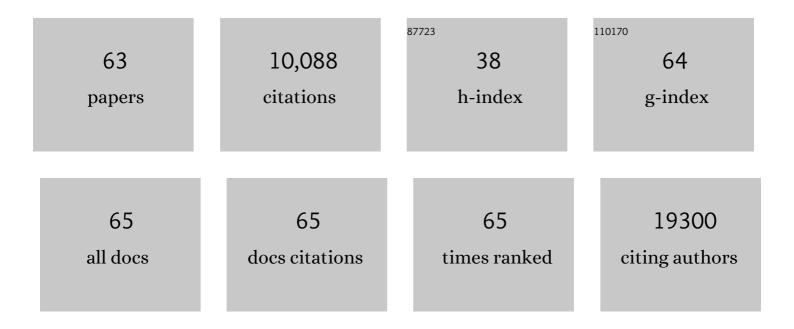
Thomas Girke

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7520852/publications.pdf Version: 2024-02-01



THOMAS CIDKE

#	Article	IF	CITATIONS
1	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
2	The Vegetative Vacuole Proteome of Arabidopsis thaliana Reveals Predicted and Unexpected Proteins[W]. Plant Cell, 2004, 16, 3285-3303.	3.1	591
3	Profiling translatomes 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
4	WUSCHEL protein movement mediates stem cell homeostasis in the <i>Arabidopsis</i> shoot apex. Genes and Development, 2011, 25, 2025-2030.	2.7	522
5	Cloning and Characterization of MicroRNAs from Rice. Plant Cell, 2005, 17, 1397-1411.	3.1	462
6	ChemMine tools: an online service for analyzing and clustering small molecules. Nucleic Acids Research, 2011, 39, W486-W491.	6.5	377
7	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
8	Gene expression map of the <i>Arabidopsis</i> shoot apical meristem stem cell niche. Proceedings of the United States of America, 2009, 106, 4941-4946.	3.3	299
9	ChemmineR: a compound mining framework for R. Bioinformatics, 2008, 24, 1733-1734.	1.8	296
10	Differential mRNA translation contributes to gene regulation under non-stress and dehydration stress conditions inArabidopsis thaliana. Plant Journal, 2004, 38, 823-839.	2.8	283
11	systemPipeR: NGS workflow and report generation environment. BMC Bioinformatics, 2016, 17, 388.	1.2	178
12	<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
13	Annotating Genes of Known and Unknown Function by Large-Scale Coexpression Analysis Â. Plant Physiology, 2008, 147, 41-57.	2.3	162
14	Tomato Susceptibility to Root-Knot Nematodes Requires an Intact Jasmonic Acid Signaling Pathway. Molecular Plant-Microbe Interactions, 2008, 21, 1205-1214.	1.4	160
15	A maximum common substructure-based algorithm for searching and predicting drug-like compounds. Bioinformatics, 2008, 24, i366-i374.	1.8	150
16	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
17	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
18	Plant stem cell maintenance involves direct transcriptional repression of differentiation program. Molecular Systems Biology, 2013, 9, 654.	3.2	126

THOMAS GIRKE

#	Article	IF	CITATIONS
19	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
20	Linking genes of unknown function with abiotic stress responses by highâ€ŧhroughput phenotype screening. Physiologia Plantarum, 2013, 148, 322-333.	2.6	123
21	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
22	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. BMC Molecular Biology, 2008, 9, 6.	3.0	120
23	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
24	Identification and characterization of endogenous small interfering RNAs from rice. Nucleic Acids Research, 2005, 33, 4443-4454.	6.5	92
25	Transcriptomes of eight Arabidopsis thaliana accessions reveal core conserved, genotype- and organ-specific responses to flooding stress. Plant Physiology, 2016, 172, pp.00472.2016.	2.3	92
26	Switching desaturase enzyme specificity by alternate subcellular targeting. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10266-10271.	3.3	87
27	Deciphering the Ubiquitin-Mediated Pathway in Apicomplexan Parasites: A Potential Strategy to Interfere with Parasite Virulence. PLoS ONE, 2008, 3, e2386.	1.1	80
28	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
29	The Cell Wall Navigator Database. A Systems-Based Approach to Organism-Unrestricted Mining of Protein Families Involved in Cell Wall Metabolism. Plant Physiology, 2004, 136, 3003-3008.	2.3	64
30	What makes species unique? The contribution of proteins with obscure features. Genome Biology, 2006, 7, R57.	13.9	64
31	ChemMine. A Compound Mining Database for Chemical Genomics. Plant Physiology, 2005, 138, 573-577.	2.3	61
32	MODIFIED VACUOLE PHENOTYPE1 Is an Arabidopsis Myrosinase-Associated Protein Involved in Endomembrane Protein Trafficking Â. Plant Physiology, 2009, 152, 120-132.	2.3	57
33	Regulation of Gene Expression Patterns in Mosquito Reproduction. PLoS Genetics, 2015, 11, e1005450.	1.5	56
34	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
35	SEED: efficient clustering of next-generation sequences. Bioinformatics, 2011, 27, 2502-2509.	1.8	54
36	Pathophysiologic and Transcriptomic Analyses of Viscerotropic Yellow Fever in a Rhesus Macaque Model. PLoS Neglected Tropical Diseases, 2014, 8, e3295.	1.3	54

THOMAS GIRKE

#	Article	IF	CITATIONS
37	fmcsR: mismatch tolerant maximum common substructure searching in R. Bioinformatics, 2013, 29, 2792-2794.	1.8	48
38	Genome Cluster Database. A Sequence Family Analysis Platform for Arabidopsis and Rice. Plant Physiology, 2005, 138, 47-54.	2.3	45
39	HOTAIRM1 IncRNA is downregulated in clear cell renal cell carcinoma and inhibits the hypoxia pathway. Cancer Letters, 2020, 472, 50-58.	3.2	41
40	Transcriptome-wide microRNA and target dynamics in the fat body during the gonadotrophic cycle ofAedes aegypti. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1895-E1903.	3.3	38
41	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
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	Gene regulatory networks shape developmental plasticity of root cell types under water extremes in rice. Developmental Cell, 2022, 57, 1177-1192.e6.	3.1	27
44	Towards a Modeling Infrastructure for Studying Plant Cells. Plant Physiology, 2003, 132, 410-414.	2.3	26
45	Alcohol Consumption Modulates Host Defense in Rhesus Macaques by Altering Gene Expression in Circulating Leukocytes. Journal of Immunology, 2016, 196, 182-195.	0.4	25
46	A novel virus from Macrosiphum euphorbiae with similarities to members of the family Flaviviridae. Journal of General Virology, 2016, 97, 1261-1271.	1.3	25
47	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
48	Acute Simian Varicella Virus Infection Causes Robust and Sustained Changes in Gene Expression in the Sensory Ganglia. Journal of Virology, 2016, 90, 10823-10843.	1.5	19
49	<i>signatureSearch</i> : environment for gene expression signature searching and functional interpretation. Nucleic Acids Research, 2020, 48, e124-e124.	6.5	17
50	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
51	Decoding the Ubiquitin-Mediated Pathway of Arthropod Disease Vectors. PLoS ONE, 2013, 8, e78077.	1.1	16
52	Sequence analysis of the potato aphid Macrosiphum euphorbiae transcriptome identified two new viruses. PLoS ONE, 2018, 13, e0193239.	1.1	14
53	bioassayR: Cross-Target Analysis of Small Molecule Bioactivity. Journal of Chemical Information and Modeling, 2016, 56, 1237-1242.	2.5	13
54	Global isoform-specific transcript alterations and deregulated networks in clear cell renal cell carcinoma. Oncotarget, 2018, 9, 23670-23680.	0.8	13

THOMAS GIRKE

#	Article	IF	CITATIONS
55	High-throughput small molecule screening reveals Nrf2-dependent and -independent pathways of cellular stress resistance. Science Advances, 2020, 6, .	4.7	12
56	Experimental Acute Exposure to Thirdhand Smoke and Changes in the Human Nasal Epithelial Transcriptome. JAMA Network Open, 2019, 2, e196362.	2.8	11
57	Genomic and functional analysis of the host response to acute simian varicella infection in the lung. Scientific Reports, 2016, 6, 34164.	1.6	9
58	Transcriptomic Evidence That Switching from Tobacco to Electronic Cigarettes Does Not Reverse Damage to the Respiratory Epithelium. Toxics, 2022, 10, 370.	1.6	7
59	Endomembrane Dissection Using Chemically Induced Bioactive Clusters. Methods in Molecular Biology, 2014, 1056, 159-168.	0.4	5
60	Genetic Support for Longevity-Enhancing Drug Targets: Issues, Preliminary Data, and Future Directions. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, S61-S71.	1.7	4
61	Large-scale bioactivity analysis of the small-molecule assayed proteome. PLoS ONE, 2017, 12, e0171413.	1.1	4
62	Cheminformatic Analysis of High-Throughput Compound Screens. Methods in Molecular Biology, 2014, 1056, 145-157.	0.4	3
63	Gene Expression Analysis of Shoot Apical Meristem Cell Types. Methods in Molecular Biology, 2013, 959, 235-245.	0.4	2