Michael Gribskov

List of Publications by Year
in descending order

93 papers	16,067 citations	87401 40 h-index	71088 80 g-index
98 all docs	98 docs citations	98 times ranked	19777 citing authors

#	Article	IF	Citations
1	Shiny-DEG: A Web Application to Analyze and Visualize Differentially Expressed Genes in RNA-seq. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 349-354.	2.2	2
2	The Evolution History of Fe–S Cluster A-Type Assembly Protein Reveals Multiple Gene Duplication Events and Essential Protein Motifs. Genome Biology and Evolution, 2020, 12, 160-173.	1.1	4
3	Chromatin-enriched RNAs mark active and repressive cis-regulation: An analysis of nuclear RNA-seq. PLoS Computational Biology, 2020, 16, e1007119.	1.5	4
4	miRNA–mediated macrophage behaviors responding to matrix stiffness and ox–LDL. Journal of Cellular Physiology, 2020, 235, 6139-6153.	2.0	15
5	MicroRNA and lncRNA Databases and Analysis. , 2019, , 165-170.		0
6	Identification of Sequence Patterns, Motifs and Domains. , 2019, , 332-340.		4
7	IRESpy: an XGBoost model for prediction of internal ribosome entry sites. BMC Bioinformatics, 2019, 20, 409.	1.2	47
8	MiPepid: MicroPeptide identification tool using machine learning. BMC Bioinformatics, 2019, 20, 559.	1.2	51
9	Comparative genome analysis reveals niche-specific genome expansion in Acinetobacter baumannii strains. PLoS ONE, 2019, 14, e0218204.	1.1	42
10	Three Genes Define a Bacterial-Like Arsenic Tolerance Mechanism in the Arsenic Hyperaccumulating Fern Pteris vittata. Current Biology, 2019, 29, 1625-1633.e3.	1.8	44
11	Transcriptome analysis identifies metallothionein as biomarkers to predict recurrence in hepatocellular cacinoma. Molecular Genetics & Genomic Medicine, 2019, 7, e693.	0.6	7
12	AUDIT: approving and tracking updates with dependencies in collaborative databases. Distributed and Parallel Databases, 2018, 36, 81-119.	1.0	3
13	COACT: a query interface language for collaborative databases. Distributed and Parallel Databases, 2018, 36, 121-151.	1.0	3
14	Comprehensive evaluation of *de novo* transcriptome assembly programs and their effects on differential gene expression analysis. Bioinformatics, 2017, 33, 327-333.	1.8	65
15	AptRank: an adaptive PageRank model for protein function prediction on bi-relational graphs. Bioinformatics, 2017, 33, 1829-1836.	1.8	40
16	DEIsoM: a hierarchical Bayesian model for identifying differentially expressed isoforms using biological replicates. Bioinformatics, 2017, 33, 3018-3027.	1.8	0
17	Effect of high-fat diet on secreted milk transcriptome in midlactation mice. Physiological Genomics, 2017, 49, 747-762.	1.0	37
18	Advancing the Representation of Women in HPC at Purdue University. , 2017, , .		1

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19	Accurate Classification of RNA Structures Using Topological Fingerprints. PLoS ONE, 2016, 11, e0164726.	1.1	8
20	Differential gene expression in Varroa jacobsoni mites following a host shift to European honey bees (Apis mellifera). BMC Genomics, 2016, 17, 926.	1.2	14
21	CellMiner Companion: an interactive web application to explore CellMiner NCI-60 data. Bioinformatics, 2016, 32, 2399-2401.	1.8	15
22	Differential gene expression in Varroa jacobsoni mites following a host shift to European honey bees (Apis mellifera). , 2015, , .		0
23	MMC-margin: Identification of maximum frequent subgraphs by metropolis Monte Carlo sampling. , 2015, , .		3
24	GenoBase: comprehensive resource database of Escherichia coli K-12. Nucleic Acids Research, 2015, 43, D606-D617.	6.5	29
25	Differential flux balance analysis of quantitative proteomic data on protein interaction networks. , 2015, , .		0
26	Ontogenetic changes in embryonic and brain gene expression in progeny produced from migratory and resident <i><scp>O</scp>ncorhynchus mykiss</i>. Molecular Ecology, 2015, 24, 1792-1809.	2.0	36
27	Making models match measurements: Model optimization for morphogen patterning networks. Seminars in Cell and Developmental Biology, 2014, 35, 109-123.	2.3	17
28	Identifying complete RNA structural ensembles including pseudoknots. RNA Biology, 2012, 9, 187-199.	1.5	6
29	Metabolite Profiles in Starved Diporeia spp. Using Liquid Chromatography-Mass Spectrometry (LC-MS) Based Metabolomics. Journal of Crustacean Biology, 2012, 32, 239-248.	0.3	28
30	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	6.0	794
31	The Role of RNA Sequence and Structure in RNAâ€"Protein Interactions. Journal of Molecular Biology, 2011, 409, 574-587.	2.0	51
32	Calcium-Dependent Protein Kinases from Arabidopsis Show Substrate Specificity Differences in an Analysis of 103 Substrates. Frontiers in Plant Science, 2011, 2, 36.	1.7	80
33	A Physical Interaction Network of Dengue Virus and Human Proteins. Molecular and Cellular Proteomics, 2011, 10, M111.012187.	2.5	153
34	Analysis of Gap Gene Regulation in a 3D Organism-Scale Model of the Drosophila melanogaster Embryo. PLoS ONE, 2011, 6, e26797.	1.1	19
35	Protein-Protein Interactions of Tandem Affinity Purified Protein Kinases from Rice. PLoS ONE, 2009, 4, e6685.	1.1	37
36	A Rice Kinase-Protein Interaction Map Â Â. Plant Physiology, 2009, 149, 1478-1492.	2.3	116

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37	The Genome of Nectria haematococca: Contribution of Supernumerary Chromosomes to Gene Expansion. PLoS Genetics, 2009, 5, e1000618.	1.5	402
38	Bioinformatics research in the Asia Pacific: a 2007 update. BMC Bioinformatics, 2008, 9, S1.	1.2	7
39	Spontaneous symmetry breaking in genome evolution. Nucleic Acids Research, 2008, 36, 2756-2763.	6.5	2
40	The Emerging World of Wikis. Science, 2008, 320, 1289-1290.	6.0	23
41	Pattern Matching in RNA Structures. , 2008, , 317-330.		6
42	Protein kinase resource: An integrated environment for phosphorylation research. Proteins: Structure, Function and Bioinformatics, 2006, 63, 78-86.	1.5	44
43	Protein-protein interactions of tandem affinity purification-tagged protein kinases in rice. Plant Journal, 2006, 46, 1-13.	2.8	164
44	The Genome of Black Cottonwood, Populus trichocarpa (Torr. & Gray). Science, 2006, 313, 1596-1604.	6.0	3,945
45	Establishing bioinformatics research in the Asia Pacific. BMC Bioinformatics, 2006, 7, 1.	1.2	356
46	Wiggleâ€"Predicting Functionally Flexible Regions from Primary Sequence. PLoS Computational Biology, 2006, 2, e90.	1.5	26
47	An Open Forum for Computational Biology. PLoS Computational Biology, 2005, 1, e5.	1.5	2
48	The ISCB: Growing and Evolving in Step with Science. PLoS Computational Biology, 2005, 1, e51.	1.5	7
49	Characteristics and regulatory elements defining constitutive splicing and different modes of alternative splicing in human and mouse. Rna, 2005, 11, 1777-1787.	1.6	75
50	MAASE: An alternative splicing database designed for supporting splicing microarray applications. Rna, 2005, 11, 1767-1776.	1.6	23
51	Examining the architecture of cellular computing through a comparative study with a computer. Journal of the Royal Society Interface, 2005, 2, 187-195.	1.5	14
52	Predicting N-terminal myristoylation sites in plant proteins. BMC Genomics, 2004, 5, 37.	1.2	137
53	Rival penalized competitive learning (RPCL): a topology-determining algorithm for analyzing gene expression data. Computational Biology and Chemistry, 2003, 27, 565-574.	1.1	20
54	modulewriter: a program for automatic generation of database interfaces. Computational Biology and Chemistry, 2003, 27, 135-139.	1.1	1

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55	The Arabidopsis CDPK-SnRK Superfamily of Protein Kinases. Plant Physiology, 2003, 132, 666-680.	2.3	898
56	Systematic Trans-Genomic Comparison of Protein Kinases between Arabidopsis and Saccharomyces cerevisiae Â. Plant Physiology, 2003, 132, 2152-2165.	2.3	75
57	Arabidopsis Proteins Containing Similarity to the Universal Stress Protein Domain of Bacteria. Plant Physiology, 2003, 131, 1209-1219.	2.3	89
58	Genomic Comparison of P-Type ATPase Ion Pumps in Arabidopsis and Rice. Plant Physiology, 2003, 132, 618-628.	2.3	320
59	Challenges in Data Management for Functional Genomics. OMICS A Journal of Integrative Biology, 2003, 7, 3-5.	1.0	6
60	2HAPI: a microarray data analysis system. Bioinformatics, 2003, 19, 1443-1445.	1.8	7
61	The PlantsP and PlantsT Functional Genomics Databases. Nucleic Acids Research, 2003, 31, 342-344.	6.5	54
62	On selecting features from splice junctions: an analysis using information theoretic and machine learning approaches. Genome Informatics, 2003, 14, 73-83.	0.4	4
63	Estimating and Evaluating the Statistics of Gapped Local-Alignment Scores. Journal of Computational Biology, 2002, 9, 575-593.	0.8	23
64	Homophila: human disease gene cognates in Drosophila. Nucleic Acids Research, 2002, 30, 149-151.	6.5	158
65	The Complement of Protein Phosphatase Catalytic Subunits Encoded in the Genome of Arabidopsis. Plant Physiology, 2002, 129, 908-925.	2.3	242
66	A Systematic Analysis of Human Disease-Associated Gene Sequences In Drosophila melanogaster. Genome Research, 2001, 11, 1114-1125.	2.4	751
67	An integrated Arabidopsis annotation database for Affymetrix GenechipÂ® data analysis, and tools for regulatory motif searches. Trends in Plant Science, 2001, 6, 448-449.	4.3	17
68	Phylogenetic Relationships within Cation Transporter Families of Arabidopsis. Plant Physiology, 2001, 126, 1646-1667.	2.3	1,110
69	The CDPK superfamily of protein kinases. New Phytologist, 2001, 151, 175-183.	3.5	188
70	PlantsP: a functional genomics database for plant phosphorylation. Nucleic Acids Research, 2001, 29, 111-113.	6.5	62
71	CDPKs â€" a kinase for every Ca2+ signal?. Trends in Plant Science, 2000, 5, 154-159.	4.3	476
72	RNA binding domain of HDV antigen is homologous to the HMG box of SRY. Archives of Virology, 1999, 144, 1139-1158.	0.9	6

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73	Methods and Statistics for Combining Motif Match Scores. Journal of Computational Biology, 1998, 5, 211-221.	0.8	180
74	Score Distributions for Simultaneous Matching to Multiple Motifs. Journal of Computational Biology, 1997, 4, 45-59.	0.8	56
75	The protein kinase resource. Trends in Biochemical Sciences, 1997, 22, 444-446.	3.7	96
76	Analysis of the structure of chemically synthesized HIV-1 protease complexed with a hexapeptide inhibitor. Part I: Crystallographic refinement of 2 Ã… data. , 1997, 27, 184-195.		15
77	Sequence comparison. , 1997, , 105-120.		1
78	A comparison of the crystal structures of bacterial l-asparaginases. Techniques in Protein Chemistry, 1996, 7, 373-IN1.	0.3	1
79	Use of receiver operating characteristic (ROC) analysis to evaluate sequence matching. Computers & Chemistry, 1996, 20, 25-33.	1.2	414
80	[13] Identification of sequence patterns with profile analysis. Methods in Enzymology, 1996, 266, 198-212.	0.4	90
81	Profile Analysis. , 1994, 25, 247-266.		27
82	A mechanistic view of proteins and their sequences. Computers & Chemistry, 1993, 17, 113-116.	1.2	0
83	The sigma 70 family: sequence conservation and evolutionary relationships. Journal of Bacteriology, 1992, 174, 3843-3849.	1.0	893
84	Translational initiation factors IF-1 and eIF-2Î± share an RNA-binding motif with prokaryotic ribosomal protein S1 and polynucleotide phosphorylase. Gene, 1992, 119, 107-111.	1.0	74
85	The language metaphor in sequence analysis. Computers & Chemistry, 1992, 16, 85-88.	1.2	4
86	[9] Profile analysis. Methods in Enzymology, 1990, 183, 146-159.	0.4	337
87	DETECTION OF PROTEIN STRUCTURAL FEATURES WITH PROFILE ANALYSIS. , 1989, , 108-117.		1
88	Profile analysis: detection of distantly related proteins.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 4355-4358.	3.3	1,225
89	Sigma factors fromE. coli, B. subtilis, phage SP01, and phage T4 are homologous proteins. Nucleic Acids Research, 1986, 14, 6745-6763.	6.5	497
90	PEPPLOT, a protein secondary structure analysis program for the UWGCG sequence analysis software package. Nucleic Acids Research, 1986, 14, 327-334.	6.5	74

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91	The codon preference plot: graphic analysis of protein coding sequences and prediction of gene expression. Nucleic Acids Research, 1984, 12, 539-549.	6.5	389
92	Overexpression and purification of the sigma subunit of Escherichia coli RNA polymerase. Gene, 1983, 26, 109-118.	1.0	171
93	Preliminary investigation of glyphosate resistance mechanism in giant ragweed using transcriptome analysis. F1000Research, 0, 5, 1354.	0.8	3