Bettina Berger

List of Publications by Year
in descending order

67	3,988	201674 27	149698 56
papers	citations	h-index	g-index
71	71	71	4378
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The R2R3-MYB transcription factor HAG1/MYB28 is a regulator of methionine-derived glucosinolate biosynthesis inArabidopsis thaliana. Plant Journal, 2007, 51, 247-261.	5.7	392
2	The transcription factor HIG1/MYB51 regulates indolic glucosinolate biosynthesis in Arabidopsis thaliana. Plant Journal, 2007, 50, 886-901.	5.7	371
3	High-throughput shoot imaging to study drought responses. Journal of Experimental Botany, 2010, 61, 3519-3528.	4.8	313
4	High-Throughput Phenotyping to Detect Drought Tolerance QTL in Wild Barley Introgression Lines. PLoS ONE, 2014, 9, e97047.	2.5	262
5	Accurate inference of shoot biomass from high-throughput images of cereal plants. Plant Methods, 2011, 7, 2.	4.3	243
6	Salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. Nature Communications, 2016, 7, 13342.	12.8	218
7	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. Journal of Experimental Botany, 2015, 66, 1817-1832.	4.8	189
8	Image-based phenotyping for non-destructive screening of different salinity tolerance traits in rice. Rice, 2014, 7, 16.	4.0	149
9	Expression of the <i><scp>A</scp>rabidopsis</i> vacuolar <scp>H</scp>⁺â€pyrophosphatase gene (<i><scp>AVP</scp>1</i>) improves the shoot biomass of transgenic barley and increases grain yield in a saline field. Plant Biotechnology Journal, 2014, 12, 378-386.	8.3	147
10	Integrating Image-Based Phenomics and Association Analysis to Dissect the Genetic Architecture of Temporal Salinity Responses in Rice. Plant Physiology, 2015, 168, 1476-1489.	4.8	146
11	Specific and coordinated control of indolic and aliphatic glucosinolate biosynthesis by R2R3-MYB transcription factors in Arabidopsis thaliana. Phytochemistry Reviews, 2009, 8, 3-13.	6.5	136
12	Investigating glutamate receptorâ€like gene coâ€expression in <i>Arabidopsis thaliana</i>. Plant, Cell and Environment, 2008, 31, 861-871.	5.7	110
13	bHLH05 Is an Interaction Partner of MYB51 and a Novel Regulator of Glucosinolate Biosynthesis in Arabidopsis. Plant Physiology, 2014, 166, 349-369.	4.8	109
14	Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. Scientific Reports, 2017, 7, 1300.	3.3	94
15	Genome-wide association of barley plant growth under drought stress using a nested association mapping population. BMC Plant Biology, 2019, 19, 134.	3.6	73
16	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. Journal of Experimental Botany, 2015, 66, 5481-5492.	4.8	67
17	Detecting spikes of wheat plants using neural networks with Laws texture energy. Plant Methods, 2017, 13, 83.	4.3	61
18	Mapping of novel salt tolerance QTL in an Excaliburâ€‰Ã—â€‰Kukri doubled haploid wheat population. Theoretical and Applied Genetics, 2018, 131, 2179-2196.	3.6	60

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19	Hyperspectral imaging and 3D technologies for plant phenotyping: From satellite to close-range sensing. Computers and Electronics in Agriculture, 2020, 175, 105621.	7.7	59
20	Accounting for variation in designing greenhouse experiments with special reference to greenhouses containing plants on conveyor systems. Plant Methods, 2013, 9, 5.	4.3	58
21	The Development of Hyperspectral Distribution Maps to Predict the Content and Distribution of Nitrogen and Water in Wheat (Triticum aestivum). Frontiers in Plant Science, 2019, 10, 1380.	3.6	56
22	A simplified method for the analysis of transcription factor-promoter interactions that allows high-throughput data generation. Plant Journal, 2007, 50, 911-916.	5.7	47
23	A Comprehensive Imageâ€based Phenomic Analysis Reveals the Complex Genetic Architecture of Shoot Growth Dynamics in Rice (<i>Oryza sativa</i>). Plant Genome, 2017, 10, plantgenome2016.07.0064.	2.8	45
24	High-Throughput Phenotyping of Plant Shoots. Methods in Molecular Biology, 2012, 918, 9-20.	0.9	37
25	Salinity tolerance in Australian wild Oryza species varies widely and matches that observed in O. sativa. Rice, 2018, 11, 66.	4.0	36
26	Comparison of Leaf Sheath Transcriptome Profiles with Physiological Traits of Bread Wheat Cultivars under Salinity Stress. PLoS ONE, 2015, 10, e0133322.	2.5	33
27	Growth curve registration for evaluating salinity tolerance in barley. Plant Methods, 2017, 13, 18.	4.3	29
28	Resource allocation to growth or luxury consumption drives mycorrhizal responses. Ecology Letters, 2019, 22, 1757-1766.	6.4	29
29	Variation in shoot tolerance mechanisms not related to ion toxicity in barley. Functional Plant Biology, 2017, 44, 1194.	2.1	28
30	Trait Dissection of Salinity Tolerance with Plant Phenomics. Methods in Molecular Biology, 2012, 913, 399-413.	0.9	26
31	Germanium as a tool to dissect boron toxicity effects in barley and wheat. Functional Plant Biology, 2013, 40, 618.	2.1	26
32	Approaches, applications, and future directions for hyperspectral vegetation studies: An emphasis on yieldâ€limiting factors inÂwheat. The Plant Phenome Journal, 2020, 3, e20007.	2.0	25
33	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages. PLoS ONE, 2020, 15, e0236037.	2.5	25
34	Using High-Throughput Phenotyping to Explore Growth Responses to Mycorrhizal Fungi and Zinc in Three Plant Species. Plant Phenomics, 2019, 2019, 5893953.	5.9	23
35	Identification of salt tolerance QTL in a wheat RIL mapping population using destructive and non-destructive phenotyping. Functional Plant Biology, 2021, 48, 131.	2.1	22
36	Salt Stress Induces Non-CG Methylation in Coding Regions of Barley Seedlings (Hordeum vulgare). Epigenomes, 2018, 2, 12.	1.8	21

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37	Different NaCl-Induced Calcium Signatures in the Arabidopsis thaliana Ecotypes Col-0 and C24. PLoS ONE, 2015, 10, e0117564.	2.5	20
38	Highâ€throughput 3D modelling to dissect the genetic control of leaf elongation in barley (<i>Hordeum vulgare</i>). Plant Journal, 2019, 98, 555-570.	5.7	20
39	Smoothing and extraction of traits in the growth analysis of noninvasive phenotypic data. Plant Methods, 2020, 16, 36.	4.3	19
40	A single nucleotide substitution in <scp><i>TaHKT1</i></scp>;<scp><i>5â€D</i></scp> controls shoot Na⁺ accumulation in bread wheat. Plant, Cell and Environment, 2020, 43, 2158-2171.	5.7	18
41	Effect of Rice GDP-L-Galactose Phosphorylase Constitutive Overexpression on Ascorbate Concentration, Stress Tolerance, and Iron Bioavailability in Rice. Frontiers in Plant Science, 2020, 11, 595439.	3.6	18
42	Genome-wide association study reveals the genetic complexity of fructan accumulation patterns in barley grain. Journal of Experimental Botany, 2021, 72, 2383-2402.	4.8	17
43	The Performances of Hyperspectral Sensors for Proximal Sensing of Nitrogen Levels in Wheat. Sensors, 2020, 20, 4550.	3.8	15
44	Sensor-based phenotyping of above-ground plant-pathogen interactions. Plant Methods, 2022, 18, 35.	4.3	14
45	Enhancement of sorghum grain yield and nutrition: A role for arbuscular mycorrhizal fungi regardless of soil phosphorus availability. Plants People Planet, 2022, 4, 143-156.	3.3	12
46	Highâ€throughput phenotyping reveals growth of Medicago truncatula is positively affected by arbuscular mycorrhizal fungi even at high soil phosphorus availability. Plants People Planet, 2020, 3, 600.	3.3	8
47	High-throughput, image-based phenotyping reveals nutrient-dependent growth facilitation in a grass-legume mixture. PLoS ONE, 2020, 15, e0239673.	2.5	8
48	A Model-Based Approach to Recovering the Structure of a Plant from Images. Lecture Notes in Computer Science, 2015, , 215-230.	1.3	7
49	Identifying the genetic control of salinity tolerance in the bread wheat landrace Mocho de Espiga Branca. Functional Plant Biology, 2021, 48, 1148-1160.	2.1	7
50	Tackling Nitrogen Use Efficiency in Cereal Crops Using High-Throughput Phenotyping. , 2018, , 121-139.		5
51	Greenhouse Spatial Effects Detected in the Barley (Hordeum vulgare L.) Epigenome Underlie Stochasticity of DNA Methylation. Frontiers in Plant Science, 2020, 11, 553907.	3.6	5
52	Evaluation of commercial composts and potting mixes and their ability to support arbuscular mycorrhizal fungi with maize (Zea mays) as host plant. Waste Management, 2021, 134, 187-196.	7.4	5
53	Investigating the effects of elevated temperature on salinity tolerance traits in grapevine rootstocks using highâ€throughput phenotyping. Australian Journal of Grape and Wine Research, 2022, 28, 276-291.	2.1	5
54	Hyperspectral imaging predicts yield and nitrogen content in grassâ€œlegume polycultures. Precision Agriculture, 2022, 23, 2270-2288.	6.0	5

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55	Applications of High-Throughput Plant Phenotyping to Study Nutrient Use Efficiency. Methods in Molecular Biology, 2013, 953, 277-290.	0.9	4
56	Integrating Ecological Stoichiometry to Understand Nutrient Limitation and Potential for Competition in Mixed Pasture Assemblages. Journal of Soil Science and Plant Nutrition, 2021, 21, 2489-2500.	3.4	3
57	Atlas of Age- and Tissue-Specific DNA Methylation during Early Development of Barley (Hordeum) Tj ETQq1 1 0.784314 rgBT /Overlock 1		2
58	Using High-Throughput Phenotyping to Explore Growth Responses to Mycorrhizal Fungi and Zinc in Three Plant Species. Plant Phenomics, 2019, 2019, 1-12.	5.9	1
59	Study on spike detection of cereal plants. , 2014, , .		0
60	Title is missing!. , 2020, 15, e0236037.		0
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62	Title is missing!. , 2020, 15, e0236037.		0
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