Petri Auvinen

List of Publications by Year in descending order

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195 papers 13,795 citations

59 h-index 24982 109 g-index

217 all docs

217 docs citations

217 times ranked 20183 citing authors

#	Article	IF	CITATIONS
1	Gut microbiota are related to Parkinson's disease and clinical phenotype. Movement Disorders, 2015, 30, 350-358.	3.9	1,457
2	Environmental biodiversity, human microbiota, and allergy are interrelated. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8334-8339.	7.1	856
3	Comparative genomic analysis of <i>Lactobacillus rhamnosus</i> GG reveals pili containing a humanmucus binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17193-17198.	7.1	654
4	Gene expression in human NAFLD. American Journal of Physiology - Renal Physiology, 2008, 294, G1281-G1287.	3.4	356
5	Bacterial diversity at different stages of the composting process. BMC Microbiology, 2010, 10, 94.	3.3	337
6	A distinct picornavirus group identified by sequence analysis Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 8847-8851.	7.1	276
7	Gut microbiota in Parkinson's disease: Temporal stability and relations to disease progression. EBioMedicine, 2019, 44, 691-707.	6.1	236
8	Rab8 promotes polarized membrane transport through reorganization of actin and microtubules in fibroblasts Journal of Cell Biology, 1996, 135, 153-167.	5.2	228
9	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. Nature Genetics, 2017, 49, 904-912.	21.4	221
10	Endosome dynamics regulated by a Rho protein. Nature, 1996, 384, 427-432.	27.8	209
10		27.8	209
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11	Endosome dynamics regulated by a Rho protein. Nature, 1996, 384, 427-432. Biogenesis of the Semliki Forest Virus RNA Replication Complex. Journal of Virology, 2001, 75, 3873-3884. Gene expression and metabolite profiling of Populus euphratica growing in the Negev desert. Genome	3.4	209
11 12	Endosome dynamics regulated by a Rho protein. Nature, 1996, 384, 427-432. Biogenesis of the Semliki Forest Virus RNA Replication Complex. Journal of Virology, 2001, 75, 3873-3884. Gene expression and metabolite profiling of Populus euphratica growing in the Negev desert. Genome Biology, 2005, 6, R101. Green areas around homes reduce atopic sensitization in children. Allergy: European Journal of	3.4 9.6	209
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19	<i>Arabidopsis</i> NAC45/86 direct sieve element morphogenesis culminating in enucleation. Science, 2014, 345, 933-937.	12.6	173
20	Cytokinin and Auxin Display Distinct but Interconnected Distribution and Signaling Profiles to Stimulate Cambial Activity. Current Biology, 2016, 26, 1990-1997.	3.9	170
21	Identification of a Novel Function of the AlphavirusCapping Apparatus. Journal of Biological Chemistry, 2000, 275, 17281-17287.	3.4	169
22	Proteomics and Transcriptomics Characterization of Bile Stress Response in Probiotic Lactobacillus rhamnosus GG. Molecular and Cellular Proteomics, 2011, 10, S1-S18.	3.8	167
23	Notum produced by Paneth cells attenuates regeneration of aged intestinal epithelium. Nature, 2019, 571, 398-402.	27.8	166
24	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
25	Oral and nasal microbiota in Parkinson's disease. Parkinsonism and Related Disorders, 2017, 38, 61-67.	2.2	159
26	Semliki Forest virus mRNA capping enzyme requires association with anionic membrane phospholipids for activity. EMBO Journal, 1999, 18, 3164-3172.	7.8	152
27	Virus-Specific mRNA Capping Enzyme Encoded by Hepatitis E Virus. Journal of Virology, 2001, 75, 6249-6255.	3.4	146
28	Combining high-throughput sequencing with fruit body surveys reveals contrasting life-history strategies in fungi. ISME Journal, 2013, 7, 1696-1709.	9.8	144
29	Hunt for the origin of allergy – comparing the Finnish and Russian Karelia. Clinical and Experimental Allergy, 2015, 45, 891-901.	2.9	131
30	Leptin-Induced mTOR Activation Defines a Specific Molecular and Transcriptional Signature Controlling CD4+ Effector T Cell Responses. Journal of Immunology, 2012, 189, 2941-2953.	0.8	121
31	Lep-MAP: fast and accurate linkage map construction for large SNP datasets. Bioinformatics, 2013, 29, 3128-3134.	4.1	114
32	More than constipation – bowel symptoms in Parkinson's disease and their connection to gut microbiota. European Journal of Neurology, 2017, 24, 1375-1383.	3.3	112
33	Taxonomically and functionally diverse microbial communities in deep crystalline rocks of the Fennoscandian shield. ISME Journal, 2014, 8, 126-138.	9.8	107
34	Genome-scale study reveals reduced metabolic adaptability in patients with non-alcoholic fatty liver disease. Nature Communications, 2016, 7, 8994.	12.8	103
35	Comparison of microbial communities in marinated and unmarinated broiler meat by metagenomics. International Journal of Food Microbiology, 2012, 157, 142-149.	4.7	101
36	Comparative genomics of Lactobacillus crispatus suggests novel mechanisms for the competitive exclusion of Gardnerella vaginalis. BMC Genomics, 2014, 15, 1070.	2.8	101

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37	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
38	Significant disparities in allergy prevalence and microbiota between the young people in Finnish and Russian Karelia. Clinical and Experimental Allergy, 2017, 47, 665-674.	2.9	97
39	Time-scale dynamics of proteome and transcriptome of the white-rot fungus Phlebia radiata: growth on spruce wood and decay effect on lignocellulose. Biotechnology for Biofuels, 2016, 9, 192.	6.2	95
40	The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. Plant Cell, 2018, 30, 2813-2837.	6.6	95
41	Mondo/ChREBP-Mlx-Regulated Transcriptional Network Is Essential for Dietary Sugar Tolerance in Drosophila. PLoS Genetics, 2013, 9, e1003438.	3.5	93
42	Membrane Binding Mechanism of an RNA Virus-capping Enzyme. Journal of Biological Chemistry, 2000, 275, 37853-37859.	3.4	82
43	An Association Analysis of Circadian Genes in Anxiety Disorders. Biological Psychiatry, 2010, 67, 1163-1170.	1.3	82
44	Human Papillomavirus 16 E5 Modulates the Expression of Host MicroRNAs. PLoS ONE, 2011, 6, e21646.	2.5	82
45	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
46	Effects of Palmitoylation of Replicase Protein nsP1 on Alphavirus Infection. Journal of Virology, 2000, 74, 6725-6733.	3.4	79
47	Growth phaseâ€associated changes in the proteome and transcriptome of <i>Lactobacillus rhamnosus</i> GG in industrialâ€type whey medium. Microbial Biotechnology, 2011, 4, 746-766.	4.2	77
48	Mouse A6/Twinfilin Is an Actin Monomer-Binding Protein That Localizes to the Regions of Rapid Actin Dynamics. Molecular and Cellular Biology, 2000, 20, 1772-1783.	2.3	76
49	Analysis of the floral transcriptome uncovers new regulators of organ determination and gene families related to flower organ differentiation in Gerbera hybrida (Asteraceae). Genome Research, 2005, 15, 475-486.	5.5	75
50	Global Changes in Cellular Gene Expression during Bacteriophage PRD1 Infection. Journal of Virology, 2006, 80, 8081-8088.	3.4	74
51	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
52	Role of Broiler Carcasses and Processing Plant Air in Contamination of Modified-Atmosphere-Packaged Broiler Products with Psychrotrophic Lactic Acid Bacteria. Applied and Environmental Microbiology, 2007, 73, 1136-1145.	3.1	71
53	Bile microbiota in primary sclerosing cholangitis: Impact on disease progression and development of biliary dysplasia. PLoS ONE, 2017, 12, e0182924.	2.5	71
54	SNP Design from 454 Sequencing of Podosphaera plantaginis Transcriptome Reveals a Genetically Diverse Pathogen Metapopulation with High Levels of Mixed-Genotype Infection. PLoS ONE, 2012, 7, e52492.	2.5	71

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55	Proteolytic processing of Semliki Forest virus-specific non-structural polyprotein by nsP2 protease. Journal of General Virology, 2001, 82, 765-773.	2.9	67
56	Identification of flowering genes in strawberry, a perennial SD plant. BMC Plant Biology, 2009, 9, 122.	3.6	65
57	The complexity of titin splicing pattern in human adult skeletal muscles. Skeletal Muscle, 2018, 8, 11.	4.2	65
58	Intracellular Distribution of Rubella Virus Nonstructural Protein P150. Journal of Virology, 1999, 73, 7805-7811.	3.4	64
59	Constitutive Ret Activity in Knock-In Multiple Endocrine Neoplasia Type B Mice Induces Profound Elevation of Brain Dopamine Concentration via Enhanced Synthesis and Increases the Number of TH-Positive Cells in the Substantia Nigra. Journal of Neuroscience, 2007, 27, 4799-4809.	3.6	63
60	Metagenomic and metatranscriptomic analysis of the microbial community in Swiss-type Maasdam cheese during ripening. International Journal of Food Microbiology, 2018, 281, 10-22.	4.7	63
61	Alphavirus Replicase Protein NSP1 Induces Filopodia and Rearrangement of Actin Filaments. Journal of Virology, 1998, 72, 10265-10269.	3.4	63
62	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
63	Identification and Validation of Human Papillomavirus Encoded microRNAs. PLoS ONE, 2013, 8, e70202.	2.5	61
64	Genes involved in cell adhesion, cell motility and mitogenic signaling are altered due to HPV 16 E5 protein expression. Oncogene, 2008, 27, 2532-2541.	5.9	60
65	Significance of Heme-Based Respiration in Meat Spoilage Caused by Leuconostoc gasicomitatum. Applied and Environmental Microbiology, 2013, 79, 1078-1085.	3.1	59
66	Linking Smoking, Coffee, Urate, and Parkinson's Disease – A Role for Gut Microbiota?. Journal of Parkinson's Disease, 2015, 5, 255-262.	2.8	59
67	Genome Sequence of a Food Spoilage Lactic Acid Bacterium, Leuconostoc gasicomitatum LMG 18811 ^T , in Association with Specific Spoilage Reactions. Applied and Environmental Microbiology, 2011, 77, 4344-4351.	3.1	56
68	Experienceâ€dependent expression of <i>NPAS4</i> regulates plasticity in adult visual cortex. Journal of Physiology, 2012, 590, 4777-4787.	2.9	54
69	Genome Sequence of Dickeya solani, 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
70	Microarray profiling of host-extract-induced genes and characterization of the type VI secretion cluster in the potato pathogen Pectobacterium atrosepticum. Microbiology (United Kingdom), 2008, 154, 2387-2396.	1.8	53
71	Alternative oxidaseâ€mediated respiration prevents lethal mitochondrial cardiomyopathy. EMBO Molecular Medicine, 2019, 11, .	6.9	53
72	Role and Regulation of the Flp/Tad Pilus in the Virulence of Pectobacterium atrosepticum SCRI1043 and Pectobacterium wasabiae SCC3193. PLoS ONE, 2013, 8, e73718.	2.5	53

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73	Gut microbiome in gestational diabetes: a crossâ€sectional study of mothers and offspring 5Âyears postpartum. Acta Obstetricia Et Gynecologica Scandinavica, 2018, 97, 38-46.	2.8	51
74	Food Spoilage-Associated Leuconostoc, Lactococcus, and Lactobacillus Species Display Different Survival Strategies in Response to Competition. Applied and Environmental Microbiology, 2018, 84, .	3.1	50
75	Comparative Genomics and Characterization of Hybrid Shigatoxigenic and Enterotoxigenic Escherichia coli (STEC/ETEC) Strains. PLoS ONE, 2015, 10, e0135936.	2.5	50
76	Virus-specific capping of tobacco mosaic virus RNA: methylation of GTP prior to formation of covalent complex p126-m7GMP. FEBS Letters, 1999, 455, 45-48.	2.8	49
77	Gene expression analysis of Drosophila Manf mutants reveals perturbations in membrane traffic and major metabolic changes. BMC Genomics, 2012, 13, 134.	2.8	49
78	Isotretinoin and lymecycline treatments modify the skin microbiota in acne. Experimental Dermatology, 2018, 27, 30-36.	2.9	48
79	Genetic Control of Myelin Plasticity after Chronic Psychosocial Stress. ENeuro, 2018, 5, ENEURO.0166-18.2018.	1.9	48
80	Developmental Changes in Scots Pine Transcriptome during Heartwood Formation. Plant Physiology, 2016, 172, 1403-1417.	4.8	46
81	Comparative study of transcriptional and physiological responses to salinity stress in two contrasting Populus alba L. genotypes. Tree Physiology, 2011, 31, 1335-1355.	3.1	44
82	Bacterial Butyrate in Parkinson's Disease Is Linked to Epigenetic Changes and Depressive Symptoms. Movement Disorders, 2022, 37, 1644-1653.	3.9	44
83	Microarray Analysis of a <i>Chlamydia pneumoniae</i> â€"Infected Human Epithelial Cell Line by Use of Gene Ontology Hierarchy. Journal of Infectious Diseases, 2008, 197, 156-162.	4.0	43
84	Multi-omics analysis identifies mitochondrial pathways associated with anxiety-related behavior. PLoS Genetics, 2019, 15, e1008358.	3.5	43
85	Spatially differing bacterial communities in water columns of the northern Baltic Sea. FEMS Microbiology Ecology, 2011, 75, 99-110.	2.7	41
86	Gut Microbiome Signatures of Risk and Prodromal Markers of Parkinson Disease. Annals of Neurology, 2021, 90, E1-E12.	5.3	41
87	Functional Characterization of Mouse Syndecan-1 Promoter. Journal of Biological Chemistry, 1996, 271, 12532-12541.	3.4	38
88	Genome Sequence of Lactobacillus crispatus ST1. Journal of Bacteriology, 2010, 192, 3547-3548.	2.2	38
89	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
90	The microbiome of the human lower airways: a next generation sequencing perspective. World Allergy Organization Journal, 2015, 8, 23.	3.5	36

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91	Network Analysis Reveals Similar Transcriptomic Responses to Intrinsic Properties of Carbon Nanomaterials <i>in Vitro</i> and <i>in Vivo</i> ACS Nano, 2017, 11, 3786-3796.	14.6	35
92	BARCOSEL: a tool for selecting an optimal barcode set for high-throughput sequencing. BMC Bioinformatics, 2018, 19, 257.	2.6	35
93	Pathogenetic differences between coxsackie A and B virus infections in newborn mice. Virus Research, 1993, 27, 71-78.	2.2	34
94	Genetic diversity of enterovirus subgroups. Archives of Virology, 1989, 104, 175-186.	2.1	32
95	Vascular endothelial growth factor C acts as a neurotrophic factor for dopamine neurons in vitro and in vivo. Neuroscience, 2011, 192, 550-563.	2.3	32
96	Genome Sequence and Transcriptome Analysis of Meat-Spoilage-Associated Lactic Acid Bacterium Lactococcus piscium MKFS47. Applied and Environmental Microbiology, 2015, 81, 3800-3811.	3.1	32
97	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. BMC Microbiology, 2012, 12, 121.	3.3	30
98	Universal ligation-detection-reaction microarray applied for compost microbes. BMC Microbiology, 2008, 8, 237.	3.3	29
99	Comparative Genomic Hybridization Analysis of Two Predominant Nordic Group I (Proteolytic) <i>Clostridium botulinum</i> Type B Clusters. Applied and Environmental Microbiology, 2009, 75, 2643-2651.	3.1	29
100	Nucleic acid sequence relationships between enterovirus serotypes. Molecular and Cellular Probes, 1987, 1, 169-176.	2.1	28
101	Flightâ€induced changes in gene expression in the Glanville fritillary butterfly. Molecular Ecology, 2015, 24, 4886-4900.	3.9	28
102	NOGO-A/RTN4A and NOGO-B/RTN4B are simultaneously expressed in epithelial, fibroblast and neuronal cells and maintain ER morphology. Scientific Reports, 2016, 6, 35969.	3.3	28
103	Complete genome sequence of Leuconostoc gelidum subsp. gasicomitatum KG16-1, isolated from vacuum-packaged vegetable sausages. Standards in Genomic Sciences, 2016, 11, 40.	1.5	28
104	Expression of BKV and JCV encoded microRNA in human cerebrospinal fluid, plasma and urine. Journal of Clinical Virology, 2015, 65, 1-5.	3.1	27
105	Lactobacillus oligofermentans glucose, ribose and xylose transcriptomes show higher similarity between glucose and xylose catabolism-induced responses in the early exponential growth phase. BMC Genomics, 2016, 17, 539.	2.8	27
106	Gene Expression Profiling of U12-Type Spliceosome Mutant Drosophila Reveals Widespread Changes in Metabolic Pathways. PLoS ONE, 2010, 5, e13215.	2.5	26
107	Skin microbiome in melanomas and melanocytic nevi. European Journal of Dermatology, 2016, 26, 49-55.	0.6	26
108	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. PLoS ONE, 2014, 9, e101467.	2.5	24

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109	Transcriptome dynamics-based operon prediction in prokaryotes. BMC Bioinformatics, 2014, 15, 145.	2.6	24
110	Bracketing phenogenotypic limits of mammalian hybridization. Royal Society Open Science, 2018, 5, 180903.	2.4	24
111	Subgingival microbiota in a population with and without cognitive dysfunction. Journal of Oral Microbiology, 2021, 13, 1854552.	2.7	24
112	Gene expression analysis in SV-40 immortalized human corneal epithelial cells cultured with an air-liquid interface. Molecular Vision, 2010, 16, 2109-20.	1.1	24
113	Physiology, Pathology and Relatedness of Human Tissues from Gene Expression Meta-Analysis. PLoS ONE, 2008, 3, e1880.	2.5	23
114	Complete genome sequence of Propionibacterium freudenreichii DSM 20271T. Standards in Genomic Sciences, 2015, 10, 83.	1.5	23
115	Dual-light photodynamic therapy administered daily provides a sustained antibacterial effect on biofilm and prevents Streptococcus mutans adaptation. PLoS ONE, 2020, 15, e0232775.	2.5	23
116	Seasonal patterns of bacterial communities in the coastal brackish sediments of the Gulf of Finland, Baltic Sea. Estuarine, Coastal and Shelf Science, 2015, 165, 86-96.	2.1	22
117	Skin Microbiome in Cutaneous T-Cell Lymphoma byÂ16S and Whole-Genome Shotgun Sequencing. Journal of Investigative Dermatology, 2020, 140, 2304-2308.e7.	0.7	22
118	Expression of multiple nebulin isoforms in human skeletal muscle and brain. Muscle and Nerve, 2012, 46, 730-737.	2.2	21
119	Loss of cutaneous microbial diversity during first 3Âweeks of life in very low birthweight infants. Experimental Dermatology, 2017, 26, 861-867.	2.9	21
120	Gut microbiota composition is associated with narcolepsy type 1. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7 , .	6.0	20
121	Functional genomics provides insights into the role of Propionibacterium freudenreichii ssp. shermanii JS in cheese ripening. International Journal of Food Microbiology, 2017, 241, 39-48.	4.7	19
122	Immuneâ€microbiota interaction in Finnish and Russian Karelia young people with high and low allergy prevalence. Clinical and Experimental Allergy, 2020, 50, 1148-1158.	2.9	19
123	Lack of RsmA-Mediated Control Results in Constant Hypervirulence, Cell Elongation, and Hyperflagellation in Pectobacterium wasabiae. PLoS ONE, 2013, 8, e54248.	2.5	19
124	High-pressure processing-induced transcriptome response during recovery of Listeria monocytogenes. BMC Genomics, 2021, 22, 117.	2.8	18
125	SARSâ€CoVâ€2 variant with mutations in N gene affecting detection by widely used PCR primers. Journal of Medical Virology, 2022, 94, 1227-1231.	5.0	18
126	Genome Sequence of Pectobacterium sp. Strain SCC3193. Journal of Bacteriology, 2012, 194, 6004-6004.	2.2	17

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127	Gene Expression Patterns Underlying the Reinstatement of Plasticity in the Adult Visual System. Neural Plasticity, 2013, 2013, 1-8.	2.2	17
128	Gut bacterial tyrosine decarboxylase associates with clinical variables in a longitudinal cohort study of Parkinsons disease. Npj Parkinson's Disease, 2021, 7, 115.	5 . 3	17
129	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
130	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
131	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
132	Genome sequence of the model plant pathogen Pectobacterium carotovorum SCC1. Standards in Genomic Sciences, 2017, 12, 87.	1.5	16
133	De novo assembly of genomes from long sequence reads reveals uncharted territories of Propionibacterium freudenreichii. BMC Genomics, 2017, 18, 790.	2.8	16
134	BK polyomavirus microRNA expression and sequence variation in polyomavirus-associated nephropathy. Journal of Clinical Virology, 2018, 102, 70-76.	3.1	16
135	Genome description of Phlebia radiata 79 with comparative genomics analysis on lignocellulose decomposition machinery of phlebioid fungi. BMC Genomics, 2019, 20, 430.	2.8	16
136	Transcriptomic time-series analysis of cold- and heat-shock response in psychrotrophic lactic acid bacteria. BMC Genomics, 2021, 22, 28.	2.8	16
137	Typing of herpes simplex virus isolates with monoclonal antibodies and by nucleic acid spot hybridization. Journal of Virological Methods, 1985, 12, 169-177.	2.1	15
138	Identification and Characterization of a Lipopolysaccharide Â,2,3-Sialyltransferase from the Human Pathogen Helicobacter bizzozeronii. Journal of Bacteriology, 2012, 194, 2540-2550.	2.2	15
139	miRSeqNovel: An R based workflow for analyzing miRNA sequencing data. Molecular and Cellular Probes, 2012, 26, 208-211.	2.1	15
140	Inconsistent Denoising and Clustering Algorithms for Amplicon Sequence Data. Journal of Computational Biology, 2015, 22, 743-751.	1.6	15
141	Secretome profiling of <i>Propionibacterium freudenreichii</i> reveals highly variable responses even among the closely related strains. Microbial Biotechnology, 2018, 11, 510-526.	4.2	15
142	HMGB4 is expressed by neuronal cells and affects the expression of genes involved in neural differentiation. Scientific Reports, 2016, 6, 32960.	3.3	14
143	gapFinisher: A reliable gap filling pipeline for SSPACE-LongRead scaffolder output. PLoS ONE, 2019, 14, e0216885.	2.5	14
144	Genomic characterization of the most barotolerant Listeria monocytogenes RO15 strain compared to reference strains used to evaluate food high pressure processing. BMC Genomics, 2020, 21, 455.	2.8	14

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145	Mapping of antigenic sites of coxsackievirus B3 by synthetic peptides. Apmis, 1993, 101, 517-528.	2.0	13
146	Evaluation of Molecular Techniques in Characterization of Deep Terrestrial Biosphere. Open Journal of Ecology, 2014, 04, 468-487.	1.0	13
147	Multilocus Sequence Typing of Leuconostoc gelidum subsp. gasicomitatum, a Psychrotrophic Lactic Acid Bacterium Causing Spoilage of Packaged Perishable Foods. Applied and Environmental Microbiology, 2015, 81, 2474-2480.	3.1	13
148	Single-Molecule Sequencing Revealing the Presence of Distinct JC Polyomavirus Populations in Patients With Progressive Multifocal Leukoencephalopathy. Journal of Infectious Diseases, 2016, 215, jiw399.	4.0	13
149	Comparison of Gene Expression Profile in Embryonic Mesencephalon and Neuronal Primary Cultures. PLoS ONE, 2009, 4, e4977.	2.5	12
150	Detection of Human Papillomaviruses by Polymerase Chain Reaction and Ligation Reaction on Universal Microarray. PLoS ONE, 2012, 7, e34211.	2.5	12
151	Differential Isoform Expression and Selective Muscle Involvement in Muscular Dystrophies. American Journal of Pathology, 2015, 185, 2833-2842.	3.8	12
152	Multiomics implicate gut microbiota in altered lipid and energy metabolism in Parkinson's disease. Npj Parkinson's Disease, 2022, 8, 39.	5.3	12
153	Use of enzyme immunoassay and nucleic acid hybridization for detecting Sindbis virus in infected mosquitoes. Journal of Virological Methods, 1987, 17, 229-236.	2.1	11
154	Microarrayâ€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
155	Red-Brown Pigmentation of Acidipropionibacterium jensenii Is Tied to Haemolytic Activity and cyl-Like Gene Cluster. Microorganisms, 2019, 7, 512.	3.6	10
156	Microbial Communities of Cladonia Lichens and Their Biosynthetic Gene Clusters Potentially Encoding Natural Products. Microorganisms, 2021, 9, 1347.	3.6	10
157	Skin Microbiome in Small- and Large-plaque Parapsoriasis. Acta Dermato-Venereologica, 2017, 97, 685-691.	1.3	9
158	A transcriptomic view to wounding response in young Scots pine stems. Scientific Reports, 2021, 11 , 3778 .	3.3	9
159	Indocyanine Green-Assisted and LED-Light-Activated Antibacterial Photodynamic Therapy Reduces Dental Plaque. Dentistry Journal, 2021, 9, 52.	2.3	9
160	Acidipropionibacterium virtanenii sp. nov., isolated from malted barley. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3175-3183.	1.7	9
161	Microbiome of the Healthy External Auditory Canal. Otology and Neurotology, 2020, Publish Ahead of Print, e609-e614.	1.3	9
162	Bayesian Hierarchical Model for Correcting Signal Saturation in Microarrays Using Pixel Intensities. Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article20.	0.6	8

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