

Bettina Berger

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68 papers	2,773 citations	24 h-index	52 g-index
71 ext. papers	3,542 ext. citations	5.4 avg, IF	5.18 L-index

#	Paper	IF	Citations
68	Investigating the effects of elevated temperature on salinity tolerance traits in grapevine rootstocks using high-throughput phenotyping. <i>Australian Journal of Grape and Wine Research</i> , 2022 , 28, 276-291	2.4	1
67	Sensor-based phenotyping of above-ground plant-pathogen interactions.. <i>Plant Methods</i> , 2022 , 18, 35	5.8	1
66	Identifying the genetic control of salinity tolerance in the bread wheat landrace Mocho de Espiga Branca. <i>Functional Plant Biology</i> , 2021 , 48, 1148-1160	2.7	1
65	Integrating Ecological Stoichiometry to Understand Nutrient Limitation and Potential for Competition in Mixed Pasture Assemblages. <i>Journal of Soil Science and Plant Nutrition</i> , 2021 , 21, 2489-2500	3.3	1
64	Identification of salt tolerance QTL in a wheat RIL mapping population using destructive and non-destructive phenotyping. <i>Functional Plant Biology</i> , 2021 , 48, 131-140	2.7	9
63	Evaluation of commercial composts and potting mixes and their ability to support arbuscular mycorrhizal fungi with maize (<i>Zea mays</i>) as host plant. <i>Waste Management</i> , 2021 , 134, 187-196	8.6	2
62	Genome-wide association study reveals the genetic complexity of fructan accumulation patterns in barley grain. <i>Journal of Experimental Botany</i> , 2021 , 72, 2383-2402	7	5
61	Smoothing and extraction of traits in the growth analysis of noninvasive phenotypic data. <i>Plant Methods</i> , 2020 , 16, 36	5.8	10
60	High-throughput phenotyping reveals growth of <i>Medicago truncatula</i> is positively affected by arbuscular mycorrhizal fungi even at high soil phosphorus availability. <i>Plants People Planet</i> , 2020 , 3, 600	4.1	3
59	High-throughput, image-based phenotyping reveals nutrient-dependent growth facilitation in a grass-legume mixture. <i>PLoS ONE</i> , 2020 , 15, e0239673	3.7	2
58	Greenhouse Spatial Effects Detected in the Barley (L.) Epigenome Underlie Stochasticity of DNA Methylation. <i>Frontiers in Plant Science</i> , 2020 , 11, 553907	6.2	3
57	A single nucleotide substitution in TaHKT1;5-D controls shoot Na accumulation in bread wheat. <i>Plant, Cell and Environment</i> , 2020 , 43, 2158-2171	8.4	11
56	Hyperspectral imaging and 3D technologies for plant phenotyping: From satellite to close-range sensing. <i>Computers and Electronics in Agriculture</i> , 2020 , 175, 105621	6.5	24
55	Approaches, applications, and future directions for hyperspectral vegetation studies: An emphasis on yield-limiting factors in wheat. <i>The Plant Phenome Journal</i> , 2020 , 3, e20007	5	15
54	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages. <i>PLoS ONE</i> , 2020 , 15, e0236037	3.7	11
53	The Performances of Hyperspectral Sensors for Proximal Sensing of Nitrogen Levels in Wheat. <i>Sensors</i> , 2020 , 20,	3.8	4
52	Effect of Rice Constitutive Overexpression on Ascorbate Concentration, Stress Tolerance, and Iron Bioavailability in Rice. <i>Frontiers in Plant Science</i> , 2020 , 11, 595439	6.2	6

51	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages 2020 , 15, e0236037		
50	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages 2020 , 15, e0236037		
49	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages 2020 , 15, e0236037		
48	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages 2020 , 15, e0236037		
47	High-throughput, image-based phenotyping reveals nutrient-dependent growth facilitation in a grass-legume mixture 2020 , 15, e0239673		
46	High-throughput, image-based phenotyping reveals nutrient-dependent growth facilitation in a grass-legume mixture 2020 , 15, e0239673		
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44	High-throughput, image-based phenotyping reveals nutrient-dependent growth facilitation in a grass-legume mixture 2020 , 15, e0239673		
43	Genome-wide association of barley plant growth under drought stress using a nested association mapping population. <i>BMC Plant Biology</i> , 2019 , 19, 134	5.3	35
42	Resource allocation to growth or luxury consumption drives mycorrhizal responses. <i>Ecology Letters</i> , 2019 , 22, 1757-1766	10	13
41	Using High-Throughput Phenotyping to Explore Growth Responses to Mycorrhizal Fungi and Zinc in Three Plant Species. <i>Plant Phenomics</i> , 2019 , 2019, 1-12	7	
40	Using High-Throughput Phenotyping to Explore Growth Responses to Mycorrhizal Fungi and Zinc in Three Plant Species. <i>Plant Phenomics</i> , 2019 , 2019, 5893953	7	13
39	The Development of Hyperspectral Distribution Maps to Predict the Content and Distribution of Nitrogen and Water in Wheat (). <i>Frontiers in Plant Science</i> , 2019 , 10, 1380	6.2	32
38	High-throughput 3D modelling to dissect the genetic control of leaf elongation in barley (<i>Hordeum vulgare</i>). <i>Plant Journal</i> , 2019 , 98, 555-570	6.9	9
37	Mapping of novel salt tolerance QTL in an Excalibur [Kukri doubled haploid wheat population. <i>Theoretical and Applied Genetics</i> , 2018 , 131, 2179-2196	6	39
36	Tackling Nitrogen Use Efficiency in Cereal Crops Using High-Throughput Phenotyping 2018 , 121-139		2
35	Salt Stress Induces Non-CG Methylation in Coding Regions of Barley Seedlings (<i>Hordeum vulgare</i>). <i>Epigenomes</i> , 2018 , 2, 12	2.3	15
34	Salinity tolerance in Australian wild <i>Oryza</i> species varies widely and matches that observed in <i>O. sativa</i> . <i>Rice</i> , 2018 , 11, 66	5.8	23

33	Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. <i>Scientific Reports</i> , 2017 , 7, 1300	4.9	57
32	Detecting spikes of wheat plants using neural networks with Laws texture energy. <i>Plant Methods</i> , 2017 , 13, 83	5.8	36
31	A Comprehensive Image-based Phenomic Analysis Reveals the Complex Genetic Architecture of Shoot Growth Dynamics in Rice (). <i>Plant Genome</i> , 2017 , 10, plantgenome2016.07.0064	4.4	31
30	Growth curve registration for evaluating salinity tolerance in barley. <i>Plant Methods</i> , 2017 , 13, 18	5.8	24
29	Variation in shoot tolerance mechanisms not related to ion toxicity in barley. <i>Functional Plant Biology</i> , 2017 , 44, 1194-1206	2.7	23
28	Salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. <i>Nature Communications</i> , 2016 , 7, 13342	17.4	134
27	Utilization of a high-throughput shoot imaging system to examine the dynamic phenotypic responses of a C4 cereal crop plant to nitrogen and water deficiency over time. <i>Journal of Experimental Botany</i> , 2015 , 66, 1817-32	7	129
26	Combining field performance with controlled environment plant imaging to identify the genetic control of growth and transpiration underlying yield response to water-deficit stress in wheat. <i>Journal of Experimental Botany</i> , 2015 , 66, 5481-92	7	56
25	Integrating Image-Based Phenomics and Association Analysis to Dissect the Genetic Architecture of Temporal Salinity Responses in Rice. <i>Plant Physiology</i> , 2015 , 168, 1476-89	6.6	109
24	Different NaCl-induced calcium signatures in the Arabidopsis thaliana ecotypes Col-0 and C24. <i>PLoS ONE</i> , 2015 , 10, e0117564	3.7	15
23	Comparison of Leaf Sheath Transcriptome Profiles with Physiological Traits of Bread Wheat Cultivars under Salinity Stress. <i>PLoS ONE</i> , 2015 , 10, e0133322	3.7	26
22	A Model-Based Approach to Recovering the Structure of a Plant from Images. <i>Lecture Notes in Computer Science</i> , 2015 , 215-230	0.9	5
21	Expression of the Arabidopsis vacuolar H ⁺ -pyrophosphatase gene (AVP1) improves the shoot biomass of transgenic barley and increases grain yield in a saline field. <i>Plant Biotechnology Journal</i> , 2014 , 12, 378-86	11.6	110
20	bHLH05 is an interaction partner of MYB51 and a novel regulator of glucosinolate biosynthesis in Arabidopsis. <i>Plant Physiology</i> , 2014 , 166, 349-69	6.6	71
19	Image-based phenotyping for non-destructive screening of different salinity tolerance traits in rice. <i>Rice</i> , 2014 , 7, 16	5.8	110
18	High-throughput phenotyping to detect drought tolerance QTL in wild barley introgression lines. <i>PLoS ONE</i> , 2014 , 9, e97047	3.7	173
17	Accounting for variation in designing greenhouse experiments with special reference to greenhouses containing plants on conveyor systems. <i>Plant Methods</i> , 2013 , 9, 5	5.8	44
16	Applications of high-throughput plant phenotyping to study nutrient use efficiency. <i>Methods in Molecular Biology</i> , 2013 , 953, 277-90	1.4	3

15	Germanium as a tool to dissect boron toxicity effects in barley and wheat. <i>Functional Plant Biology</i> , 2013 , 40, 618-627	2.7	22
14	Trait dissection of salinity tolerance with plant phenomics. <i>Methods in Molecular Biology</i> , 2012 , 913, 399-413	4.1	19
13	High-throughput phenotyping of plant shoots. <i>Methods in Molecular Biology</i> , 2012 , 918, 9-20	1.4	27
12	Accurate inference of shoot biomass from high-throughput images of cereal plants. <i>Plant Methods</i> , 2011 , 7, 2	5.8	194
11	High-throughput shoot imaging to study drought responses. <i>Journal of Experimental Botany</i> , 2010 , 61, 3519-28	7	232
10	Specific and coordinated control of indolic and aliphatic glucosinolate biosynthesis by R2R3-MYB transcription factors in <i>Arabidopsis thaliana</i> . <i>Phytochemistry Reviews</i> , 2009 , 8, 3-13	7.7	98
9	Investigating glutamate receptor-like gene co-expression in <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2008 , 31, 861-71	8.4	95
8	The R2R3-MYB transcription factor HAG1/MYB28 is a regulator of methionine-derived glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2007 , 51, 247-61	6.9	296
7	A simplified method for the analysis of transcription factor-promoter interactions that allows high-throughput data generation. <i>Plant Journal</i> , 2007 , 50, 911-6	6.9	43
6	The transcription factor HIG1/MYB51 regulates indolic glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2007 , 50, 886-901	6.9	294
5	Genetic Determinants of Salinity Tolerance in Crop Plants	81-111	
4	A single nucleotide substitution in TaHKT1;5-D controls shoot Na ⁺ accumulation in bread wheat		3
3	Atlas of Age- and Tissue-Specific DNA Methylation during Early Development of Barley (<i>Hordeum vulgare</i>)		1
2	Enhancement of sorghum grain yield and nutrition: A role for arbuscular mycorrhizal fungi regardless of soil phosphorus availability. <i>Plants People Planet</i> ,	4.1	1
1	GWAS reveals the genetic complexity of fructan accumulation patterns in barley grain		1