## William L Poehlman

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4148216/publications.pdf

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1307594 1199594 14 254 7 12 citations g-index h-index papers 15 15 15 248 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	<scp>RNA</scp> â€seq analyses of <i>Arabidopsis thaliana</i> seedlings after exposure to blueâ€light phototropic stimuli in microgravity. American Journal of Botany, 2019, 106, 1466-1476.	1.7	53
2	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific Reports, 2017, 7, 8617.	3.3	44
3	RNAseq Analysis of the Response of Arabidopsis thaliana to Fractional Gravity Under Blue-Light Stimulation During Spaceflight. Frontiers in Plant Science, 2019, 10, 1529.	3.6	42
4	The Evolution of an Invasive Plant, Sorghum halepense L. (â€Johnsongrass'). Frontiers in Genetics, 2020, 11, 317.	2.3	30
5	OSG-GEM: Gene Expression Matrix Construction Using the Open Science Grid. Bioinformatics and Biology Insights, 2016, 10, BBI.S38193.	2.0	18
6	Discovery and validation of a glioblastoma co-expressed gene module. Oncotarget, 2018, 9, 10995-11008.	1.8	15
7	Linking Binary Gene Relationships to Drivers of Renal Cell Carcinoma Reveals Convergent Function in Alternate Tumor Progression Paths. Scientific Reports, 2019, 9, 2899.	3.3	13
8	Sorting Five Human Tumor Types Reveals Specific Biomarkers and Background Classification Genes. Scientific Reports, 2018, 8, 8180.	3.3	8
9	Integrity Protection for Scientific Workflow Data. , 2019, , .		7
10	Identifying Temporally Regulated Root Nodulation Biomarkers Using Time Series Gene Co-Expression Network Analysis. Frontiers in Plant Science, 2019, 10, 1409.	3.6	7
11	OSG-KINC: High-throughput gene co-expression network construction using the open science grid., 2017,,.		6
12	Time Series Transcriptome Analysis in Medicago truncatula Shoot and Root Tissue During Early Nodulation. Frontiers in Plant Science, 2022, 13, 861639.	3.6	5
13	Exploration into biomarker potential of region-specific brain gene co-expression networks. Scientific Reports, 2020, 10, 17089.	3.3	4
14	Moving Just Enough Deep Sequencing Data to Get the Job Done. Bioinformatics and Biology Insights, 2019, 13, 117793221985635.	2.0	2