Daniel A Jacobson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7096072/publications.pdf

Version: 2024-02-01

59 papers 2,320 citations

304743

22

h-index

243625 44 g-index

78 all docs 78 docs citations

78 times ranked 4086 citing authors

#	Article	IF	Citations
1	Response to comment on $\hat{a}\in SARS$ -CoV-2 suppresses anticoagulant and fibrinolytic gene expression in the lung $\hat{a}\in M$. ELife, 2022, 11 , .	6.0	1
2	Protoplast fusion in Bacillus species produces frequent, unbiased, genome-wide homologous recombination. Nucleic Acids Research, 2022, , .	14.5	4
3	NF-ÎB perturbation reveals unique immunomodulatory functions in Prx1 ⁺ fibroblasts that promote development of atopic dermatitis. Science Translational Medicine, 2022, 14, eabj0324.	12.4	22
4	Antiviral Strategies Against SARS-CoV-2: A Systems Biology Approach. Methods in Molecular Biology, 2022, 2452, 317-351.	0.9	1
5	Potential Pathogenicity Determinants Identified from Structural Proteomics of SARS-CoV and SARS-CoV-2. Molecular Biology and Evolution, 2021, 38, 702-715.	8.9	23
6	Image-Based Methods to Score Fungal Pathogen Symptom Progression and Severity in Excised Arabidopsis Leaves. Plants, 2021, 10, 158.	3.5	15
7	Early initiation of prophylactic anticoagulation for prevention of coronavirus disease 2019 mortality in patients admitted to hospital in the United States: cohort study. BMJ, The, 2021, 372, n311.	6.0	166
8	Characterization of aromatic acid/proton symporters in Pseudomonas putida KT2440 toward efficient microbial conversion of lignin-related aromatics. Metabolic Engineering, 2021, 64, 167-179.	7.0	24
9	SARS-CoV-2 suppresses anticoagulant and fibrinolytic gene expression in the lung. ELife, 2021, 10, .	6.0	46
10	Integration of evidence across human and model organism studies: A meeting report. Genes, Brain and Behavior, 2021, 20, e12738.	2.2	12
11	COVID-19 Insights Partnership: Leveraging big data from the Department of Veterans Affairs and supercomputers at the Department of Energy under the public health authority. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1578-1581.	4.4	2
12	A vision of immuno-oncology: the Siena think tank of the Italian network for tumor biotherapy (NIBIT) foundation. Journal of Experimental and Clinical Cancer Research, 2021, 40, 240.	8.6	3
13	Quinoa Phenotyping Methodologies: An International Consensus. Plants, 2021, 10, 1759.	3.5	24
14	Polypharmacy-associated risk of hospitalisation among people ageing with and without HIV: an observational study. The Lancet Healthy Longevity, 2021, 2, e639-e650.	4.6	18
15	Reusability First: Toward FAIR Workflows. , 2021, , .		9
16	A k-mer based approach for classifying viruses without taxonomy identifies viral associations in human autism and plant microbiomes. Computational and Structural Biotechnology Journal, 2021, 19, 5911-5919.	4.1	10
17	Genome-Wide Association Study of Wood Anatomical and Morphological Traits in Populus trichocarpa. Frontiers in Plant Science, 2020, 11, 545748.	3.6	21
18	Isoflurane anesthesia disrupts the cortical metabolome. Journal of Neurophysiology, 2020, 124, 2012-2021.	1.8	5

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19	Can exascale computing and explainable artificial intelligence applied to plant biology deliver on the United Nations sustainable development goals?. Current Opinion in Biotechnology, 2020, 61, 217-225.	6.6	32
20	Neurotransmitter networks in mouse prefrontal cortex are reconfigured by isoflurane anesthesia. Journal of Neurophysiology, 2020, 123, 2285-2296.	1.8	10
21	The Phylogenetic Roots of Addiction: Compulsive Drug Seeking, Natural and Drug-Sensitive Reward, and the Acquisition of Learned Habits. Brain, Behavior and Evolution, 2020, 95, 1-5.	1.7	0
22	Network Modeling of Complex Data Sets. Methods in Molecular Biology, 2020, 2096, 197-215.	0.9	5
23	Potentially adaptive SARS-CoV-2 mutations discovered with novel spatiotemporal and explainable Al models. Genome Biology, 2020, 21, 304.	8.8	55
24	Development and validation of a 30-day mortality index based on pre-existing medical administrative data from 13,323 COVID-19 patients: The Veterans Health Administration COVID-19 (VACO) Index. PLoS ONE, 2020, 15, e0241825.	2.5	79
25	A mechanistic model and therapeutic interventions for COVID-19 involving a RAS-mediated bradykinin storm. ELife, 2020, 9, .	6.0	296
26	Title is missing!. , 2020, 15, e0241825.		O
27	Title is missing!. , 2020, 15, e0241825.		0
28	Title is missing!. , 2020, 15, e0241825.		0
29	Title is missing!. , 2020, 15, e0241825.		O
30	Mediation of plant–mycorrhizal interaction by a lectin receptor-like kinase. Nature Plants, 2019, 5, 676-680.	9.3	42
31	Data Integration in Poplar: †Omics Layers and Integration Strategies. Frontiers in Genetics, 2019, 10, 874.	2.3	15
32	Finding New Cell Wall Regulatory Genes in Populus trichocarpa Using Multiple Lines of Evidence. Frontiers in Plant Science, 2019, 10, 1249.	3.6	13
33	Plant Host-Associated Mechanisms for Microbial Selection. Frontiers in Plant Science, 2019, 10, 862.	3.6	139
34	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. Frontiers in Genetics, 2019, 10, 487.	2.3	11
35	Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. Trends in Biotechnology, 2019, 37, 1217-1235.	9.3	134
36	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. Frontiers in Genetics, 2019, 10, 417.	2.3	20

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37	Differences in resource use lead to coexistence of seed-transmitted microbial populations. Scientific Reports, 2019, 9, 6648.	3.3	17
38	Multitrait genomeâ€wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. New Phytologist, 2019, 223, 293-309.	7.3	85
39	Parallel accelerated Custom Correlation Coefficient calculations for genomics applications. Parallel Computing, 2019, 84, 15-23.	2.1	12
40	Fungal-Bacterial Networks in the Populus Rhizobiome Are Impacted by Soil Properties and Host Genotype. Frontiers in Microbiology, 2019, 10, 481.	3.5	71
41	Epigenetic effects of paternal cocaine on reward stimulus behavior and accumbens gene expression in mice. Behavioural Brain Research, 2019, 367, 68-81.	2.2	14
42	A High-Performance Computing Implementation of Iterative Random Forest for the Creation of Predictive Expression Networks. Genes, 2019, 10, 996.	2.4	26
43	The Sphagnome Project: enabling ecological and evolutionary insights through a genusâ€level sequencing project. New Phytologist, 2018, 217, 16-25.	7.3	54
44	Attacking the Opioid Epidemic: Determining the Epistatic and Pleiotropic Genetic Architectures for Chronic Pain and Opioid Addiction. , 2018 , , .		29
45	High Throughput Screening Technologies in Biomass Characterization. Frontiers in Energy Research, 2018, 6, .	2.3	28
46	Hardwood Tree Genomics: Unlocking Woody Plant Biology. Frontiers in Plant Science, 2018, 9, 1799.	3.6	50
47	Phytobiome and Transcriptional Adaptation of <i>Populus deltoides</i> to Acute Progressive Drought and Cyclic Drought. Phytobiomes Journal, 2018, 2, 249-260.	2.7	23
48	Defining the genetic components of callus formation: A GWAS approach. PLoS ONE, 2018, 13, e0202519.	2.5	27
49	A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a <i>Populus</i> ANGUSTIFOLIA Protein. G3: Genes, Genomes, Genetics, 2018, 8, 2631-2641.	1.8	9
50	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. Frontiers in Energy Research, 2018, 6, .	2.3	32
51	Parallel accelerated vector similarity calculations for genomics applications. Parallel Computing, 2018, 75, 130-145.	2.1	16
52	The Kalancho \tilde{A} « genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications, 2017, 8, 1899.	12.8	159
53	Network Metamodeling: Effect of Correlation Metric Choice on Phylogenomic and Transcriptomic Network Topology. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 143-183.	1.1	27
54	Sensory effect of acetaldehyde on the perception of 3-mercaptohexan-1-ol and 3-isobutyl-2-methoxypyrazine. Australian Journal of Grape and Wine Research, 2016, 22, 197-204.	2.1	17

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55	Sequence-based Analysis of the Vitis vinifera L. cv Cabernet Sauvignon Grape Must Mycobiome in Three South African Vineyards Employing Distinct Agronomic Systems. Frontiers in Microbiology, 2015, 6, 1358.	3.5	64
56	3-way Networks: Application of Hypergraphs for Modelling Increased Complexity in Comparative Genomics. PLoS Computational Biology, 2015, 11, e1004079.	3.2	29
57	Sensory interaction between 3-mercaptohexan-1-ol, 3-isobutyl-2-methoxypyrazine and oxidation-related compounds. Australian Journal of Grape and Wine Research, 2015, 21, 179-188.	2.1	25
58	Sensory interaction between 3-mercaptohexan-1-ol and 2-isobutyl-3-methoxypyrazine in dearomatised Sauvignon Blanc wine. Australian Journal of Grape and Wine Research, 2014, 20, 178-185.	2.1	26
59	The Vineyard Yeast Microbiome, a Mixed Model Microbial Map. PLoS ONE, 2012, 7, e52609.	2.5	176