

Thomas Girke

List of Publications by Year in descending order

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63
papers

10,088
citations

87723

38
h-index

110170

64
g-index

65
all docs

65
docs citations

65
times ranked

19300
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene regulatory networks shape developmental plasticity of root cell types under water extremes in rice. <i>Developmental Cell</i> , 2022, 57, 1177-1192.e6.	3.1	27
2	Transcriptomic Evidence That Switching from Tobacco to Electronic Cigarettes Does Not Reverse Damage to the Respiratory Epithelium. <i>Toxics</i> , 2022, 10, 370.	1.6	7
3	HOTAIRM1 lncRNA is downregulated in clear cell renal cell carcinoma and inhibits the hypoxia pathway. <i>Cancer Letters</i> , 2020, 472, 50-58.	3.2	41
4	High-throughput small molecule screening reveals Nrf2-dependent and -independent pathways of cellular stress resistance. <i>Science Advances</i> , 2020, 6, .	4.7	12
5	<i>signatureSearch</i> : environment for gene expression signature searching and functional interpretation. <i>Nucleic Acids Research</i> , 2020, 48, e124-e124.	6.5	17
6	Experimental Acute Exposure to Thirdhand Smoke and Changes in the Human Nasal Epithelial Transcriptome. <i>JAMA Network Open</i> , 2019, 2, e196362.	2.8	11
7	Genetic Support for Longevity-Enhancing Drug Targets: Issues, Preliminary Data, and Future Directions. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, S61-S71.	1.7	4
8	Sequence analysis of the potato aphid <i>Macrosiphum euphorbiae</i> transcriptome identified two new viruses. <i>PLoS ONE</i> , 2018, 13, e0193239.	1.1	14
9	Global isoform-specific transcript alterations and deregulated networks in clear cell renal cell carcinoma. <i>Oncotarget</i> , 2018, 9, 23670-23680.	0.8	13
10	Transcriptome-wide microRNA and target dynamics in the fat body during the gonadotrophic cycle of <i>Aedes aegypti</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1895-E1903.	3.3	38
11	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	5.8	147
12	Large-scale bioactivity analysis of the small-molecule assayed proteome. <i>PLoS ONE</i> , 2017, 12, e0171413.	1.1	4
13	bioassayR: Cross-Target Analysis of Small Molecule Bioactivity. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1237-1242.	2.5	13
14	systemPipeR: NGS workflow and report generation environment. <i>BMC Bioinformatics</i> , 2016, 17, 388.	1.2	178
15	Genomic and functional analysis of the host response to acute simian varicella infection in the lung. <i>Scientific Reports</i> , 2016, 6, 34164.	1.6	9
16	Acute Simian Varicella Virus Infection Causes Robust and Sustained Changes in Gene Expression in the Sensory Ganglia. <i>Journal of Virology</i> , 2016, 90, 10823-10843.	1.5	19
17	Transcriptomes of eight <i>Arabidopsis thaliana</i> accessions reveal core conserved, genotype- and organ-specific responses to flooding stress. <i>Plant Physiology</i> , 2016, 172, pp.00472.2016.	2.3	92
18	Alcohol Consumption Modulates Host Defense in Rhesus Macaques by Altering Gene Expression in Circulating Leukocytes. <i>Journal of Immunology</i> , 2016, 196, 182-195.	0.4	25

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19	Hairy and Groucho mediate the action of juvenile hormone receptor Methoprene-tolerant in gene repression. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E735-43.	3.3	55
20	A novel virus from <i>Macrosiphum euphorbiae</i> with similarities to members of the family Flaviviridae. Journal of General Virology, 2016, 97, 1261-1271.	1.3	25
21	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
22	Regulation of Gene Expression Patterns in Mosquito Reproduction. PLoS Genetics, 2015, 11, e1005450.	1.5	56
23	Translational dynamics revealed by genome-wide profiling of ribosome footprints in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E203-12.	3.3	367
24	Pathophysiologic and Transcriptomic Analyses of Viscerotropic Yellow Fever in a Rhesus Macaque Model. PLoS Neglected Tropical Diseases, 2014, 8, e3295.	1.3	54
25	Cheminformatic Analysis of High-Throughput Compound Screens. Methods in Molecular Biology, 2014, 1056, 145-157.	0.4	3
26	A high-resolution gene expression map of the <i>Arabidopsis</i> shoot meristem stem cell niche. Development (Cambridge), 2014, 141, 2735-2744.	1.2	110
27	Endomembrane Dissection Using Chemically Induced Bioactive Clusters. Methods in Molecular Biology, 2014, 1056, 159-168.	0.4	5
28	Isolation and Analysis of mRNAs from Specific Cell Types of Plants by Ribosome Immunopurification. Methods in Molecular Biology, 2013, 959, 277-302.	0.4	16
29	Juvenile hormone and its receptor, methoprene-tolerant, control the dynamics of mosquito gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2173-81.	3.3	124
30	fmcsR: mismatch tolerant maximum common substructure searching in R. Bioinformatics, 2013, 29, 2792-2794.	1.8	48
31	Gene Expression Analysis of Shoot Apical Meristem Cell Types. Methods in Molecular Biology, 2013, 959, 235-245.	0.4	2
32	Plant stem cell maintenance involves direct transcriptional repression of differentiation program. Molecular Systems Biology, 2013, 9, 654.	3.2	126
33	Linking genes of unknown function with abiotic stress responses by high-throughput phenotype screening. Physiologia Plantarum, 2013, 148, 322-333.	2.6	123
34	In Planta Expression or Delivery of Potato Aphid <i>Macrosiphum euphorbiae</i> Effectors <i>Me10</i> and <i>Me23</i> Enhances Aphid Fecundity. Molecular Plant-Microbe Interactions, 2013, 26, 67-74.	1.4	150
35	Microarray Analysis of Tomato's Early and Late Wound Response Reveals New Regulatory Targets for Leucine Aminopeptidase A. PLoS ONE, 2013, 8, e77889.	1.1	35
36	Decoding the Ubiquitin-Mediated Pathway of Arthropod Disease Vectors. PLoS ONE, 2013, 8, e78077.	1.1	16

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37	<i>Arabidopsis</i> LATERAL ORGAN BOUNDARIES negatively regulates brassinosteroid accumulation to limit growth in organ boundaries. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21146-21151.	3.3	167
38	WUSCHEL protein movement mediates stem cell homeostasis in the <i>Arabidopsis</i> shoot apex. Genes and Development, 2011, 25, 2025-2030.	2.7	522
39	ChemMine tools: an online service for analyzing and clustering small molecules. Nucleic Acids Research, 2011, 39, W486-W491.	6.5	377
40	SEED: efficient clustering of next-generation sequences. Bioinformatics, 2011, 27, 2502-2509.	1.8	54
41	Clusters of bioactive compounds target dynamic endomembrane networks in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17850-17855.	3.3	122
42	Accelerated similarity searching and clustering of large compound sets by geometric embedding and locality sensitive hashing. Bioinformatics, 2010, 26, 953-959.	1.8	34
43	Profiling translomes of discrete cell populations resolves altered cellular priorities during hypoxia in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18843-18848.	3.3	553
44	Gene expression map of the <i>Arabidopsis</i> shoot apical meristem stem cell niche. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4941-4946.	3.3	299
45	MODIFIED VACUOLE PHENOTYPE1 Is an Arabidopsis Myosinase-Associated Protein Involved in Endomembrane Protein Trafficking Â. Plant Physiology, 2009, 152, 120-132.	2.3	57
46	The Synthetic Elicitor 3,5-Dichloroanthranilic Acid Induces <i>NPR1</i>-Dependent and <i>NPR1</i>-Independent Mechanisms of Disease Resistance in Arabidopsis Â. Plant Physiology, 2009, 150, 333-347.	2.3	74
47	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. BMC Molecular Biology, 2008, 9, 6.	3.0	120
48	A maximum common substructure-based algorithm for searching and predicting drug-like compounds. Bioinformatics, 2008, 24, i366-i374.	1.8	150
49	ChemmineR: a compound mining framework for R. Bioinformatics, 2008, 24, 1733-1734.	1.8	296
50	Tomato Susceptibility to Root-Knot Nematodes Requires an Intact Jasmonic Acid Signaling Pathway. Molecular Plant-Microbe Interactions, 2008, 21, 1205-1214.	1.4	160
51	Expression analysis of Arabidopsis vacuolar sorting receptor 3 reveals a putative function in guard cells. Journal of Experimental Botany, 2008, 59, 1149-1161.	2.4	22
52	Annotating Genes of Known and Unknown Function by Large-Scale Coexpression Analysis Â. Plant Physiology, 2008, 147, 41-57.	2.3	162
53	Deciphering the Ubiquitin-Mediated Pathway in Apicomplexan Parasites: A Potential Strategy to Interfere with Parasite Virulence. PLoS ONE, 2008, 3, e2386.	1.1	80
54	What makes species unique? The contribution of proteins with obscure features. Genome Biology, 2006, 7, R57.	13.9	64

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55	ChemMine. A Compound Mining Database for Chemical Genomics. <i>Plant Physiology</i> , 2005, 138, 573-577.	2.3	61
56	Genome Cluster Database. A Sequence Family Analysis Platform for Arabidopsis and Rice. <i>Plant Physiology</i> , 2005, 138, 47-54.	2.3	45
57	Cloning and Characterization of MicroRNAs from Rice. <i>Plant Cell</i> , 2005, 17, 1397-1411.	3.1	462
58	Identification and characterization of endogenous small interfering RNAs from rice. <i>Nucleic Acids Research</i> , 2005, 33, 4443-4454.	6.5	92
59	The Cell Wall Navigator Database. A Systems-Based Approach to Organism-Unrestricted Mining of Protein Families Involved in Cell Wall Metabolism. <i>Plant Physiology</i> , 2004, 136, 3003-3008.	2.3	64
60	Switching desaturase enzyme specificity by alternate subcellular targeting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10266-10271.	3.3	87
61	Differential mRNA translation contributes to gene regulation under non-stress and dehydration stress conditions in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 38, 823-839.	2.8	283
62	The Vegetative Vacuole Proteome of <i>Arabidopsis thaliana</i> Reveals Predicted and Unexpected Proteins[W]. <i>Plant Cell</i> , 2004, 16, 3285-3303.	3.1	591
63	Towards a Modeling Infrastructure for Studying Plant Cells. <i>Plant Physiology</i> , 2003, 132, 410-414.	2.3	26