Astrid Junker

List of Publications by Year
in descending order

42 papers	1,913 citations	361296 20 h-index	276775 41 g-index
44 all docs	44 docs citations	44 times ranked	3196 citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	VANTED v2: a framework for systems biology applications. BMC Systems Biology, 2012, 6, 139.	3.0	158
3	Phenotypic and metabolic responses to drought and salinity of four contrasting lentil accessions. Journal of Experimental Botany, 2015, 66, 5467-5480.	2.4	146
4	Toward the identification and regulation of the Arabidopsis thaliana ABI3 regulon. Nucleic Acids Research, 2012, 40, 8240-8254.	6.5	145
5	Elongation-related functions of LEAFY COTYLEDON1 during the development of *Arabidopsis thaliana*. Plant Journal, 2012, 71, 427-442.	2.8	133
6	Multiscale Metabolic Modeling: Dynamic Flux Balance Analysis on a Whole-Plant Scale. Plant Physiology, 2013, 163, 637-647.	2.3	130
7	Measures for interoperability of phenotypic data: minimum information requirements and formatting. Plant Methods, 2016, 12, 44.	1.9	109
8	PGP repository: a plant phenomics and genomics data publication infrastructure. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw033.	1.4	90
9	Genetic variation of growth dynamics in maize (*Zea mays* L.) revealed through automated non-invasive phenotyping. Plant Journal, 2017, 89, 366-380.	2.8	85
10	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	3.5	84
11	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
12	Establishment of integrated protocols for automated high throughput kinetic chlorophyll fluorescence analyses. Plant Methods, 2017, 13, 54.	1.9	66
13	MetaCrop 2.0: managing and exploring information about crop plant metabolism. Nucleic Acids Research, 2012, 40, D1173-D1177.	6.5	56
14	An engineer's view on regulation of seed development. Trends in Plant Science, 2010, 15, 303-307.	4.3	33
15	Semi-automated Root Image Analysis (saRIA). Scientific Reports, 2019, 9, 19674.	1.6	33
16	FluxMap: A VANTED add-on for the visual exploration of flux distributions in biological networks. BMC Systems Biology, 2012, 6, 33.	3.0	31
17	Identification of Rapeseed (Brassica napus) Cultivars With a High Tolerance to Boron-Deficient Conditions. Frontiers in Plant Science, 2018, 9, 1142.	1.7	31
18	Quantitative monitoring of Arabidopsis thaliana growth and development using high-throughput plant phenotyping. Scientific Data, 2016, 3, 160055.	2.4	30

#	Article	IF	Citations
19	Demystifying roots: A need for clarification and extended concepts in root phenotyping. Plant Science, 2019, 282, 11-13.	1.7	28
20	Opportunities and limits of controlled-environment plant phenotyping for climate response traits. Theoretical and Applied Genetics, 2022, 135, 1-16.	1.8	28
21	Creating interactive, web-based and data-enriched maps with the Systems Biology Graphical Notation. Nature Protocols, 2012, 7, 579-593.	5.5	26
22	Multifunctionality of the LEC1 transcription factor during plant development. Plant Signaling and Behavior, 2012, 7, 1718-1720.	1.2	20
23	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
24	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
25	Phenotyping roots in darkness: disturbance-free root imaging with near infrared illumination. Functional Plant Biology, 2018, 45, 400.	1.1	17
26	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
27	Fully-automated root image analysis (faRIA). Scientific Reports, 2021, 11, 16047.	1.6	15
28	Wiring diagrams in biology: towards the standardized representation of biological information. Trends in Biotechnology, 2012, 30, 555-557.	4.9	13
29	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
30	The on-premise data sharing infrastructure e!DAL: Foster FAIR data for faster data acquisition. GigaScience, 2020, 9, .	3.3	11
31	From data to knowledge â€" big data needs stewardship, a plant phenomics perspective. Plant Journal, 2022, 111, 335-347.	2.8	11
32	Programmatic Access to FAIRified Digital Plant Genetic Resources. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	9
33	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
34	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
35	Visual Analysis of Transcriptome Data in the Context of Anatomical Structures and Biological Networks. Frontiers in Plant Science, 2012, 3, 252.	1.7	6
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	isa4j: a scalable Java library for creating ISA-Tab metadata. F1000Research, 2020, 9, 1388.	0.8	4
39	Synthetic Gene Networks in Plant Systems. Methods in Molecular Biology, 2012, 813, 343-358.	0.4	3
40	Flux Visualization Using VANTED/FluxMap. Methods in Molecular Biology, 2014, 1191, 225-233.	0.4	2
41	Flux Balance Analysis as an Alternative Method to Estimate Fluxes Without Labeling. Methods in Molecular Biology, 2014, 1090, 281-299.	0.4	1
42	Novel developments in SBGN-ED and applications. Nature Precedings, 2011, , .	0.1	0