

Kathleen Marchal

List of Publications by Year in descending order

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205
papers

17,488
citations

47006

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h-index

17592

121
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218
all docs

218
docs citations

218
times ranked

24774
citing authors

#	ARTICLE	IF	CITATIONS
1	Halvade somatic: Somatic variant calling with Apache Spark. <i>CigaScience</i> , 2022, 11, .	6.4	2
2	Extracting functional insights from loss-of-function screens using deep link prediction. <i>Cell Reports Methods</i> , 2022, 2, 100171.	2.9	1
3	OMEN: network-based driver gene identification using mutual exclusivity. <i>Bioinformatics</i> , 2022, 38, 3245-3251.	4.1	4
4	First detection of a plasmid-encoded New-Delhi metallo-beta-lactamase-1 (NDM-1) producing <i>Acinetobacter baumannii</i> using whole genome sequencing, isolated in a clinical setting in Benin. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 5.	3.8	6
5	Low immunogenicity of common cancer hot spot mutations resulting in false immunogenic selection signals. <i>PLoS Genetics</i> , 2021, 17, e1009368.	3.5	19
6	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
7	DNA-SIP and repeated isolation corroborate <i>Variovorax</i> as a key organism in maintaining the genetic memory for linuron biodegradation in an agricultural soil. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	0
8	Phylogenomic Investigation of Increasing Fluoroquinolone Resistance among Belgian Cases of Shigellosis between 2013 and 2018 Indicates Both Travel-Related Imports and Domestic Circulation. <i>Microorganisms</i> , 2021, 9, 767.	3.6	4
9	Application of a strain-level shotgun metagenomics approach on food samples: resolution of the source of a <i>Salmonella</i> food-borne outbreak. <i>Microbial Genomics</i> , 2021, 7, .	2.0	16
10	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
11	Genome-wide expression and network analyses of mutants in key brassinosteroid signaling genes. <i>BMC Genomics</i> , 2021, 22, 465.	2.8	4
12	Dynamic partitioning of search patterns for approximate pattern matching using search schemes. <i>IScience</i> , 2021, 24, 102687.	4.1	3
13	A shotgun metagenomics approach to detect and characterize unauthorized genetically modified microorganisms in microbial fermentation products. <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100023.	2.1	5
14	Network-Based Analysis to Identify Drivers of Metastatic Prostate Cancer Using GoNetic. <i>Cancers</i> , 2021, 13, 5291.	3.7	2
15	Whole Genome Sequencing Provides an Added Value to the Investigation of Staphylococcal Food Poisoning Outbreaks. <i>Frontiers in Microbiology</i> , 2021, 12, 750278.	3.5	7
16	Evaluation of WGS performance for bacterial pathogen characterization with the Illumina technology optimized for time-critical situations. <i>Microbial Genomics</i> , 2021, 7, .	2.0	4
17	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
18	Whole-Genome Sequencing-Based Antimicrobial Resistance Characterization and Phylogenomic Investigation of 19 Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Positive <i>Escherichia coli</i> Strains Collected From Hospital Patients in Benin in 2019. <i>Frontiers in Microbiology</i> , 2021, 12, 752883.	3.5	8

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19	A multiplex oligonucleotide ligation-PCR method for the genosero-typing of common Salmonella using a liquid bead suspension assay. Food Microbiology, 2020, 87, 103394.	4.2	6
20	Comparative analysis of somatic variant calling on matched FF and FFPE WGS samples. BMC Medical Genomics, 2020, 13, 94.	1.5	12
21	The Benefits of Whole Genome Sequencing for Foodborne Outbreak Investigation from the Perspective of a National Reference Laboratory in a Smaller Country. Foods, 2020, 9, 1030.	4.3	23
22	Development of an NGS-Based Workflow for Improved Monitoring of Circulating Plasmids in Support of Risk Assessment of Antimicrobial Resistance Gene Dissemination. Antibiotics, 2020, 9, 503.	3.7	13
23	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. International Journal of Molecular Sciences, 2020, 21, 5688.	4.1	14
24	A Practical Method to Implement Strain-Level Metagenomics-Based Foodborne Outbreak Investigation and Source Tracking in Routine. Microorganisms, 2020, 8, 1191.	3.6	14
25	Impact of DNA extraction on whole genome sequencing analysis for characterization and relatedness of Shiga toxin-producing Escherichia coli isolates. Scientific Reports, 2020, 10, 14649.	3.3	32
26	Culture-Independent Analysis of Linuron-Mineralizing Microbiota and Functions in on-Farm Biopurification Systems via DNA-Stable Isotope Probing: Comparison with Enrichment Culture. Environmental Science & Technology, 2020, 54, 9387-9397.	10.0	19
27	A genosero-typing system for a fast and objective identification of Salmonella serotypes commonly isolated from poultry and pork food sectors in Belgium. Food Microbiology, 2020, 91, 103534.	4.2	12
28	Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified Bacillus. Scientific Reports, 2020, 10, 4310.	3.3	57
29	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	12.8	73
30	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
31	Distinct Expression and Methylation Patterns for Genes with Different Fates following a Single Whole-Genome Duplication in Flowering Plants. Molecular Biology and Evolution, 2020, 37, 2394-2413.	8.9	75
32	Image-Based Dynamic Phenotyping Reveals Genetic Determinants of Filamentation-Mediated Î ² -Lactam Tolerance. Frontiers in Microbiology, 2020, 11, 374.	3.5	17
33	First detection of a plasmid located carbapenem resistant blaVIM-1 gene in E. coli isolated from meat products at retail in Belgium in 2015. International Journal of Food Microbiology, 2020, 324, 108624.	4.7	16
34	Managing evidence in food safety and nutrition. EFSA Journal, 2019, 17, e170704.	1.8	7
35	IAMBEE: a web-service for the identification of adaptive pathways from parallel evolved clonal populations. Nucleic Acids Research, 2019, 47, W151-W157.	14.5	1
36	Development of a real-time PCR method for the genosero-typing of Salmonella Paratyphi B variant Java. Applied Microbiology and Biotechnology, 2019, 103, 4987-4996.	3.6	7

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37	Associating expression and genomic data using co-occurrence measures. <i>Biology Direct</i> , 2019, 14, 10.	4.6	7
38	Organellar carbon metabolism is coordinated with distinct developmental phases of secondary xylem. <i>New Phytologist</i> , 2019, 222, 1832-1845.	7.3	11
39	Detailed Evaluation of Data Analysis Tools for Subtyping of Bacterial Isolates Based on Whole Genome Sequencing: <i>Neisseria meningitidis</i> as a Proof of Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 2897.	3.5	8
40	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
41	Modeling multi-valued biological interaction networks using fuzzy answer set programming. <i>Fuzzy Sets and Systems</i> , 2018, 345, 63-82.	2.7	3
42	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
43	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
44	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
45	1-((2,4-Dichlorophenethyl)Amino)-3-Phenoxypropan-2-ol Kills <i>Pseudomonas aeruginosa</i> through Extensive Membrane Damage. <i>Frontiers in Microbiology</i> , 2018, 9, 129.	3.5	9
46	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
47	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
48	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. <i>Diabetologia</i> , 2017, 60, 475-489.	6.3	31
49	The evolutionary significance of polyploidy. <i>Nature Reviews Genetics</i> , 2017, 18, 411-424.	16.3	1,288
50	Molecular Subtyping of <i>Salmonella</i> Typhimurium with Multiplex Oligonucleotide Ligation-PCR (MOL-PCR). <i>Methods in Molecular Biology</i> , 2017, 1616, 39-69.	0.9	1
51	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
52	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
53	Effect of genomic distance on coexpression of coregulated genes in <i>E. coli</i> . <i>PLoS ONE</i> , 2017, 12, e0174887.	2.5	28
54	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

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55	Simultaneous discovery of cancer subtypes and subtype features by molecular data integration. <i>Bioinformatics</i> , 2016, 32, i445-i454.	4.1	25
56	SSA-ME Detection of cancer driver genes using mutual exclusivity by small subnetwork analysis. <i>Scientific Reports</i> , 2016, 6, 36257.	3.3	12
57	Network-Based Analysis of eQTL Data to Prioritize Driver Mutations. <i>Genome Biology and Evolution</i> , 2016, 8, 481-494.	2.5	13
58	EXPLoRA-web: linkage analysis of quantitative trait loci using bulk segregant analysis. <i>Nucleic Acids Research</i> , 2016, 44, W142-W146.	14.5	9
59	Optimized MOLâ€PCR for Characterization of Microbial Pathogens. <i>Current Protocols in Cytometry</i> , 2016, 75, 13.15.1-13.15.15.	3.7	0
60	FabR regulates Salmonella biofilm formation via its direct target FabB. <i>BMC Genomics</i> , 2016, 17, 253.	2.8	9
61	Emergent adaptive behaviour of GRN-controlled simulated robots in a changing environment. <i>PeerJ</i> , 2016, 4, e2812.	2.0	4
62	Pathway Relevance Ranking for Tumor Samples through Network-Based Data Integration. <i>PLoS ONE</i> , 2015, 10, e0133503.	2.5	24
63	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. <i>PLoS Genetics</i> , 2015, 11, e1005635.	3.5	173
64	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
65	Obg 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
66	SomlnaClust: detection of cancer genes based on somatic mutation patterns of inactivation and clustering. <i>BMC Bioinformatics</i> , 2015, 16, 125.	2.6	36
67	PheNetic: network-based interpretation of molecular profiling data. <i>Nucleic Acids Research</i> , 2015, 43, W244-W250.	14.5	24
68	Frequency-based haplotype reconstruction from deep sequencing data of bacterial populations. <i>Nucleic Acids Research</i> , 2015, 43, e105-e105.	14.5	45
69	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
70	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
71	A multiplex oligonucleotide ligation-PCR as a complementary tool for subtyping of <i>Salmonella Typhimurium</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8137-8149.	3.6	12
72	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

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73	Whole Genome Sequence Analysis of Salmonella Enteritidis PT4 Outbreaks from a National Reference Laboratory's Viewpoint. PLOS Currents, 2015, 7, .	1.4	29
74	Improving the Adaptability of Simulated Evolutionary Swarm Robots in Dynamically Changing Environments. PLoS ONE, 2014, 9, e90695.	2.5	9
75	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia: Table 1.. Nucleic Acids Research, 2014, 42, D649-D653.	14.5	38
76	MAGIC: access portal to a cross-platform gene expression compendium for maize. Bioinformatics, 2014, 30, 1316-1318.	4.1	2
77	Inferring the relation between transcriptional and posttranscriptional regulation from expression compendia. BMC Microbiology, 2014, 14, 14.	3.3	21
78	Assessing Genetic Diversity among Brettanomyces Yeasts by DNA Fingerprinting and Whole-Genome Sequencing. Applied and Environmental Microbiology, 2014, 80, 4398-4413.	3.1	66
79	Phenotypical and molecular responses of <i>Arabidopsis thaliana</i> roots as a result of inoculation with the auxin-producing bacterium <i>Zoosporium brasiliense</i> . New Phytologist, 2014, 201, 850-861.	7.3	172
80	Photoreceptor-Mediated Bending towards UV-B in Arabidopsis. Molecular Plant, 2014, 7, 1041-1052.	8.3	68
81	ASP-G: an ASP-based method for finding attractors in genetic regulatory networks. Bioinformatics, 2014, 30, 3086-3092.	4.1	13
82	Improved linkage analysis of Quantitative Trait Loci using bulk segregants unveils a novel determinant of high ethanol tolerance in yeast. BMC Genomics, 2014, 15, 207.	2.8	50
83	A network-based approach to identify substrate classes of bacterial glycosyltransferases. BMC Genomics, 2014, 15, 349.	2.8	337
84	A putative de-N-acetylase of the PIG-L superfamily affects fluoroquinolone tolerance in <i>Pseudomonas aeruginosa</i> . Pathogens and Disease, 2014, 71, 39-54.	2.0	25
85	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. PLoS ONE, 2014, 9, e102871.	2.5	16
86	Path Finding in Biological Networks. , 2014, , 289-309.		0
87	Synthetic Biology and Microdevices. ACM Journal on Emerging Technologies in Computing Systems, 2013, 9, 1-22.	2.3	0
88	PheNetic: network-based interpretation of unstructured gene lists in E. coli. Molecular BioSystems, 2013, 9, 1594.	2.9	35
89	Expression Divergence between Escherichia coli and Salmonella enterica serovar Typhimurium Reflects Their Lifestyles. Molecular Biology and Evolution, 2013, 30, 1302-1314.	8.9	27
90	Dynamics of the Saccharomyces cerevisiae Transcriptome during Bread Dough Fermentation. Applied and Environmental Microbiology, 2013, 79, 7325-7333.	3.1	24

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91	EPSILON: an eQTL prioritization framework using similarity measures derived from local networks. <i>Bioinformatics</i> , 2013, 29, 1308-1316.	4.1	9
92	Identifying differentially expressed genes in the absence of replication. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 71.	0.2	1
93	MLVA as a Tool for Public Health Surveillance of Human <i>Salmonella Typhimurium</i> : Prospective Study in Belgium and Evaluation of MLVA Loci Stability. <i>PLoS ONE</i> , 2013, 8, e84055.	2.5	40
94	Identifying Common Structural DNA Properties in Transcription Factor Binding Site Sets of the LacI-GalR Family. <i>Current Bioinformatics</i> , 2013, 8, 483-488.	1.5	4
95	Omics Derived Networks in Bacteria. <i>Current Bioinformatics</i> , 2013, 8, 489-495.	1.5	2
96	Nucleosomes affect local transformation efficiency. <i>Nucleic Acids Research</i> , 2012, 40, 9506-9512.	14.5	6
97	MotifSuite: workflow for probabilistic motif detection and assessment. <i>Bioinformatics</i> , 2012, 28, 1931-1932.	4.1	23
98	DNA Structural Properties in the Classification of Genomic Transcription Regulation Elements. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9426.	2.0	27
99	Identification of a complex genetic network underlying <i>Saccharomyces cerevisiae</i> colony morphology. <i>Molecular Microbiology</i> , 2012, 86, 225-239.	2.5	71
100	Mining Local Staircase Patterns in Noisy Data. , 2012, , .		0
101	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
102	Association of the Vascular Endothelial Growth Factor Gene Polymorphisms (â€“460C/T, +405G/C and) Tj ETQq0 0 0 rgBT /Overlock 10	0.8	15
103	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
104	Directed Module Detection in a Large-Scale Expression Compendium. <i>Methods in Molecular Biology</i> , 2012, 804, 131-165.	0.9	3
105	A combined approach to study the protein glycosylation potential of <i>Lactobacillus rhamnosus</i> GG (LGG). <i>Communications in Agricultural and Applied Biological Sciences</i> , 2012, 77, 15-9.	0.0	1
106	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
107	Network-based functional modeling of genomics, transcriptomics and metabolism in bacteria. <i>Current Opinion in Microbiology</i> , 2011, 14, 599-607.	5.1	21
108	COLOMBOS: Access Port for Cross-Platform Bacterial Expression Compendia. <i>PLoS ONE</i> , 2011, 6, e20938.	2.5	25

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109	An Alignment-Free Approach for Eukaryotic ITS2 Annotation and Phylogenetic Inference. PLoS ONE, 2011, 6, e26638.	2.5	10
110	A Comparative Transcriptome Analysis of <i>Rhizobium etli</i> Bacteroids: Specific Gene Expression During Symbiotic Nongrowth. Molecular Plant-Microbe Interactions, 2011, 24, 1553-1561.	2.6	28
111	Transcriptome Analysis of the Rhizosphere Bacterium <i>Azospirillum brasilense</i> Reveals an Extensive Auxin Response. Microbial Ecology, 2011, 61, 723-728.	2.8	81
112	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. BMC Systems Biology, 2011, 5, 8.	3.0	128
113	Query-based biclustering of gene expression data using Probabilistic Relational Models. BMC Bioinformatics, 2011, 12, S37.	2.6	14
114	COMODO: an adaptive coclustering strategy to identify conserved coexpression modules between organisms. Nucleic Acids Research, 2011, 39, e41-e41.	14.5	20
115	Use of structural DNA properties for the prediction of transcription-factor binding sites in <i>Escherichia coli</i> . Nucleic Acids Research, 2011, 39, e6-e6.	14.5	42
116	An ensemble biclustering approach for querying gene expression compendia with experimental lists. Bioinformatics, 2011, 27, 1948-1956.	4.1	9
117	Genome Sequence of <i>Rhizobium etli</i> CNPAF512, a Nitrogen-Fixing Symbiont Isolated from Bean Root Nodules in Brazil. Journal of Bacteriology, 2011, 193, 3158-3159.	2.2	10
118	The Potential for pathogenicity was present in the ancestor of the Ascomycete subphylum Pezizomycotina. BMC Evolutionary Biology, 2010, 10, 318.	3.2	4
119	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. BMC Genomics, 2010, 11, 53.	2.8	42
120	The small regulatory RNA molecule MicA is involved in <i>Salmonella enterica</i> serovar Typhimurium biofilm formation. BMC Microbiology, 2010, 10, 276.	3.3	48
121	Advantages and limitations of current network inference methods. Nature Reviews Microbiology, 2010, 8, 717-729.	28.6	452
122	The Effect of Orthology and Coregulation on Detecting Regulatory Motifs. PLoS ONE, 2010, 5, e8938.	2.5	5
123	Module Network Inference from a Cancer Gene Expression Data Set Identifies MicroRNA Regulated Modules. PLoS ONE, 2010, 5, e10162.	2.5	46
124	The AI-2-dependent regulator LsrR has a limited regulon in <i>Salmonella Typhimurium</i> . Cell Research, 2010, 20, 966-969.	12.0	8
125	Alternative Experimental Design with an Applied Normalization Scheme Can Improve Statistical Power in 2D-DIGE Experiments. Journal of Proteome Research, 2010, 9, 4919-4926.	3.7	6
126	Integration of "omics" data: does it lead to new insights into host-microbe interactions?. Future Microbiology, 2010, 5, 313-328.	2.0	32

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127	Cis-regulatory module detection using constraint programming. , 2010, , .		3
128	An ensemble method for querying gene expression compendia with experimental lists. , 2010, , .		0
129	Systems Microbiology: Gaining Insights in Transcriptional Networks. , 2010, , 93-122.		0
130	Layout and Post-Processing of Transcriptional Modules. , 2009, , .		0
131	A Nonlinear Mixed-Effects Model for Estimating Calibration Intervals for Unknown Concentrations in Two-Color Microarray Data with Spike-Ins. Statistical Applications in Genetics and Molecular Biology, 2009, 8, 1-25.	0.6	1
132	Module networks revisited: computational assessment and prioritization of model predictions. Bioinformatics, 2009, 25, 490-496.	4.1	82
133	ViTraM: visualization of transcriptional modules. Bioinformatics, 2009, 25, 2450-2451.	4.1	2
134	ModuleDigger: an itemset mining framework for the detection of cis-regulatory modules. BMC Bioinformatics, 2009, 10, S30.	2.6	10
135	Comparative analysis of module-based versus direct methods for reverse-engineering transcriptional regulatory networks. BMC Systems Biology, 2009, 3, 49.	3.0	55
136	The Conditionâ€Dependent Transcriptional Network in <i>Escherichia coli</i> . Annals of the New York Academy of Sciences, 2009, 1158, 29-35.	3.8	4
137	Reverseâ€Engineering Transcriptional Modules from Gene Expression Data. Annals of the New York Academy of Sciences, 2009, 1158, 36-43.	3.8	5
138	Conditional Random Fields Feature Subset Selection Based on Genetic Algorithms for Phosphorylation Site Prediction. , 2009, , .		0
139	DISTILLER: a data integration framework to reveal condition dependency of complex regulons in <i>Escherichia coli</i> . Genome Biology, 2009, 10, R27.	9.6	52
140	Inferring the transcriptional network of <i>Bacillus subtilis</i> . Molecular BioSystems, 2009, 5, 1840.	2.9	30
141	Microarray analysis of MCF-7 breast cancer cells treated with 1,25-dihydroxyvitamin D3 or a 17-methyl-D-ring analog. Anticancer Research, 2009, 29, 3585-90.	1.1	9
142	Genome-wide expression analysis reveals TORC1-dependent and -independent functions of Sch9. FEMS Yeast Research, 2008, 8, 1276-1288.	2.3	35
143	Expression of the BRCA1-interacting protein Brip1/BACH1/FANCI is driven by E2F and correlates with human breast cancer malignancy. Oncogene, 2008, 27, 4233-4241.	5.9	41
144	Evaluation of time profile reconstruction from complex two-color microarray designs. BMC Bioinformatics, 2008, 9, 1.	2.6	875

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145	Brominated Furanones Inhibit Biofilm Formation by <i>Salmonella enterica</i> Serovar Typhimurium. Applied and Environmental Microbiology, 2008, 74, 6639-6648.	3.1	184
146	Meta Analysis of Gene Expression Data within and Across Species. Current Genomics, 2008, 9, 525-534.	1.6	31
147	Exploring the Operational Characteristics of Inference Algorithms for Transcriptional Networks by Means of Synthetic Data. Artificial Life, 2008, 14, 49-63.	1.3	1
148	Using Ribosomal Protein Genes as Reference: A Tale of Caution. PLoS ONE, 2008, 3, e1854.	2.5	180
149	Functional Analysis of luxS in the Probiotic Strain Lactobacillus rhamnosus GG Reveals a Central Metabolic Role Important for Growth and Biofilm Formation. Journal of Bacteriology, 2007, 189, 860-871.	2.2	142
150	CALIB: a Bioconductor package for estimating absolute expression levels from two-color microarray data. Bioinformatics, 2007, 23, 1700-1701.	4.1	4
151	Query-driven module discovery in microarray data. Bioinformatics, 2007, 23, 2573-2580.	4.1	25
152	Delineation of the Salmonella enterica Serovar Typhimurium HilA Regulon through Genome-Wide Location and Transcript Analysis. Journal of Bacteriology, 2007, 189, 4587-4596.	2.2	65
153	The E2F-Regulated Gene <i>Chk1</i> Is Highly Expressed in Triple-Negative Estrogen Receptor ⁺ /Progesterone Receptor ⁺ /HER-2 ⁺ Breast Carcinomas. Cancer Research, 2007, 67, 6574-6581.	0.9	134
154	1 α ,25-Dihydroxyvitamin D ₃ -induced down-regulation of the checkpoint proteins, Chk1 and Claspin, is mediated by the pocket proteins p107 and p130. Journal of Steroid Biochemistry and Molecular Biology, 2007, 103, 411-415.	2.5	14
155	Joint mapping of genes and conditions via multidimensional unfolding analysis. BMC Bioinformatics, 2007, 8, 181.	2.6	10
156	Validating module network learning algorithms using simulated data. BMC Bioinformatics, 2007, 8, S5.	2.6	34
157	Inferring transcriptional modules from ChIP-chip, motif and microarray data. Genome Biology, 2006, 7, R37.	9.6	89
158	Predicting the clinical behavior of ovarian cancer from gene expression profiles. International Journal of Gynecological Cancer, 2006, 16, 147-151.	2.5	23
159	Strong antimicrobial activity of <i>Lactobacillus rhamnosus</i> GG against <i>Salmonella typhimurium</i> is due to accumulation of lactic acid. FEMS Microbiology Letters, 2006, 259, 89-96.	1.8	257
160	Integration of omics data: how well does it work for bacteria?. Molecular Microbiology, 2006, 62, 1239-1250.	2.5	49
161	More robust detection of motifs in coexpressed genes by using phylogenetic information. BMC Bioinformatics, 2006, 7, 160.	2.6	16
162	SynTREN: a generator of synthetic gene expression data for design and analysis of structure learning algorithms. BMC Bioinformatics, 2006, 7, 43.	2.6	233

#	ARTICLE	IF	CITATIONS
163	Inferring Transcriptional Networks by Mining Omics Data. <i>Current Bioinformatics</i> , 2006, 1, 301-313.	1.5	19
164	A calibration method for estimating absolute expression levels from microarray data. <i>Bioinformatics</i> , 2006, 22, 1251-1258.	4.1	8
165	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
166	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
167	Advances in Cluster Analysis of Microarray Data. , 2005, , 153-173.		7
168	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
169	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
170	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
171	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
172	M@CBETH: a microarray classification benchmarking tool. <i>Bioinformatics</i> , 2005, 21, 3185-3186.	4.1	14
173	A novel approach to identifying regulatory motifs in distantly related genomes. <i>Genome Biology</i> , 2005, 6, R113.	9.6	12
174	Computational Biology and Toxicogenomics. , 2005, , 37-92.		0
175	Discovering transcriptional modules from motif, chip-chip and microarray data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 483-94.	0.7	5
176	The Effects of 1 α ,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
177	Screening genomes of Gram-positive bacteria for double-glycine-motif-containing peptides. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1121-1126.	1.8	37
178	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
179	Genetic and Physical Map of the pLAFR1 Vector. <i>DNA Sequence</i> , 2004, 15, 225-227.	0.7	13
180	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

#	ARTICLE	IF	CITATIONS
181	Differential regulation of the insulin-like growth factor II mRNA-binding protein genes by architectural transcription factor HMGA2. FEBS Letters, 2004, 569, 277-283.	2.8	78
182	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. Peptides, 2004, 25, 1425-1440.	2.4	108
183	DISCOVERING TRANSCRIPTIONAL MODULES FROM MOTIF, ChIP-CHIP AND MICROARRAY DATA. , 2004, , .		4
184	Genome-specific higher-order background models to improve motif detection. Trends in Microbiology, 2003, 11, 61-66.	7.7	29
185	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. European Journal of Control, 2003, 9, 237-278.	2.6	10
186	MARAN: normalizing micro-array data. Bioinformatics, 2003, 19, 893-894.	4.1	20
187	INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis. Nucleic Acids Research, 2003, 31, 3468-3470.	14.5	46
188	Computational Approaches to Identify Promoters and cis-Regulatory Elements in Plant Genomes. Plant Physiology, 2003, 132, 1162-1176.	4.8	158
189	Adaptive quality-based clustering of gene expression profiles. Bioinformatics, 2002, 18, 735-746.	4.1	170
190	COMPARISON OF DIFFERENT METHODOLOGIES TO IDENTIFY DIFFERENTIALLY EXPRESSED GENES IN TWO-SAMPLE cDNA MICROARRAYS. Journal of Biological Systems, 2002, 10, 409-430.	1.4	14
191	INCLUSive: Integrated Clustering, Upstream sequence retrieval and motif Sampling. Bioinformatics, 2002, 18, 331-332.	4.1	78
192	SENSITIVITY FUNCTION BASED MODEL REDUCTION: A BACTERIAL GENE EXPRESSION CASE STUDY. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2002, 35, 443-448.	0.4	0
193	PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. Nucleic Acids Research, 2002, 30, 325-327.	14.5	4,875
194	Prediction and overview of the RpoN-regulon in closely related species of the Rhizobiales. Genome Biology, 2002, 3, research0076.1.	9.6	62
195	A Gibbs Sampling Method to Detect Overrepresented Motifs in the Upstream Regions of Coexpressed Genes. Journal of Computational Biology, 2002, 9, 447-464.	1.6	301
196	Functional bioinformatics of microarray data: from expression to regulation. Proceedings of the IEEE, 2002, 90, 1722-1743.	21.3	37
197	Sensitivity function-based model reduction: A bacterial gene expression case study. Biotechnology and Bioengineering, 2002, 80, 195-200.	3.3	26
198	A higher-order background model improves the detection of promoter regulatory elements by Gibbs sampling. Bioinformatics, 2001, 17, 1113-1122.	4.1	344

#	ARTICLE	IF	CITATIONS
199	Quantitative Analysis of Bacterial Gene Expression by Using the gusA Reporter Gene System. Applied and Environmental Microbiology, 2001, 67, 3350-3357.	3.1	5
200	Characterization of an <i>Azospirillum brasilense</i> Tn5 mutant with enhanced N ₂ fixation: the effect of ORF280 on nifH expression. FEMS Microbiology Letters, 2000, 183, 23-29.	1.8	15
201	The "oxygen paradox" of dinitrogen-fixing bacteria. Biology and Fertility of Soils, 2000, 30, 363-373.	4.3	61
202	A Cytochrome <i>cbb</i> ₃ (Cytochrome c) Terminal Oxidase in <i>Azospirillum brasilense</i> Sp7 Supports Microaerobic Growth. Journal of Bacteriology, 1998, 180, 5689-5696.	2.2	29
203	Gene Regulation Bioinformatics of Microarray Data. , 0, , 55-98.		0
204	Adaptive Self-Organizing Organisms Using A Bio-Inspired Gene Regulatory Network Controller. Advances in Computational Intelligence and Robotics Book Series, 0, , 68-82.	0.4	3
205	Comparative transcriptome analysis of two maize genotypes with different tolerance to salt stress. Cereal Research Communications, 0, , 1.	1.6	0