54248.	2.5	19
111	Role and Regulation of the Flp/Tad Pilus in the Virulence of <i>Pectobacterium atrosepticum</i> SCRI1043 and <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS ONE</i> , 2013, 8, e73718.	2.5	53
112	Genome Sequence of <i>Pectobacterium</i> sp. Strain SCC3193. <i>Journal of Bacteriology</i> , 2012, 194, 6004-6004.	2.2	17
113	Leptin-Induced mTOR Activation Defines a Specific Molecular and Transcriptional Signature Controlling CD4+ Effector T Cell Responses. <i>Journal of Immunology</i> , 2012, 189, 2941-2953.	0.8	121
114	Environmental biodiversity, human microbiota, and allergy are interrelated. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8334-8339.	7.1	856
115	Identification and Characterization of a Lipopolysaccharide \hat{A} ,2,3-Sialyltransferase from the Human Pathogen <i>Helicobacter bizzozeronii</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2540-2550.	2.2	15
116	Expression of multiple nebulin isoforms in human skeletal muscle and brain. <i>Muscle and Nerve</i> , 2012, 46, 730-737.	2.2	21
117	Gene expression analysis of <i>Drosophila</i> Manf mutants reveals perturbations in membrane traffic and major metabolic changes. <i>BMC Genomics</i> , 2012, 13, 134.	2.8	49
118	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. <i>BMC Microbiology</i> , 2012, 12, 121.	3.3	30
119	Cell culture model predicts human disease: Altered expression of junction proteins and matrix metalloproteinases in cervical dysplasia. <i>BMC Clinical Pathology</i> , 2012, 12, 9.	1.8	4
120	miRSeqNovel: An R based workflow for analyzing miRNA sequencing data. <i>Molecular and Cellular Probes</i> , 2012, 26, 208-211.	2.1	15
121	Detection of Human Papillomaviruses by Polymerase Chain Reaction and Ligation Reaction on Universal Microarray. <i>PLoS ONE</i> , 2012, 7, e34211.	2.5	12
122	Comparison of microbial communities in marinated and unmarinated broiler meat by metagenomics. <i>International Journal of Food Microbiology</i> , 2012, 157, 142-149.	4.7	101
123	Experience-dependent expression of <i>NPAS4</i> regulates plasticity in adult visual cortex. <i>Journal of Physiology</i> , 2012, 590, 4777-4787.	2.9	54
124	Re-analysis of Bipolar Disorder and Schizophrenia Gene Expression Complements the Kraepelinian Dichotomy. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 563-577.	1.6	4
125	SNP Design from 454 Sequencing of <i>Podosphaera plantaginis</i> Transcriptome Reveals a Genetically Diverse Pathogen Metapopulation with High Levels of Mixed-Genotype Infection. <i>PLoS ONE</i> , 2012, 7, e52492.	2.5	71
126	Vascular endothelial growth factor C acts as a neurotrophic factor for dopamine neurons in vitro and in vivo. <i>Neuroscience</i> , 2011, 192, 550-563.	2.3	32

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127	Spatially differing bacterial communities in water columns of the northern Baltic Sea. FEMS Microbiology Ecology, 2011, 75, 99-110.	2.7	41
128	Growth phase-associated changes in the proteome and transcriptome of <i>Lactobacillus rhamnosus</i> GG in industrial-type whey medium. Microbial Biotechnology, 2011, 4, 746-766.	4.2	77
129	Characterization of psychrotrophic bacterial communities in modified atmosphere-packed meat with terminal restriction fragment length polymorphism. International Journal of Food Microbiology, 2011, 144, 360-366.	4.7	73
130	Molecular profiling of fungal communities in moisture damaged buildings before and after remediation - a comparison of culture-dependent and culture-independent methods. BMC Microbiology, 2011, 11, 235.	3.3	80
131	Comparative study of transcriptional and physiological responses to salinity stress in two contrasting <i>Populus alba</i> L. genotypes. Tree Physiology, 2011, 31, 1335-1355.	3.1	44
132	Genome Sequence of a Food Spoilage Lactic Acid Bacterium, <i>Leuconostoc gasicomitatum</i> LMG 18811, in Association with Specific Spoilage Reactions. Applied and Environmental Microbiology, 2011, 77, 4344-4351.	3.1	56
133	Proteomics and Transcriptomics Characterization of Bile Stress Response in Probiotic <i>Lactobacillus rhamnosus</i> GG. Molecular and Cellular Proteomics, 2011, 10, S1-S18.	3.8	167
134	Human Papillomavirus 16 E5 Modulates the Expression of Host MicroRNAs. PLoS ONE, 2011, 6, e21646.	2.5	82
135	Comparison of Dorsocervical With Abdominal Subcutaneous Adipose Tissue in Patients With and Without Antiretroviral Therapy-associated Lipodystrophy. Diabetes, 2011, 60, 1894-1900.	0.6	16
136	Bayesian integrated modeling of expression data: a case study on RhoG. BMC Bioinformatics, 2010, 11, 295.	2.6	2
137	Bacterial diversity at different stages of the composting process. BMC Microbiology, 2010, 10, 94.	3.3	337
138	Microarray-based comparison of genetic differences between strains of <i>Streptomyces turgidiscabies</i> with focus on the pathogenicity island. Molecular Plant Pathology, 2010, 11, 733-746.	4.2	10
139	Differential gene expression in senescing leaves of two silver birch genotypes in response to elevated CO ₂ and tropospheric ozone. Plant, Cell and Environment, 2010, 33, 1016-1028.	5.7	37
140	Determination of fungal succession during municipal solid waste composting using a cloning-based analysis. Journal of Applied Microbiology, 2010, 108, 472-487.	3.1	62
141	Gene Expression Profiling of U12-Type Spliceosome Mutant <i>Drosophila</i> Reveals Widespread Changes in Metabolic Pathways. PLoS ONE, 2010, 5, e13215.	2.5	26
142	Genome Sequence of <i>Lactobacillus crispatus</i> ST1. Journal of Bacteriology, 2010, 192, 3547-3548.	2.2	38
143	Identifying wood-inhabiting fungi with 454 sequencing - what is the probability that BLAST gives the correct species?. Fungal Ecology, 2010, 3, 274-283.	1.6	97
144	An Association Analysis of Circadian Genes in Anxiety Disorders. Biological Psychiatry, 2010, 67, 1163-1170.	1.3	82

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145	Gene expression analysis in SV-40 immortalized human corneal epithelial cells cultured with an air-liquid interface. <i>Molecular Vision</i> , 2010, 16, 2109-20.	1.1	24
146	Comparison of Gene Expression Profile in Embryonic Mesencephalon and Neuronal Primary Cultures. <i>PLoS ONE</i> , 2009, 4, e4977.	2.5	12
147	Comparative Genomic Hybridization Analysis of Two Predominant Nordic Group I (Proteolytic) <i>Clostridium botulinum</i> Type B Clusters. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2643-2651.	3.1	29
148	A Naive Bayes Classifier for Protein Function Prediction. <i>In Silico Biology</i> , 2009, 9, 23-34.	0.9	8
149	Identification of flowering genes in strawberry, a perennial SD plant. <i>BMC Plant Biology</i> , 2009, 9, 122.	3.6	65
150	Application of hybridization control probe to increase accuracy on ligation detection or minisequencing diagnostic microarrays. <i>BMC Research Notes</i> , 2009, 2, 249.	1.4	7
151	Comparative genomic analysis of <i>Lactobacillus rhamnosus</i> GG reveals pili containing a human-mucus binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17193-17198.	7.1	654
152	Microarray profiling of host-extract-induced genes and characterization of the type VI secretion cluster in the potato pathogen <i>Pectobacterium atrosepticum</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 2387-2396.	1.8	53
153	Genes involved in cell adhesion, cell motility and mitogenic signaling are altered due to HPV 16 E5 protein expression. <i>Oncogene</i> , 2008, 27, 2532-2541.	5.9	60
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