Susanne Barth

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Improving phenotyping in winter barley cultivars towards waterlogging tolerance by combining field trials under natural conditions with controlled growth condition experiments. European Journal of Agronomy, 2022, 133, 126432.	4.1	6
2	A novel 3D Xâ€ray computed tomography (CT) method for spatioâ€temporal evaluation of waterloggingâ€induced aerenchyma formation in barley. The Plant Phenome Journal, 2022, 5, .	2.0	6
3	A new genetic locus for self-compatibility in the outcrossing grass species perennial ryegrass (Lolium) Tj ETQq1 1	0.784314 2.9	rgBT /Overl
4	Physiological and transcriptional response to drought stress among bioenergy grass Miscanthus species. Biotechnology for Biofuels, 2021, 14, 60.	6.2	13
5	Experimental comparison of two methods to study barley responses to partial submergence. Plant Methods, 2021, 17, 40.	4.3	13
6	First Detection and Characterization of Cross- and Multiple Resistance to Acetyl-CoA Carboxylase (ACCase)- and Acetolactate Synthase (ALS)-Inhibiting Herbicides in Black-Grass (Alopecurus) Tj ETQq0 0 0 rgBT /C (Switzerland), 2021, 11, 1272.	Dverlock 1	0 Jf 50 542
7	Genome biology of the paleotetraploid perennial biomass crop Miscanthus. Nature Communications, 2020, 11, 5442.	12.8	67
8	Diurnal patterns of growth and transient reserves of sink and source tissues are affected by cold nights in barley. Plant, Cell and Environment, 2020, 43, 1404-1420.	5.7	1
9	First Report on Assessing the Severity of Herbicide Resistance to ACCase Inhibitors Pinoxaden, Propaquizafop and Cycloxydim in Six Avena fatua Populations in Ireland. Agronomy, 2020, 10, 1362.	3.0	8
10	Genotyping by Sequencing and Plastome Analysis Finds High Genetic Variability and Geographical Structure in Dactylis glomerata L. in Northwest Europe Despite Lack of Ploidy Variation. Agronomy, 2019, 9, 342.	3.0	6
11	Transcriptome characterization and differentially expressed genes under flooding and drought stress in the biomass grasses Phalaris arundinacea and Dactylis glomerata. Annals of Botany, 2019, 124, 717-730.	2.9	7
12	Transcriptome sequencing of Festulolium accessions under salt stress. BMC Research Notes, 2019, 12, 311.	1.4	6
13	An Immortalized Genetic Mapping Population for Perennial Ryegrass: A Resource for Phenotyping and Complex Trait Mapping. Frontiers in Plant Science, 2018, 9, 717.	3.6	5
14	Plastid genome sequencing reveals biogeographical structure and extensive population genetic variation in wild populations of <i>Phalaris arundinacea</i> L. in northâ€western Europe. GCB Bioenergy, 2017, 9, 46-56.	5.6	30
15	An Irish perennial ryegrass genetic resource collection clearly divides into two major gene pools. Plant Genetic Resources: Characterisation and Utilisation, 2017, 15, 269-278.	0.8	1
16	Using variable importance measures to identify a small set of SNPs to predict heading date in perennial ryegrass. Scientific Reports, 2017, 7, 3566.	3.3	17
17	Quantitative trait loci associated with different polar metabolites in perennial ryegrass - providing scope for breeding towards increasing certain polar metabolites. BMC Genetics, 2017, 18, 84.	2.7	1
18	Markers associated with heading and aftermath heading in perennial ryegrass full-sib families. BMC Plant Biology, 2016, 16, 160.	3.6	16

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19	An ultra-high density genetic linkage map of perennial ryegrass (<i>Lolium perenne</i>) using genotyping by sequencing (GBS) based on a reference shotgun genome assembly. Annals of Botany, 2016, 118, 71-87.	2.9	31
20	Variation in sequences containing microsatellite motifs in the perennial biomass and forage grass, Phalaris arundinacea (Poaceae). BMC Research Notes, 2016, 9, 184.	1.4	5
21	A Gene Encoding a DUF247 Domain Protein Cosegregates with the <i>S</i> Self-Incompatibility Locus in Perennial Ryegrass. Molecular Biology and Evolution, 2016, 33, 870-884.	8.9	78
22	<i>Miscanthus</i> : a case study for the utilization of natural genetic variation. Plant Genetic Resources: Characterisation and Utilisation, 2015, 13, 219-237.	0.8	37
23	Quantitative trait loci analysis to study the genetic regulation of non-polar metabolites in perennial ryegrass. Metabolomics, 2015, 11, 412-424.	3.0	11
24	Seasonal and genetic variations in water-soluble carbohydrates and other quality traits in ecotypes and cultivars of perennial ryegrass (Lolium perenneL.). Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 236-247.	0.8	4
25	Comparative exomics of Phalariscultivars under salt stress. BMC Genomics, 2014, 15, S18.	2.8	13
26	A hybrid next generation transcript sequencing-based approach to identify allelic and homeolog-specific single nucleotide polymorphisms in allotetraploid white clover. BMC Genomics, 2013, 14, 100.	2.8	18
27	Short-term response in leaf metabolism of perennial ryegrass (Lolium perenne) to alterations in nitrogen supply. Metabolomics, 2013, 9, 145-156.	3.0	42
28	Nuclear SSR Markers for Miscanthus, Saccharum, and Related Grasses (Saccharinae, Poaceae). Applications in Plant Sciences, 2013, 1, 1300042.	2.1	7
29	Old Age Sex: A Parentage Study of Different Age Cohorts in a Native Veteran Pedunculate Oak (<i>Quercus Robur L.</i>) Woodland Using Microsatellite Markers. Biology and Environment, 2013, 113, 1-13.	0.3	2
30	Breeding strategies for forage and grass improvement. Annals of Botany, 2012, 110, 1261-1262.	2.9	5
31	New chloroplast microsatellite markers suitable for assessing genetic diversity of Lolium perenne and other related grass species. Annals of Botany, 2012, 110, 1327-1339.	2.9	33
32	Genetic linkage mapping in an F2 perennial ryegrass population using DArT markers. Plant Breeding, 2012, 131, 345-349.	1.9	17
33	Progress towards elucidating the mechanisms of self-incompatibility in the grasses: further insights from studies in Lolium. Annals of Botany, 2011, 108, 677-685.	2.9	49
34	Early response mechanisms of perennial ryegrass (Lolium perenne) to phosphorus deficiency. Annals of Botany, 2011, 107, 243-254.	2.9	60
35	Fine Mapping of Quantitative Trait Loci for Biomass Yield in Perennial Ryegrass. , 2010, , 461-464.		5
36	The genetic location of the self-incompatibility locus in white clover (Trifolium repens L.). Theoretical and Applied Genetics, 2010, 121, 567-576.	3.6	17

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37	Identification of ABC transporters from Lolium perenne L. that are regulated by toxic levels of selenium. Planta, 2010, 231, 901-911.	3.2	29

Chloroplast DNA markers (cpSSRs, SNPs) for Miscanthus, Saccharum and related grasses (Panicoideae,) Tj ETQq0 0.0 rgBT /Overlock 10

39	EST-derived SSR markers used as anchor loci for the construction of a consensus linkage map in ryegrass (Lolium spp.). BMC Plant Biology, 2010, 10, 177.	3.6	42
40	Variation in inflorescence characters and inflorescence development in ecotypes and cultivars of <i>Lolium perenne</i> L. Grass and Forage Science, 2010, 65, 398-409.	2.9	12
41	Localized hypermutation and associated gene losses in legume chloroplast genomes. Genome Research, 2010, 20, 1700-1710.	5.5	244
42	The Complete Chloroplast Genome Sequence of Perennial Ryegrass (Lolium perenne L.) Reveals Useful Polymorphisms Among European Ecotypes. , 2010, , 409-413.		1
43	Complete Chloroplast Genome Sequence of a Major Allogamous Forage Species, Perennial Ryegrass (Lolium perenne L.). DNA Research, 2009, 16, 165-176.	3.4	72
44	Identification of genes expressed during the self-incompatibility response in perennial ryegrass (Lolium perenne L.). Plant Molecular Biology, 2009, 70, 709-723.	3.9	28
45	Identification of coincident QTL for days to heading, spike length and spikelets per spike in Lolium perenne L Euphytica, 2009, 166, 61-70.	1.2	33
46	Quantitative trait loci mapping for biomass yield traits in a Lolium inbred line derived F2 population. Euphytica, 2009, 170, 99-107.	1.2	30
47	Genotypes and phenotypes of an ex situ Vitis vinifera ssp. sylvestris (Gmel.) Beger germplasm collection from the Upper Rhine Valley. Genetic Resources and Crop Evolution, 2009, 56, 1171-1181.	1.6	22
48	Identification of genes involved in the floral transition at the shoot apical meristem of Lolium perenne L. by use of suppression subtractive hybridisation. Plant Growth Regulation, 2009, 59, 215-225.	3.4	2
49	Transcriptional and metabolic profiles of <i>Lolium perenne</i> L. genotypes in response to a PEGâ€induced water stress. Plant Biotechnology Journal, 2009, 7, 719-732.	8.3	79
50	Understanding the Genetic Basis of Flowering and Fertility in the Ryegrasses (Lolium spp.). , 2009, , 185-192.		1
51	Expressed sequence tag-derived microsatellite markers of perennial ryegrass (Lolium perenne L.). Molecular Breeding, 2008, 21, 533-548.	2.1	31
52	Segregation distortion in Lolium: evidence for genetic effects. Theoretical and Applied Genetics, 2008, 117, 297-306.	3.6	54
53	How far are we from unravelling selfâ€incompatibility in grasses?. New Phytologist, 2008, 178, 740-753.	7.3	59
54	An Optimized Chloroplast DNA Extraction Protocol for Grasses (Poaceae) Proves Suitable for Whole Plastid Genome Sequencing and SNP Detection. PLoS ONE, 2008, 3, e2813.	2.5	49

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55	Analysis of a Triple Testcross Design With Recombinant Inbred Lines Reveals a Significant Role of Epistasis in Heterosis for Biomass-Related Traits in Arabidopsis. Genetics, 2007, 175, 2009-2017.	2.9	65
56	Extremely high cytoplasmic diversity in natural and breeding populations of Lolium (Poaceae). Heredity, 2007, 99, 531-544.	2.6	40
57	Development and testing of novel chloroplast microsatellite markers for Lolium perenne and other grasses (Poaceae) from de novo sequencing and in silico sequences. Molecular Ecology Notes, 2006, 6, 449-452.	1.7	17
58	Monitoring Lactobacillus plantarum in grass silages with the aid of 16S rDNA-based quantitative real-time PCR assays. Systematic and Applied Microbiology, 2006, 29, 49-58.	2.8	38
59	Genetic diversity in European perennial ryegrass cultivars investigated with RAPD markers. Plant Breeding, 2005, 124, 161-166.	1.9	56
60	Molecular genetic diversity within and among German ecotypes in comparison to European perennial ryegrass cultivars. Plant Breeding, 2005, 124, 257-262.	1.9	40
61	Molecular characterization of genetic diversity in European germplasm of perennial ryegrass. Euphytica, 2005, 146, 39-44.	1.2	21
62	Heterosis for biomass yield and related traits in five hybrids of Arabidopsis thaliana L. Heynh. Heredity, 2003, 91, 36-42.	2.6	86
63	Genetic diversity in Arabidopsis thaliana L. Heynh. investigated by cleaved amplified polymorphic sequence (CAPS) and inter-simple sequence repeat (ISSR) markers. Molecular Ecology, 2002, 11, 495-505.	3.9	80
64	Influence of genetic background and heterozygosity on meiotic recombination in <i>Arabidopsis thaliana</i> . Genome, 2001, 44, 971-978.	2.0	28
65	Influence of genetic background and heterozygosity on meiotic recombination in <i>Arabidopsis thaliana</i> . Genome, 2001, 44, 971-978.	2.0	5
66	A high-throughput system for genome-wide measurement of genetic recombination in Arabidopsis thaliana based on transgenic markers. Functional and Integrative Genomics, 2000, 1, 200-206.	3.5	19