Astrid Junker

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4624576/publications.pdf

Version: 2024-02-01

42	1,913	361296	276775
papers	citations	20 h-index	41 g-index

44	44	44	3196
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Opportunities and limits of controlled-environment plant phenotyping for climate response traits. Theoretical and Applied Genetics, 2022, 135, 1-16.	1.8	28
2	From data to knowledge â€“ big data needs stewardship, a plant phenomics perspective. Plant Journal, 2022, 111, 335-347.	2.8	11
3	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. Briefings in Bioinformatics, 2021, 22, .	3.2	18
4	Dynamics of Maize Vegetative Growth and Drought Adaptability Using Image-Based Phenotyping Under Controlled Conditions. Frontiers in Plant Science, 2021, 12, 652116.	1.7	13
5	The Arabidopsis AAC Proteins CIL and CIA2 Are Sub-functionalized Paralogs Involved in Chloroplast Development. Frontiers in Plant Science, 2021, 12, 681375.	1.7	6
6	Fully-automated root image analysis (faRIA). Scientific Reports, 2021, 11, 16047.	1.6	15
7	Mutation of the ALBOSTRIANS Ohnologous Gene HvCMF3 Impairs Chloroplast Development and Thylakoid Architecture in Barley. Frontiers in Plant Science, 2021, 12, 732608.	1.7	7
8	A two-step registration-classification approach to automated segmentation of multimodal images for high-throughput greenhouse plant phenotyping. Plant Methods, 2020, 16, 95.	1.9	6
9	Image Phenotyping of Spring Barley (Hordeum vulgare L.) RIL Population Under Drought: Selection of Traits and Biological Interpretation. Frontiers in Plant Science, 2020, 11, 743.	1.7	8
10	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	3.5	84
11	isa4j: a scalable Java library for creating ISA-Tab metadata. F1000Research, 2020, 9, 1388.	0.8	4
12	The on-premise data sharing infrastructure e!DAL: Foster FAIR data for faster data acquisition. GigaScience, 2020, 9, .	3.3	11
13	Image-Derived Traits Related to Mid-Season Growth Performance of Maize Under Nitrogen and Water Stress. Frontiers in Plant Science, 2019, 10, 814.	1.7	18
14	Semi-automated Root Image Analysis (saRIA). Scientific Reports, 2019, 9, 19674.	1.6	33
15	Demystifying roots: A need for clarification and extended concepts in root phenotyping. Plant Science, 2019, 282, 11-13.	1.7	28
16	Programmatic Access to FAIRified Digital Plant Genetic Resources. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	9
17	Phenotyping roots in darkness: disturbance-free root imaging with near infrared illumination. Functional Plant Biology, 2018, 45, 400.	1.1	17
18	Identification of Rapeseed (Brassica napus) Cultivars With a High Tolerance to Boron-Deficient Conditions. Frontiers in Plant Science, 2018, 9, 1142.	1.7	31

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19	Genetic variation of growth dynamics in maize (Zea mays L.) revealed through automated nonâ€invasive phenotyping. Plant Journal, 2017, 89, 366-380.	2.8	85
20	Establishment of integrated protocols for automated high throughput kinetic chlorophyll fluorescence analyses. Plant Methods, 2017, 13, 54.	1.9	66
21	PGP repository: a plant phenomics and genomics data publication infrastructure. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw033.	1.4	90
22	Measures for interoperability of phenotypic data: minimum information requirements and formatting. Plant Methods, 2016, 12, 44.	1.9	109
23	Quantitative monitoring of Arabidopsis thaliana growth and development using high-throughput plant phenotyping. Scientific Data, 2016, 3, 160055.	2.4	30
24	Nonâ€canonical structure, function and phylogeny of the B sister MADS â€box gene O s MADS 30 of rice () Tj ETQq0 0 0 rgBT /Overlock	2.8	16
25	Phenotypic and metabolic responses to drought and salinity of four contrasting lentil accessions. Journal of Experimental Botany, 2015, 66, 5467-5480.	2.4	146
26	AtRD22 and AtUSPL1, Members of the Plant-Specific BURP Domain Family Involved in Arabidopsis thaliana Drought Tolerance. PLoS ONE, 2014, 9, e110065.	1.1	74
27	Flux Balance Analysis as an Alternative Method to Estimate Fluxes Without Labeling. Methods in Molecular Biology, 2014, 1090, 281-299.	0.4	1
28	Optimizing experimental procedures for quantitative evaluation of crop plant performance in high throughput phenotyping systems. Frontiers in Plant Science, 2014, 5, 770.	1.7	187
29	Flux Visualization Using VANTED/FluxMap. Methods in Molecular Biology, 2014, 1191, 225-233.	0.4	2
30	Multiscale Metabolic Modeling: Dynamic Flux Balance Analysis on a Whole-Plant Scale. Plant Physiology, 2013, 163, 637-647.	2.3	130
31	Visual Analysis of Transcriptome Data in the Context of Anatomical Structures and Biological Networks. Frontiers in Plant Science, 2012, 3, 252.	1.7	6
32	MetaCrop 2.0: managing and exploring information about crop plant metabolism. Nucleic Acids Research, 2012, 40, D1173-D1177.	6.5	56
33	Toward the identification and regulation of the Arabidopsis thaliana ABI3 regulon. Nucleic Acids Research, 2012, 40, 8240-8254.	6.5	145
34	Multifunctionality of the LEC1 transcription factor during plant development. Plant Signaling and Behavior, 2012, 7, 1718-1720.	1.2	20
35	Creating interactive, web-based and data-enriched maps with the Systems Biology Graphical Notation. Nature Protocols, 2012, 7, 579-593.	5.5	26
36	FluxMap: A VANTED add-on for the visual exploration of flux distributions in biological networks. BMC Systems Biology, 2012, 6, 33.	3.0	31

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37	Wiring diagrams in biology: towards the standardized representation of biological information. Trends in Biotechnology, 2012, 30, 555-557.	4.9	13
38	VANTED v2: a framework for systems biology applications. BMC Systems Biology, 2012, 6, 139.	3.0	158
39	Elongationâ€related functions of LEAFY COTYLEDON1 during the development of Arabidopsis thaliana. Plant Journal, 2012, 71, 427-442.	2.8	133
40	Synthetic Gene Networks in Plant Systems. Methods in Molecular Biology, 2012, 813, 343-358.	0.4	3
41	Novel developments in SBGN-ED and applications. Nature Precedings, 2011, , .	0.1	0
42	An engineer's view on regulation of seed development. Trends in Plant Science, 2010, 15, 303-307.	4.3	33