## Philip Zimmermann

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6935390/publications.pdf

Version: 2024-02-01

26 papers 7,301 citations

331538
21
h-index

25 g-index

26 all docs

 $\begin{array}{c} 26 \\ \\ \text{docs citations} \end{array}$ 

26 times ranked 10844 citing authors

#	Article	IF	CITATIONS
1	GENEVESTIGATOR. Arabidopsis Microarray Database and Analysis Toolbox. Plant Physiology, 2004, 136, 2621-2632.	2.3	2,232
2	Genevestigator V3: A Reference Expression Database for the Meta-Analysis of Transcriptomes. Advances in Bioinformatics, 2008, 2008, 1-5.	5.7	1,692
3	A systematic comparison and evaluation of biclustering methods for gene expression data. Bioinformatics, 2006, 22, 1122-1129.	1.8	782
4	Genome-Scale Proteomics Reveals <i>Arabidopsis thaliana</i> Gene Models and Proteome Dynamics. Science, 2008, 320, 938-941.	6.0	490
5	Genome-Wide Analysis of Hydrogen Peroxide-Regulated Gene Expression in Arabidopsis Reveals a High Light-Induced Transcriptional Cluster Involved in Anthocyanin Biosynthesis Â. Plant Physiology, 2005, 139, 806-821.	2.3	476
6	Sparse graphical Gaussian modeling of the isoprenoid gene network in Arabidopsis thaliana. Genome Biology, 2004, 5, R92.	13.9	290
7	RefGenes: identification of reliable and condition specific reference genes for RT-qPCR data normalization. BMC Genomics, 2011, 12, 156.	1.2	260
8	Gene-expression analysis and network discovery using Genevestigator. Trends in Plant Science, 2005, 10, 407-409.	4.3	254
9	Genevestigator Transcriptome Meta-Analysis and Biomarker Search using Rice and Barley Gene Expression Databases. Molecular Plant, 2008, 1, 851-857.	3.9	98
10	Gene Expression Analysis, Proteomics, and Network Discovery. Plant Physiology, 2010, 152, 402-410.	2.3	97
11	Engineering the root-soil interface via targeted expression of a synthetic phytase gene in trichoblasts. Plant Biotechnology Journal, 2003, $1$ , 353-360.	4.1	87
12	Largeâ€scale gene expression profiling data for the model moss <i><scp>P</scp>hyscomitrella patens</i> aid understanding of developmental progression, culture and stress conditions. Plant Journal, 2014, 79, 530-539.	2.8	82
13	The Arabidopsis Rho of Plants GTPase AtROP6 Functions in Developmental and Pathogen Response Pathways   Â. Plant Physiology, 2013, 161, 1172-1188.	2.3	77
14	Expression analysis suggests novel roles for the plastidic phosphate transporter Pht2;1 in auto- and heterotrophic tissues in potato and Arabidopsis. Plant Journal, 2004, 39, 13-28.	2.8	73
15	MIAME/Plant - adding value to plant microarrray experiments. Plant Methods, 2006, 2, 1.	1.9	61
16	The Expression of an Extensin-Like Protein Correlates with Cellular Tip Growth in Tomato. Plant Physiology, 2002, 128, 911-923.	2.3	54
17	Effects of timing and duration of brackish irrigation water on fruit yield and quality of late summer melons. Agricultural Water Management, 2005, 74, 123-134.	2.4	35
18	Exploring the role of sphingolipid machinery during the epithelial to mesenchymal transition program using an integrative approach. Oncotarget, 2016, 7, 22295-22323.	0.8	27

#	Article	lF	CITATIONS
19	Integrative genome-wide expression profiling identifies three distinct molecular subgroups of renal cell carcinoma with different patient outcome. BMC Cancer, 2012, 12, 310.	1.1	25
20	Web-based analysis of the mouse transcriptome using Genevestigator. BMC Bioinformatics, 2006, 7, 311.	1.2	24
21	ExpressionData - A public resource of high quality curated datasets representing gene expression across anatomy, development and experimental conditions. BioData Mining, 2014, 7, 18.	2.2	22
22	Global regulatory architecture of human, mouse and rat tissue transcriptomes. BMC Genomics, 2013, 14, 716.	1.2	19
23	AID/APOBEC-network reconstruction identifies pathways associated with survival in ovarian cancer. BMC Genomics, 2016, 17, 643.	1.2	19
24	Interrelations of Sphingolipid and Lysophosphatidate Signaling with Immune System in Ovarian Cancer. Computational and Structural Biotechnology Journal, 2019, 17, 537-560.	1.9	19
25	Network analysis of systems elements. , 2007, 97, 331-351.		5
26	A Multilevel Gamma-Clustering Layout Algorithm for Visualization of Biological Networks. Advances in Bioinformatics, 2013, 2013, 1-10.	5 <b>.</b> 7	1