Michael A Langston

List of Publications by Year
in descending order

75 papers	2,543 citations	236925 25 h-index	206112 48 g-index
78 all docs	78 docs citations	78 times ranked	3315 citing authors

#	Article	IF	Citations
1	Detecting Differential and Correlated Protein Expression in Label-Free Shotgun Proteomics. Journal of Proteome Research, 2006, 5, 2909-2918.	3.7	361
2	The Public Health Exposome: A Population-Based, Exposure Science Approach to Health Disparities Research. International Journal of Environmental Research and Public Health, 2014, 11, 12866-12895.	2.6	137
3	On finding bicliques in bipartite graphs: a novel algorithm and its application to the integration of diverse biological data types. BMC Bioinformatics, 2014, 15, 110.	2.6	131
4	Cross-Species Integrative Functional Genomics in GeneWeaver Reveals a Role for Pafah1b1 in Altered Response to Alcohol. Frontiers in Behavioral Neuroscience, 2016, 10, 1.	2.0	123
5	GeneWeaver: a web-based system for integrative functional genomics. Nucleic Acids Research, 2012, 40, D1067-D1076.	14.5	112
6	Genetic Dissection of Acute Ethanol Responsive Gene Networks in Prefrontal Cortex: Functional and Mechanistic Implications. PLoS ONE, 2012, 7, e33575.	2.5	109
7	Crown Structures for Vertex Cover Kernelization. Theory of Computing Systems, 2007, 41, 411-430.	1.1	97
8	Extracting Gene Networks for Low-Dose Radiation Using Graph Theoretical Algorithms. PLoS Computational Biology, 2006, 2, e89.	3.2	86
9	Nonconstructive advances in polynomial-time complexity. Information Processing Letters, 1987, 26, 157-162.	0.6	72
10	Threshold selection in gene co-expression networks using spectral graph theory techniques. BMC Bioinformatics, 2009, 10, S4.	2.6	71
11	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. PLoS Genetics, 2014, 10, e1004059.	3.5	70
12	On Well-Partial-Order Theory and Its Application to Combinatorial Problems of VLSI Design. SIAM Journal on Discrete Mathematics, 1992, 5, 117-126.	0.8	69
13	On search, decision, and the efficiency of polynomial-time algorithms. Journal of Computer and System Sciences, 1994, 49, 769-779.	1.2	67
14	Interstage Transportation Planning in the Deterministic Flow-Shop Environment. Operations Research, 1987, 35, 556-564.	1.9	62
15	Scalable Parallel Algorithms for FPT Problems. Algorithmica, 2006, 45, 269-284.	1.3	62
16	A systematic comparison of genome-scale clustering algorithms. BMC Bioinformatics, 2012, 13, S7.	2.6	55
17	Practical in-place merging. Communications of the ACM, 1988, 31, 348-352.	4.5	50
18	Genome-level analysis of genetic regulation of liver gene expression networks. Hepatology, 2007, 46, 548-557.	7.3	49

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19	Obstruction set isolation for the gate matrix layout problem. Discrete Applied Mathematics, 1994, 54, 169-213.	0.9	44
20	Comparison of threshold selection methods for microarray gene co-expression matrices. BMC Research Notes, 2009, 2, 240.	1.4	37
21	Ontological discovery environment: A system for integrating gene–phenotype associations. Genomics, 2009, 94, 377-387.	2.9	35
22	Efficient prediction of human protein-protein interactions at a global scale. BMC Bioinformatics, 2014, 15, 383.	2.6	32
23	Genome-wide DNA methylation analysis reveals loci that distinguish different types of adipose tissue in obese individuals. Clinical Epigenetics, 2017, 9, 48.	4.1	32
24	GeneWeaver: data driven alignment of cross-species genomics in biology and disease. Nucleic Acids Research, 2016, 44, D555-D559.	14.5	30
25	Online variable-sized bin packing. Discrete Applied Mathematics, 1988, 22, 143-148.	0.9	29
26	Computational, Integrative, and Comparative Methods for the Elucidation of Genetic Coexpression Networks. Journal of Biomedicine and Biotechnology, 2005, 2005, 172-180.	3.0	29
27	Analysis of a Compound Bin Packing Algorithm. SIAM Journal on Discrete Mathematics, 1991, 4, 61-79.	0.8	27
28	A network-based analysis of the late-phase reaction of the skin. Journal of Allergy and Clinical Immunology, 2006, 118, 220-225.	2.9	27
29	Combinatorial Genetic Regulatory Network Analysis Tools for High Throughput Transcriptomic Data. , 2005, , 150-165.		27
30	The Maximum Common Subgraph Problem: Faster Solutions via Vertex Cover. , 2007, , .		25
31	Exploration of Preterm Birth Rates Using the Public Health Exposome Database and Computational Analysis Methods. International Journal of Environmental Research and Public Health, 2014, 11, 12346-12366.	2.6	25
32	Scalable Combinatorial Tools for Health Disparities Research. International Journal of Environmental Research and Public Health, 2014, 11, 10419-10443.	2.6	22
33	EntropyExplorer: an R package for computing and comparing differential Shannon entropy, differential coefficient of variation and differential expression. BMC Research Notes, 2015, 8, 832.	1.4	21
34	Improved 0/1-interchange scheduling. BIT Numerical Mathematics, 1982, 22, 282-290.	2.0	17
35	Lower bounds on paraclique density. Discrete Applied Mathematics, 2016, 204, 208-212.	0.9	17
36	Polynomial-time self-reducibility: theoretical motivations and practical resultsâˆ—. International Journal of Computer Mathematics, 1989, 31, 1-9.	1.8	15

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37	Approximating the pathwidth of outerplanar graphs. Information Processing Letters, 1998, 68, 17-23.	0.6	15
38	Validation of research trajectory 1 of an Exposome framework: Exposure to benzo(a)pyrene confers enhanced susceptibility to bacterial infection. Environmental Research, 2016, 146, 173-184.	7.5	15
39	A multifactorial obesity model developed from nationwide public health exposome data and modern computational analyses. Obesity Research and Clinical Practice, 2017, 11, 522-533.	1.8	15
40	Chapter 8 Algorithmic implications of the graph minor theorem. Handbooks in Operations Research and Management Science, 1995, 7, 481-502.	0.6	14
41	Robust Inference of Genetic Exchange Communities from Microbial Genomes Using TF-IDF. Frontiers in Microbiology, 2017, 8, 21.	3.5	14
42	The Effects of Social, Personal, and Behavioral Risk Factors and PM2.5 on Cardio-Metabolic Disparities in a Cohort of Community Health Center Patients. International Journal of Environmental Research and Public Health, 2020, 17, 3561.	2.6	14
43	On algorithmic applications of the immersion order. Discrete Mathematics, 1998, 182, 191-196.	0.7	13
44	A robustness metric for biological data clustering algorithms. BMC Bioinformatics, 2019, 20, 503.	2.6	13
45	Structural and Social Determinants of Health Factors Associated with County-Level Variation in Non-Adherence to Antihypertensive Medication Treatment. International Journal of Environmental Research and Public Health, 2020, 17, 6684.	2.6	13
46	Stable duplicate-key extraction with optimal time and space bounds. Acta Informatica, 1989, 26, 473-484.	0.5	12
47	Differential Shannon entropy and differential coefficient of variation: alternatives and augmentations to differential expression in the search for disease-related genes. International Journal of Computational Biology and Drug Design, 2014, 7, 183.	0.3	12
48	GeneWeaver: finding consilience in heterogeneous cross-species functional genomics data. Mammalian Genome, 2015, 26, 556-566.	2.2	12
49	Social Determinants and the Classification of Disease: Descriptive Epidemiology of Selected Socially Mediated Disease Constellations. PLoS ONE, 2014, 9, e110271.	2.5	12
50	MicroRNA Profiling in Adipose Before and After Weight Loss Highlights the Role of miRâ€223â€3p and the NLRP3 Inflammasome. Obesity, 2020, 28, 570-580.	3.0	11
51	On Finding and Enumerating Maximal and Maximum k-Partite Cliques in k-Partite Graphs. Algorithms, 2019, 12, 23.	2.1	10
52	A novel approach to analyzing lung cancer mortality disparities: Using the exposome and a graph-theoretical toolchain. Environmental Disease, 2017, 2, 33-44.	0.1	10
53	Fast Algorithms forK4Immersion Testing. Journal of Algorithms, 1999, 30, 344-378.	0.9	9
54	Graph Theoretical Analysis of Genome-Scale Data: Examination of Gene Activation Occurring in the Setting of Community-Acquired Pneumonia. Shock, 2018, 50, 53-59.	2.1	9

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55	Biclique: an R package for maximal biclique enumeration in bipartite graphs. BMC Research Notes, 2020, 13, 88.	1.4	9
56	Graph Algorithms for Integrated Biological Analysis, with Applications to Type 1 Diabetes Data. , 2009, , 207-222.		7
57	Integrative Functional Genomics for Systems Genetics in GeneWeaver.org. Methods in Molecular Biology, 2017, 1488, 131-152.	0.9	6
58	Association of Cardiovascular Disease and Long-Term Exposure to Fine Particulate Matter (PM2.5) in the Southeastern United States. Atmosphere, 2021, 12, 947.	2.3	4
59	Scalable multipartite subgraph enumeration for integrative analysis of heterogeneous experimental functional genomics data. , 2015, , .		3
60	Using out-of-core techniques to produce exact solutions to the maximum clique problem on extremely large graphs. , 2009, , .		2
61	Toward an efficient, highly scalable maximum clique solver for massive graphs. , 2014, , .		2
62	Compound Analytics: Templates for Integrating Graph Algorithms and Machine Learning. , 2017, , .		2
63	Multiscale graph theoretical tools reveal subtle patterns in big geospatial data. , 2017, , .		2
64	Genetic analysis of BDNF expression cliques and adult neurogenesis in the hippocampus. , 2010, , .		1
65	Rural congestive heart failure mortality among US elderly, 1999â€"2013: Identifying counties with promising outcomes and opportunities for implementation research. Family Medicine and Community Health, 2015, 3, 27-38.	1.6	1
66	Infant Deaths and Mortality from Gun Violence: Causal or Casual?. Journal of the National Medical Association, 2017, 109, 246-251.	0.8	1
67	Classification and Anomaly Detection in Traffic Patterns of New York City Taxis: A Case Study in Compound Analytics. , 2018, , .		1
68	Molecular Subtyping and Outlier Detection in Human Disease Using the Paraclique Algorithm. Algorithms, 2021, 14, 63.	2.1	1
69	Examining the Drivers of Racial/Ethnic Disparities in Non-Adherence to Antihypertensive Medications and Mortality Due to Heart Disease and Stroke: A County-Level Analysis. International Journal of Environmental Research and Public Health, 2021, 18, 12702.	2.6	1
70	A Study of Composite Heuristic Algorithms. Journal of the Operational Research Society, 1987, 38, 539.	3.4	0
71	MIMD VERSUS SIMD COMPUTATION: EXPERIENCE WITH NON-NUMERIC PARALLEL ALGORITHMSâˆˆâ€. International Journal of Parallel, Emergent and Distributed Systems, 1994, 2, 123-138.	0.4	0
72	AN INTRODUCTION TO THE SPECIAL ISSUE. International Journal of Parallel, Emergent and Distributed Systems, 1996, 8, 1-2.	0.4	0

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73	Graph Algorithm Alternatives via Polynomial-Time Transformations: An Empirical Study Using Boolean Satisfiability and Integer Linear Programming. , 2017, , .		0
74	Compound Analytics using Combinatorics for Feature Selection: A Case Study in Biomarker Detection. , 2019, , .		0
75	Molecular Subtyping in Human Disease Using the Paraclique Algorithm. Communications in Computer and Information Science, 2019, , 54-58.	0.5	0