

# Kathleen Marchal

## List of Publications by Year in descending order

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205  
papers

17,488  
citations

47006

47  
h-index

17592

121  
g-index

218  
all docs

218  
docs citations

218  
times ranked

24774  
citing authors

#	ARTICLE	IF	CITATIONS
1	PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. <i>Nucleic Acids Research</i> , 2002, 30, 325-327.	14.5	4,875
2	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
3	The evolutionary significance of polyploidy. <i>Nature Reviews Genetics</i> , 2017, 18, 411-424.	16.3	1,288
4	Evaluation of time profile reconstruction from complex two-color microarray designs. <i>BMC Bioinformatics</i> , 2008, 9, 1.	2.6	875
5	Advantages and limitations of current network inference methods. <i>Nature Reviews Microbiology</i> , 2010, 8, 717-729.	28.6	452
6	A higher-order background model improves the detection of promoter regulatory elements by Gibbs sampling. <i>Bioinformatics</i> , 2001, 17, 1113-1122.	4.1	344
7	A network-based approach to identify substrate classes of bacterial glycosyltransferases. <i>BMC Genomics</i> , 2014, 15, 349.	2.8	337
8	A Gibbs Sampling Method to Detect Overrepresented Motifs in the Upstream Regions of Coexpressed Genes. <i>Journal of Computational Biology</i> , 2002, 9, 447-464.	1.6	301
9	O <sub>2</sub> and Membrane Depolarization Are Part of a Microbial Bet-Hedging Strategy that Leads to Antibiotic Tolerance. <i>Molecular Cell</i> , 2015, 59, 9-21.	9.7	261
10	Strong antimicrobial activity of <i>Lactobacillus rhamnosus</i> GG against <i>Salmonella typhimurium</i> is due to accumulation of lactic acid. <i>FEMS Microbiology Letters</i> , 2006, 259, 89-96.	1.8	257
11	SynTRen: a generator of synthetic gene expression data for design and analysis of structure learning algorithms. <i>BMC Bioinformatics</i> , 2006, 7, 43.	2.6	233
12	Vitamin D3 Induces Tolerance in Human Dendritic Cells by Activation of Intracellular Metabolic Pathways. <i>Cell Reports</i> , 2015, 10, 711-725.	6.4	228
13	Brominated Furanones Inhibit Biofilm Formation by <i>Salmonella enterica</i> Serovar Typhimurium. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6639-6648.	3.1	184
14	Using Ribosomal Protein Genes as Reference: A Tale of Caution. <i>PLoS ONE</i> , 2008, 3, e1854.	2.5	180
15	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. <i>PLoS Genetics</i> , 2015, 11, e1005635.	3.5	173
16	Phenotypical and molecular responses of <i>Arabidopsis thaliana</i> roots as a result of inoculation with the auxin-producing bacterium <i>Zostera brasiliense</i> . <i>New Phytologist</i> , 2014, 201, 850-861.	7.3	172
17	Adaptive quality-based clustering of gene expression profiles. <i>Bioinformatics</i> , 2002, 18, 735-746.	4.1	170
18	PKA and Sch9 control a molecular switch important for the proper adaptation to nutrient availability. <i>Molecular Microbiology</i> , 2005, 55, 862-880.	2.5	170

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19	Computational Approaches to Identify Promoters and cis-Regulatory Elements in Plant Genomes. <i>Plant Physiology</i> , 2003, 132, 1162-1176.	4.8	158
20	Functional Analysis of luxS in the Probiotic Strain <i>Lactobacillus rhamnosus</i> GG Reveals a Central Metabolic Role Important for Growth and Biofilm Formation. <i>Journal of Bacteriology</i> , 2007, 189, 860-871.	2.2	142
21	The E2F-Regulated Gene <i>Chk1</i> Is Highly Expressed in Triple-Negative Estrogen Receptor <sup>+</sup> /Progesterone Receptor <sup>+</sup> /HER-2 <sup>+</sup> Breast Carcinomas. <i>Cancer Research</i> , 2007, 67, 6574-6581.	0.9	134
22	The Effect of a Sertoli Cell-Selective Knockout of the Androgen Receptor on Testicular Gene Expression in Prepubertal Mice. <i>Molecular Endocrinology</i> , 2006, 20, 321-334.	3.7	130
23	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. <i>BMC Systems Biology</i> , 2011, 5, 8.	3.0	128
24	Chemical Synthesis of (S)-4,5-Dihydroxy-2,3-pentanedione, a Bacterial Signal Molecule Precursor, and Validation of Its Activity in <i>Salmonella typhimurium</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 19563-19568.	3.4	127
25	Peptide signal molecules and bacteriocins in Gram-negative bacteria: a genome-wide in silico screening for peptides containing a double-glycine leader sequence and their cognate transporters. <i>Peptides</i> , 2004, 25, 1425-1440.	2.4	108
26	Comparison of the PhoPQ Regulon in <i>Escherichia coli</i> and <i>Salmonella typhimurium</i> . <i>Journal of Molecular Evolution</i> , 2005, 60, 462-474.	1.8	106
27	Inferring transcriptional modules from ChIP-chip, motif and microarray data. <i>Genome Biology</i> , 2006, 7, R37.	9.6	89
28	Module networks revisited: computational assessment and prioritization of model predictions. <i>Bioinformatics</i> , 2009, 25, 490-496.	4.1	82
29	Transcriptome Analysis of the Rhizosphere Bacterium <i>Azospirillum brasilense</i> Reveals an Extensive Auxin Response. <i>Microbial Ecology</i> , 2011, 61, 723-728.	2.8	81
30	INCLUSive: INtegrated Clustering, Upstream sequence retrieval and motif Sampling. <i>Bioinformatics</i> , 2002, 18, 331-332.	4.1	78
31	Differential regulation of the insulin-like growth factor II mRNA-binding protein genes by architectural transcription factor HMGA2. <i>FEBS Letters</i> , 2004, 569, 277-283.	2.8	78
32	Distinct Expression and Methylation Patterns for Genes with Different Fates following a Single Whole-Genome Duplication in Flowering Plants. <i>Molecular Biology and Evolution</i> , 2020, 37, 2394-2413.	8.9	75
33	Stress response regulators identified through genome-wide transcriptome analysis of the (p)ppGpp-dependent response in <i>Rhizobium etli</i> . <i>Genome Biology</i> , 2011, 12, R17.	9.6	74
34	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	12.8	73
35	Identification of a complex genetic network underlying <i>Saccharomyces cerevisiae</i> colony morphology. <i>Molecular Microbiology</i> , 2012, 86, 225-239.	2.5	71
36	Photoreceptor-Mediated Bending towards UV-B in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2014, 7, 1041-1052.	8.3	68

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37	The Effects of 1 $\alpha$ ,25-Dihydroxyvitamin D3 on the Expression of DNA Replication Genes. <i>Journal of Bone and Mineral Research</i> , 2004, 19, 133-146.	2.8	66
38	Assessing Genetic Diversity among <i>Brettanomyces</i> Yeasts by DNA Fingerprinting and Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4398-4413.	3.1	66
39	Delineation of the <i>Salmonella enterica</i> Serovar Typhimurium HilA Regulon through Genome-Wide Location and Transcript Analysis. <i>Journal of Bacteriology</i> , 2007, 189, 4587-4596.	2.2	65
40	Prediction and overview of the RpoN-regulon in closely related species of the Rhizobiales. <i>Genome Biology</i> , 2002, 3, research0076.1.	9.6	62
41	The "oxygen paradox" of dinitrogen-fixing bacteria. <i>Biology and Fertility of Soils</i> , 2000, 30, 363-373.	4.3	61
42	Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified <i>Bacillus</i> . <i>Scientific Reports</i> , 2020, 10, 4310.	3.3	57
43	Comparative analysis of module-based versus direct methods for reverse-engineering transcriptional regulatory networks. <i>BMC Systems Biology</i> , 2009, 3, 49.	3.0	55
44	Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1195-1200.	7.1	55
45	In silico identification and experimental validation of PmrAB targets in <i>Salmonella typhimurium</i> by regulatory motif detection. <i>Genome Biology</i> , 2004, 5, R9.	9.6	53
46	DISTILLER: a data integration framework to reveal condition dependency of complex regulons in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2009, 10, R27.	9.6	52
47	Microarray Analysis and Motif Detection Reveal New Targets of the <i>Salmonella enterica</i> Serovar Typhimurium HilA Regulatory Protein, Including hilA Itself. <i>Journal of Bacteriology</i> , 2005, 187, 4381-4391.	2.2	50
48	Improved linkage analysis of Quantitative Trait Loci using bulk segregants unveils a novel determinant of high ethanol tolerance in yeast. <i>BMC Genomics</i> , 2014, 15, 207.	2.8	50
49	Integration of omics data: how well does it work for bacteria?. <i>Molecular Microbiology</i> , 2006, 62, 1239-1250.	2.5	49
50	The small regulatory RNA molecule MicA is involved in <i>Salmonella enterica</i> serovar Typhimurium biofilm formation. <i>BMC Microbiology</i> , 2010, 10, 276.	3.3	48
51	Comparative phenomics and targeted use of genomics reveals variation in carbon and nitrogen assimilation among different <i>Brettanomyces bruxellensis</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9123-9134.	3.6	47
52	INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3468-3470.	14.5	46
53	Module Network Inference from a Cancer Gene Expression Data Set Identifies MicroRNA Regulated Modules. <i>PLoS ONE</i> , 2010, 5, e10162.	2.5	46
54	The Crabtree Effect Shapes the <i>Saccharomyces cerevisiae</i> Lag Phase during the Switch between Different Carbon Sources. <i>MBio</i> , 2018, 9, .	4.1	46

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55	Frequency-based haplotype reconstruction from deep sequencing data of bacterial populations. <i>Nucleic Acids Research</i> , 2015, 43, e105-e105.	14.5	45
56	Characterization of the Condensin Component Cnap1 and Protein Kinase Melk as Novel E2F Target Genes Down-regulated by 1,25-Dihydroxyvitamin D3. <i>Journal of Biological Chemistry</i> , 2005, 280, 37319-37330.	3.4	43
57	Genome-wide detection of predicted non-coding RNAs in <i>Rhizobium etli</i> expressed during free-living and host-associated growth using a high-resolution tiling array. <i>BMC Genomics</i> , 2010, 11, 53.	2.8	42
58	Use of structural DNA properties for the prediction of transcription-factor binding sites in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2011, 39, e6-e6.	14.5	42
59	Expression of the BRCA1-interacting protein Brip1/BACH1/FANCI is driven by E2F and correlates with human breast cancer malignancy. <i>Oncogene</i> , 2008, 27, 4233-4241.	5.9	41
60	MLVA as a Tool for Public Health Surveillance of Human <i>Salmonella</i> Typhimurium: Prospective Study in Belgium and Evaluation of MLVA Loci Stability. <i>PLoS ONE</i> , 2013, 8, e84055.	2.5	40
61	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia: Table 1.. <i>Nucleic Acids Research</i> , 2014, 42, D649-D653.	14.5	38
62	Functional bioinformatics of microarray data: from expression to regulation. <i>Proceedings of the IEEE</i> , 2002, 90, 1722-1743.	21.3	37
63	Screening genomes of Gram-positive bacteria for double-glycine-motif-containing peptides. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1121-1126.	1.8	37
64	Annotation of the pRhico plasmid of <i>Azospirillum brasilense</i> reveals its role in determining the outer surface composition. <i>FEMS Microbiology Letters</i> , 2004, 232, 165-172.	1.8	37
65	SomlnaClust: detection of cancer genes based on somatic mutation patterns of inactivation and clustering. <i>BMC Bioinformatics</i> , 2015, 16, 125.	2.6	36
66	Genome-wide expression analysis reveals TORC1-dependent and -independent functions of Sch9. <i>FEMS Yeast Research</i> , 2008, 8, 1276-1288.	2.3	35
67	PheNetic: network-based interpretation of unstructured gene lists in <i>E. coli</i> . <i>Molecular BioSystems</i> , 2013, 9, 1594.	2.9	35
68	Ultraviolet-B radiation stimulates downward leaf curling in <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2015, 93, 9-17.	5.8	35
69	Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5.	2.6	34
70	Fermentation assays reveal differences in sugar and (off-) flavor metabolism across different <i>Brettanomyces bruxellensis</i> strains. <i>FEMS Yeast Research</i> , 2017, 17, .	2.3	34
71	Integration of omics data: does it lead to new insights into host-microbe interactions?. <i>Future Microbiology</i> , 2010, 5, 313-328.	2.0	32
72	Impact of DNA extraction on whole genome sequencing analysis for characterization and relatedness of Shiga toxin-producing <i>Escherichia coli</i> isolates. <i>Scientific Reports</i> , 2020, 10, 14649.	3.3	32

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73	Meta Analysis of Gene Expression Data within and Across Species. <i>Current Genomics</i> , 2008, 9, 525-534.	1.6	31
74	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. <i>Diabetologia</i> , 2017, 60, 475-489.	6.3	31
75	Inferring the transcriptional network of <i>Bacillus subtilis</i> . <i>Molecular BioSystems</i> , 2009, 5, 1840.	2.9	30
76	Elucidation of the Mode of Action of a New Antibacterial Compound Active against <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2016, 11, e0155139.	2.5	30
77	Genome-specific higher-order background models to improve motif detection. <i>Trends in Microbiology</i> , 2003, 11, 61-66.	7.7	29
78	Comparison of SNP-based subtyping workflows for bacterial isolates using WGS data, applied to <i>Salmonella enterica</i> serotype Typhimurium and serotype 1,4,[5],12:i:-. <i>PLoS ONE</i> , 2018, 13, e0192504.	2.5	29
79	A Cytochrome <i>cbb</i> <sub>3</sub> (Cytochrome c) Terminal Oxidase in <i>Azospirillum brasilense</i> Sp7 Supports Microaerobic Growth. <i>Journal of Bacteriology</i> , 1998, 180, 5689-5696.	2.2	29
80	Whole Genome Sequence Analysis of <i>Salmonella Enteritidis</i> PT4 Outbreaks from a National Reference Laboratory's Viewpoint. <i>PLOS Currents</i> , 2015, 7, .	1.4	29
81	A Comparative Transcriptome Analysis of <i>Rhizobium etli</i> Bacteroids: Specific Gene Expression During Symbiotic Nongrowth. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1553-1561.	2.6	28
82	Effect of genomic distance on coexpression of coregulated genes in <i>E. coli</i> . <i>PLoS ONE</i> , 2017, 12, e0174887.	2.5	28
83	DNA Structural Properties in the Classification of Genomic Transcription Regulation Elements. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9426.	2.0	27
84	Expression Divergence between <i>Escherichia coli</i> and <i>Salmonella enterica</i> serovar Typhimurium Reflects Their Lifestyles. <i>Molecular Biology and Evolution</i> , 2013, 30, 1302-1314.	8.9	27
85	Sensitivity function-based model reduction: A bacterial gene expression case study. <i>Biotechnology and Bioengineering</i> , 2002, 80, 195-200.	3.3	26
86	Query-driven module discovery in microarray data. <i>Bioinformatics</i> , 2007, 23, 2573-2580.	4.1	25
87	COLOMBOS: Access Port for Cross-Platform Bacterial Expression Compendia. <i>PLoS ONE</i> , 2011, 6, e20938.	2.5	25
88	Follicle stimulating hormone receptor G-29A, 919A>G, 2039A>G polymorphism and the risk of male infertility: A meta-analysis. <i>Gene</i> , 2012, 505, 388-392.	2.2	25
89	A putative de-N-acetylase of the PIG-L superfamily affects fluoroquinolone tolerance in <i>Pseudomonas aeruginosa</i> . <i>Pathogens and Disease</i> , 2014, 71, 39-54.	2.0	25
90	Simultaneous discovery of cancer subtypes and subtype features by molecular data integration. <i>Bioinformatics</i> , 2016, 32, i445-i454.	4.1	25

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91	Dynamics of the <i>Saccharomyces cerevisiae</i> Transcriptome during Bread Dough Fermentation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7325-7333.	3.1	24
92	Pathway Relevance Ranking for Tumor Samples through Network-Based Data Integration. <i>PLoS ONE</i> , 2015, 10, e0133503.	2.5	24
93	PheNetic: network-based interpretation of molecular profiling data. <i>Nucleic Acids Research</i> , 2015, 43, W244-W250.	14.5	24
94	Predicting the clinical behavior of ovarian cancer from gene expression profiles. <i>International Journal of Gynecological Cancer</i> , 2006, 16, 147-151.	2.5	23
95	MotifSuite: workflow for probabilistic motif detection and assessment. <i>Bioinformatics</i> , 2012, 28, 1931-1932.	4.1	23
96	Unveiling combinatorial regulation through the combination of ChIP information and in silico cis-regulatory module detection. <i>Nucleic Acids Research</i> , 2012, 40, e90-e90.	14.5	23
97	The Benefits of Whole Genome Sequencing for Foodborne Outbreak Investigation from the Perspective of a National Reference Laboratory in a Smaller Country. <i>Foods</i> , 2020, 9, 1030.	4.3	23
98	Network-based functional modeling of genomics, transcriptomics and metabolism in bacteria. <i>Current Opinion in Microbiology</i> , 2011, 14, 599-607.	5.1	21
99	Inferring the relation between transcriptional and posttranscriptional regulation from expression compendia. <i>BMC Microbiology</i> , 2014, 14, 14.	3.3	21
100	MARAN: normalizing micro-array data. <i>Bioinformatics</i> , 2003, 19, 893-894.	4.1	20
101	COMODO: an adaptive coclustering strategy to identify conserved coexpression modules between organisms. <i>Nucleic Acids Research</i> , 2011, 39, e41-e41.	14.5	20
102	Validation strategy of a bioinformatics whole genome sequencing workflow for Shiga toxin-producing <i>Escherichia coli</i> using a reference collection extensively characterized with conventional methods. <i>Microbial Genomics</i> , 2021, 7, .	2.0	20
103	Inferring Transcriptional Networks by Mining Omics Data. <i>Current Bioinformatics</i> , 2006, 1, 301-313.	1.5	19
104	Catabolic task division between two near-isogenic subpopulations co-existing in a herbicide-degrading bacterial consortium: consequences for the interspecies consortium metabolic model. <i>Environmental Microbiology</i> , 2018, 20, 85-96.	3.8	19
105	Culture-Independent Analysis of Linuron-Mineralizing Microbiota and Functions in on-Farm Biopurification Systems via DNA-Stable Isotope Probing: Comparison with Enrichment Culture. <i>Environmental Science &amp; Technology</i> , 2020, 54, 9387-9397.	10.0	19
106	Low immunogenicity of common cancer hot spot mutations resulting in false immunogenic selection signals. <i>PLoS Genetics</i> , 2021, 17, e1009368.	3.5	19
107	Towards Real-Time and Affordable Strain-Level Metagenomics-Based Foodborne Outbreak Investigations Using Oxford Nanopore Sequencing Technologies. <i>Frontiers in Microbiology</i> , 2021, 12, 738284.	3.5	19
108	A Bioinformatics Whole-Genome Sequencing Workflow for Clinical <i>Mycobacterium tuberculosis</i> Complex Isolate Analysis, Validated Using a Reference Collection Extensively Characterized with Conventional Methods and <i>In Silico</i> Approaches. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	18

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109	Image-Based Dynamic Phenotyping Reveals Genetic Determinants of Filamentation-Mediated $\beta$ -Lactam Tolerance. <i>Frontiers in Microbiology</i> , 2020, 11, 374.	3.5	17
110	More robust detection of motifs in coexpressed genes by using phylogenetic information. <i>BMC Bioinformatics</i> , 2006, 7, 160.	2.6	16
111	Network-Based Identification of Adaptive Pathways in Evolved Ethanol-Tolerant Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2927-2943.	8.9	16
112	First detection of a plasmid located carbapenem resistant blaVIM-1 gene in E. coli isolated from meat products at retail in Belgium in 2015. <i>International Journal of Food Microbiology</i> , 2020, 324, 108624.	4.7	16
113	Application of a strain-level shotgun metagenomics approach on food samples: resolution of the source of a Salmonella food-borne outbreak. <i>Microbial Genomics</i> , 2021, 7, .	2.0	16
114	Genome-Scale Co-Expression Network Comparison across Escherichia coli and Salmonella enterica Serovar Typhimurium Reveals Significant Conservation at the Regulon Level of Local Regulators Despite Their Dissimilar Lifestyles. <i>PLoS ONE</i> , 2014, 9, e102871.	2.5	16
115	Characterization of an Azospirillum brasilense Tn5 mutant with enhanced N <sub>2</sub> fixation: the effect of ORF280 on nifH expression. <i>FEMS Microbiology Letters</i> , 2000, 183, 23-29.	1.8	15
116	Association of the Vascular Endothelial Growth Factor Gene Polymorphisms (â€“460C/T, +405G/C and) Tj ETQq0 0 0 r gBT /Overlock 10	0.8	15
117	Guidelines for Optimisation of a Multiplex Oligonucleotide Ligation-PCR for Characterisation of Microbial Pathogens in a Microsphere Suspension Array. <i>BioMed Research International</i> , 2015, 2015, 1-10.	1.9	15
118	COMPARISON OF DIFFERENT METHODOLOGIES TO IDENTIFY DIFFERENTIALLY EXPRESSED GENES IN TWO-SAMPLE cDNA MICROARRAYS. <i>Journal of Biological Systems</i> , 2002, 10, 409-430.	1.4	14
119	M@CBETH: a microarray classification benchmarking tool. <i>Bioinformatics</i> , 2005, 21, 3185-3186.	4.1	14
120	1 $\alpha$ ,25-Dihydroxyvitamin D <sub>3</sub> -induced down-regulation of the checkpoint proteins, Chk1 and Claspin, is mediated by the pocket proteins p107 and p130. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2007, 103, 411-415.	2.5	14
121	Query-based biclustering of gene expression data using Probabilistic Relational Models. <i>BMC Bioinformatics</i> , 2011, 12, S37.	2.6	14
122	Strain-Level Metagenomic Data Analysis of Enriched In Vitro and In Silico Spiked Food Samples: Paving the Way towards a Culture-Free Foodborne Outbreak Investigation Using STEC as a Case Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5688.	4.1	14
123	A Practical Method to Implement Strain-Level Metagenomics-Based Foodborne Outbreak Investigation and Source Tracking in Routine. <i>Microorganisms</i> , 2020, 8, 1191.	3.6	14
124	Genetic and Physical Map of the pLAFR1 Vector. <i>DNA Sequence</i> , 2004, 15, 225-227.	0.7	13
125	ASP-G: an ASP-based method for finding attractors in genetic regulatory networks. <i>Bioinformatics</i> , 2014, 30, 3086-3092.	4.1	13
126	Network-Based Analysis of eQTL Data to Prioritize Driver Mutations. <i>Genome Biology and Evolution</i> , 2016, 8, 481-494.	2.5	13

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127	Development of an NGS-Based Workflow for Improved Monitoring of Circulating Plasmids in Support of Risk Assessment of Antimicrobial Resistance Gene Dissemination. <i>Antibiotics</i> , 2020, 9, 503.	3.7	13
128	A novel approach to identifying regulatory motifs in distantly related genomes. <i>Genome Biology</i> , 2005, 6, R113.	9.6	12
129	A multiplex oligonucleotide ligation-PCR as a complementary tool for subtyping of <i>Salmonella</i> Typhimurium. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8137-8149.	3.6	12
130	SSA-ME Detection of cancer driver genes using mutual exclusivity by small subnetwork analysis. <i>Scientific Reports</i> , 2016, 6, 36257.	3.3	12
131	Molecular processes underlying synergistic linuron mineralization in a triple-species bacterial consortium biofilm revealed by differential transcriptomics. <i>MicrobiologyOpen</i> , 2018, 7, e00559.	3.0	12
132	Comparative analysis of somatic variant calling on matched FF and FFPE WGS samples. <i>BMC Medical Genomics</i> , 2020, 13, 94.	1.5	12
133	A genoserotyping system for a fast and objective identification of <i>Salmonella</i> serotypes commonly isolated from poultry and pork food sectors in Belgium. <i>Food Microbiology</i> , 2020, 91, 103534.	4.2	12
134	Organellar carbon metabolism is coordinated with distinct developmental phases of secondary xylem. <i>New Phytologist</i> , 2019, 222, 1832-1845.	7.3	11
135	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. <i>European Journal of Control</i> , 2003, 9, 237-278.	2.6	10
136	Joint mapping of genes and conditions via multidimensional unfolding analysis. <i>BMC Bioinformatics</i> , 2007, 8, 181.	2.6	10
137	ModuleDigger: an itemset mining framework for the detection of cis-regulatory modules. <i>BMC Bioinformatics</i> , 2009, 10, S30.	2.6	10
138	An Alignment-Free Approach for Eukaryotic ITS2 Annotation and Phylogenetic Inference. <i>PLoS ONE</i> , 2011, 6, e26638.	2.5	10
139	Genome Sequence of <i>Rhizobium etli</i> CNPAF512, a Nitrogen-Fixing Symbiont Isolated from Bean Root Nodules in Brazil. <i>Journal of Bacteriology</i> , 2011, 193, 3158-3159.	2.2	10
140	An ensemble biclustering approach for querying gene expression compendia with experimental lists. <i>Bioinformatics</i> , 2011, 27, 1948-1956.	4.1	9
141	EPSILON: an eQTL prioritization framework using similarity measures derived from local networks. <i>Bioinformatics</i> , 2013, 29, 1308-1316.	4.1	9
142	Improving the Adaptability of Simulated Evolutionary Swarm Robots in Dynamically Changing Environments. <i>PLoS ONE</i> , 2014, 9, e90695.	2.5	9
143	EXPLoRA-web: linkage analysis of quantitative trait loci using bulk segregant analysis. <i>Nucleic Acids Research</i> , 2016, 44, W142-W146.	14.5	9
144	FabR regulates <i>Salmonella</i> biofilm formation via its direct target FabB. <i>BMC Genomics</i> , 2016, 17, 253.	2.8	9

#	ARTICLE	IF	CITATIONS
145	Identification of novel genes involved in acetic acid tolerance of <i>Saccharomyces cerevisiae</i> using pooled-segregant RNA sequencing. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	9
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