

Andreas Bärner

List of Publications by Year in descending order

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225
papers

10,601
citations

44444

50
h-index

53065

89
g-index

231
all docs

231
docs citations

231
times ranked

8397
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping of additive and epistatic QTLs linked to seed longevity in bread wheat (<i>Triticum aestivum</i> L.). <i>Cereal Research Communications</i> , 2022, 50, 709-715.	0.8	8
2	Genetic Insight Into the Insect Resistance in Bread Wheat Exploiting the Untapped Natural Diversity. <i>Frontiers in Genetics</i> , 2022, 13, 828905.	1.1	16
3	Genetic Aspects and Molecular Causes of Seed Longevity in Plants—A Review. <i>Plants</i> , 2022, 11, 598.	1.6	15
4	Relationship between the Characteristics of Bread Wheat Grains, Storage Time and Germination. <i>Plants</i> , 2022, 11, 35.	1.6	2
5	Physiological and molecular aspects of seed longevity: exploring intra-species variation in eight <i>Pisum sativum</i> L. accessions. <i>Physiologia Plantarum</i> , 2022, 174, e13698.	2.6	8
6	Recombination Landscape Divergence Between Populations is Marked by Larger Low-Recombining Regions in Domesticated Rye. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
7	Old and modern wheat (<i>Triticum aestivum</i> L.) cultivars and their potential to elicit celiac disease. <i>Food Chemistry</i> , 2021, 339, 127952.	4.2	17
8	QTL analysis of seed germination traits in tobacco (<i>Nicotiana tabacum</i> L.). <i>Journal of Applied Genetics</i> , 2021, 62, 441-444.	1.0	7
9	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
10	Regions of Chromosome 2A of Bread Wheat (<i>Triticum aestivum</i> L.) Associated with Variation in Physiological and Agronomical Traits under Contrasting Water Regimes. <i>Plants</i> , 2021, 10, 1023.	1.6	8
11	Genetic Diversity, Linkage Disequilibrium and Population Structure of Bulgarian Bread Wheat Assessed by Genome-Wide Distributed SNP Markers: From Old Germplasm to Semi-Dwarf Cultivars. <i>Plants</i> , 2021, 10, 1116.	1.6	15
12	A SNP-based genetic dissection of versatile traits in bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Journal</i> , 2021, 108, 960-976.	2.8	22
13	Inheritance of seed quality and seed germination in two doubled haploid populations of oilseed rape segregating for acid detergent lignin (ADL) content. <i>Euphytica</i> , 2021, 217, 1.	0.6	6
14	Insight into the genetic contribution of maximum yield potential, spikelet development and abortion in barley. <i>Plants People Planet</i> , 2021, 3, 721-736.	1.6	4
15	Global range expansion history of pepper (<i>Capsicum</i> spp.) revealed by over 10,000 genebank accessions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
16	Comparative Proteomics at the Critical Node of Vigor Loss in Wheat Seeds Differing in Storability. <i>Frontiers in Plant Science</i> , 2021, 12, 707184.	1.7	4
17	Genetic Mapping Reveals Novel Exotic and Elite QTL Alleles for Salinity Tolerance in Barley. <i>Agronomy</i> , 2021, 11, 1774.	1.3	11
18	A mechanistic view on lodging resistance in rye and wheat: a multiscale comparative study. <i>Plant Biotechnology Journal</i> , 2021, 19, 2646-2661.	4.1	16

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19	WHEAT SEED (<i>TRITICUM AESTIVUM</i> L.) RADIOCARBON CONCENTRATION OVER THE LAST 75 YEARS. <i>Radiocarbon</i> , 2021, 63, 1387-1396.	0.8	3
20	Genetic dissection of grain architecture-related traits in a winter wheat population. <i>BMC Plant Biology</i> , 2021, 21, 417.	1.6	16
21	Detection and Verification of QTL for Salinity Tolerance at Germination and Seedling Stages Using Wild Barley Introgression Lines. <i>Plants</i> , 2021, 10, 2246.	1.6	4
22	Mapping Resistance to Argentinean Fusarium (<i>Graminearum</i>) Head Blight Isolates in Wheat. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13653.	1.8	5
23	Analyses of MADS-box Genes Suggest HvMADS56 to Regulate Lateral Spikelet Development in Barley. <i>Plants</i> , 2021, 10, 2825.	1.6	3
24	Identification of Candidate Genes and Genomic Regions Associated with Adult Plant Resistance to Stripe Rust in Spring Wheat. <i>Agronomy</i> , 2021, 11, 2585.	1.3	11
25	GWAS: Fast-forwarding gene identification and characterization in temperate Cereals: lessons from Barley – A review. <i>Journal of Advanced Research</i> , 2020, 22, 119-135.	4.4	227
26	Age-dependent loss of seed viability is associated with increased lipid oxidation and hydrolysis. <i>Plant, Cell and Environment</i> , 2020, 43, 303-314.	2.8	49
27	Genome-wide association mapping reveals putative candidate genes for drought tolerance in barley. <i>Environmental and Experimental Botany</i> , 2020, 180, 104237.	2.0	14
28	Fingerprinting of wheat protein profiles for improved distinction between wheat cultivars and species. <i>Cereal Chemistry</i> , 2020, 97, 999-1009.	1.1	8
29	The relationship between root system development and vernalization under contrasting irrigation in bread wheat lines with the introgressions from a synthetic hexaploid. <i>Plant Growth Regulation</i> , 2020, 92, 583-595.	1.8	3
30	DEFECTIVE ENDOSPERM-D1 (Dee-D1) is crucial for endosperm development in hexaploid wheat. <i>Communications Biology</i> , 2020, 3, 791.	2.0	3
31	Screening for Drought Tolerance in Maize (<i>Zea mays</i> L.) Germplasm Using Germination and Seedling Traits under Simulated Drought Conditions. <i>Plants</i> , 2020, 9, 565.	1.6	61
32	Wheat (<i>Triticum aestivum</i> L.) Breeding from 1891 to 2010 Contributed to Increasing Yield and Glutenin Contents but Decreasing Protein and Gliadin Contents. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 13247-13256.	2.4	51
33	Melanin formation in barley grain occurs within plastids of pericarp and husk cells. <i>Scientific Reports</i> , 2020, 10, 179.	1.6	26
34	Genome-wide and SNP network analyses reveal genetic control of spikelet sterility and yield-related traits in wheat. <i>Scientific Reports</i> , 2020, 10, 2098.	1.6	26
35	An SNP based GWAS analysis of seed longevity in wheat. <i>Cereal Research Communications</i> , 2020, 48, 149-156.	0.8	19
36	Identification of stable reference genes for qPCR studies in common wheat (<i>Triticum aestivum</i> L.) seedlings under short-term drought stress. <i>Plant Methods</i> , 2020, 16, 58.	1.9	31

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37	Mapping of QTLs Associated with Yield and Yield Related Traits in Durum Wheat (<i>Triticum durum</i> Desf.) Under Irrigated and Drought Conditions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2372.	1.8	21
38	An SNP Based GWAS analysis of seed longevity in wheat. <i>Cereal Research Communications</i> , 2020, 48, 149.	0.8	2
39	Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. <i>Scientific Data</i> , 2019, 6, 137.	2.4	13
40	Identification of consistent QTL with large effect on anther extrusion in doubled haploid populations developed from spring wheat accessions in German Federal ex situ Genebank. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3035-3045.	1.8	12
41	Drought Stress Tolerance in Wheat and Barley: Advances in Physiology, Breeding and Genetics Research. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3137.	1.8	353
42	Uncovering the Genetic Architecture of Fruiting Efficiency in Bread Wheat: A Viable Alternative to Increase Yield Potential. <i>Crop Science</i> , 2019, 59, 1853-1869.	0.8	11
43	Spike developmental stages and ABA role in spikelet primordia abortion contribute to the final yield in barley (<i>Hordeum vulgare</i> L.). , 2019, 60, 13.		25
44	Using intervarietal substitution lines for the identification of wheat chromosomes involved in early responses to water-deficit stress. <i>PLoS ONE</i> , 2019, 14, e0221849.	1.1	2
45	The search for candidate genes associated with natural variation of grain Zn accumulation in barley. <i>Biochemical Journal</i> , 2019, 476, 1889-1909.	1.7	12
46	Wheat seed ageing viewed through the cellular redox environment and changes in pH. <i>Free Radical Research</i> , 2019, 53, 641-654.	1.5	23
47	Analysis of wheat gene expression related to the oxidative stress response and signal transduction under short-term osmotic stress. <i>Scientific Reports</i> , 2019, 9, 2743.	1.6	64
48	Mapping of QTL associated with seed longevity in durum wheat (<i>Triticum durum</i> Desf.). <i>Journal of Applied Genetics</i> , 2019, 60, 33-36.	1.0	26
49	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322
50	Novel loci and a role for nitric oxide for seed dormancy and preharvest sprouting in barley. <i>Plant, Cell and Environment</i> , 2019, 42, 1318-1327.	2.8	32
51	Genetic diversity and relationship between domesticated rye and its wild relatives as revealed through genotyping-by-sequencing. <i>Evolutionary Applications</i> , 2019, 12, 66-77.	1.5	50
52	QTL analysis of falling number and seed longevity in wheat (<i>Triticum aestivum</i> L.). <i>Journal of Applied Genetics</i> , 2018, 59, 35-42.	1.0	31
53	Photosynthetic Responses of a Wheat Mutant (Rht-B1c) with Altered DELLA Proteins to Salt Stress. <i>Journal of Plant Growth Regulation</i> , 2018, 37, 645-656.	2.8	25
54	Variability of fat content and fatty acids profiles in seeds of a Polish white lupin (<i>Lupinus albus</i> L.) collection. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 417-431.	0.8	24

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55	Genome-Wide Association Mapping of Major Root Length QTLs Under PEG Induced Water Stress in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1759.	1.7	34
56	Antioxidant Potential of Grass Pea Seeds from European Countries. <i>Foods</i> , 2018, 7, 142.	1.9	18
57	Changes in tocochromanols and glutathione reveal differences in the mechanisms of seed ageing under seedbank conditions and controlled deterioration in barley. <i>Environmental and Experimental Botany</i> , 2018, 156, 8-15.	2.0	39
58	Unlocking historical phenotypic data from an ex situ collection to enhance the informed utilization of genetic resources of barley (<i>Hordeum</i> sp.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 2009-2019.	1.8	16
59	Association genetics studies on frost tolerance in wheat (<i>Triticum aestivum</i> L.) reveal new highly conserved amino acid substitutions in CBF-A3, CBF-A15, VRN3 and PPD1 genes. <i>BMC Genomics</i> , 2018, 19, 409.	1.2	31
60	Leveraging the Use of Historical Data Gathered During Seed Regeneration of an ex Situ Genebank Collection of Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 609.	1.7	15
61	Machine learning links seed composition, glucosinolates and viability of oilseed rape after 31 years of long-term storage. <i>Seed Science Research</i> , 2018, 28, 340-348.	0.8	5
62	Unbalanced historical phenotypic data from seed regeneration of a barley ex situ collection. <i>Scientific Data</i> , 2018, 5, 180278.	2.4	12
63	Genetic architecture of seed longevity in bread wheat (<i>Triticum aestivum</i> L.). <i>Journal of Biosciences</i> , 2017, 42, 81-89.	0.5	31
64	The wheat mutant DELLA-encoding gene (<i>Rht-B1c</i>) affects plant photosynthetic responses to cadmium stress. <i>Plant Physiology and Biochemistry</i> , 2017, 114, 10-18.	2.8	43
65	The changes in the reproductive barrier between hexaploid wheat (<i>Triticum aestivum</i> L.) and rye (<i>Secale cereale</i> L.): different states lead to different fates. <i>Planta</i> , 2017, 246, 377-388.	1.6	3
66	Metabolic profiling of glucosinolates and their hydrolysis products in a germplasm collection of <i>Brassica rapa</i> turnips. <i>Food Research International</i> , 2017, 100, 392-403.	2.9	57
67	Diversity of leaf pubescence in bread wheat and relative species. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 1761-1773.	0.8	6
68	Genome-wide association mapping of genetic factors controlling <i>Septoria tritici</i> blotch resistance and their associations with plant height and heading date in wheat. <i>Euphytica</i> , 2017, 213, 1.	0.6	17
69	Genotypic and phenotypic changes in wild barley (<i>Hordeum vulgare</i> subsp. <i>spontaneum</i>) during a period of climate change in Jordan. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 1295-1312.	0.8	17
70	Identification and characterization of regulatory network components for anthocyanin synthesis in barley aleurone. <i>BMC Plant Biology</i> , 2017, 17, 184.	1.6	39
71	Genetic Architecture of Anther Extrusion in Spring and Winter Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 754.	1.7	53
72	Metabolic pathways and genes identified by RNA-seq analysis of barley near-isogenic lines differing by allelic state of the Black lemma and pericarp (<i>Blp</i>) gene. <i>BMC Plant Biology</i> , 2017, 17, 182.	1.6	22

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73	Regulation of the Flavonoid Biosynthesis Pathway Genes in Purple and Black Grains of <i>Hordeum vulgare</i> . PLoS ONE, 2016, 11, e0163782.	1.1	90
74	Genome-Wide Association Mapping of Anther Extrusion in Hexaploid Spring Wheat. PLoS ONE, 2016, 11, e0155494.	1.1	23
75	Barley Seed Aging: Genetics behind the Dry Elevated Pressure of Oxygen Aging and Moist Controlled Deterioration. Frontiers in Plant Science, 2016, 7, 388.	1.7	40
76	The inheritance of wheat grain longevity: a comparison between induced and natural ageing. Journal of Applied Genetics, 2016, 57, 477-481.	1.0	23
77	Comparative proteomic analysis of \hat{I}^2 -aminobutyric acid-mediated alleviation of salt stress in barley. Plant Physiology and Biochemistry, 2016, 99, 150-161.	2.8	35
78	Regions of the bread wheat D genome associated with variation in key photosynthesis traits and shoot biomass under both well watered and water deficient conditions. Journal of Applied Genetics, 2016, 57, 151-163.	1.0	16
79	Geography of Genetic Structure in Barley Wild Relative <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> in Jordan. PLoS ONE, 2016, 11, e0160745.	1.1	13
80	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat"™. Genetics, 2015, 201, 155-165.	1.2	109
81	Barley <i>scp>A</scp>nt1</i> is a homolog of maize <i>scp>C</scp>1</i> and its product is part of the regulatory machinery governing anthocyanin synthesis in the leaf sheath. Plant Breeding, 2015, 134, 400-405.</i></i>	1.0	20
82	<i>Aegilops tauschii</i> Introgressions in Wheat. , 2015, , 245-271.		19
83	Diversity of germination and seedling traits in a spring barley (<i>Hordeum vulgare</i> L.) collection under drought simulated conditions. Genetic Resources and Crop Evolution, 2015, 62, 275-292.	0.8	32
84	Mapping quantitative trait loci determining seed longevity in tobacco (<i>Nicotiana tabacum</i> L.). Euphytica, 2015, 202, 479-486.	0.6	21
85	Estimation of mechanical properties of seeds of common vetch accessions (<i>Vicia sativa</i> L.) and their chemical composition. Genetic Resources and Crop Evolution, 2015, 62, 361-375.	0.8	8
86	Genetic dissection of earliness by analysis of a recombinant chromosome substitution double haploid mapping population of bread wheat (<i>Triticum aestivum</i> L.) in different geographic regions. Euphytica, 2015, 206, 191-202.	0.6	3
87	Alterations in root proteome of salt-sensitive and tolerant barley lines under salt stress conditions. Journal of Plant Physiology, 2015, 174, 166-176.	1.6	69
88	Hybrid dwarfness in crosses between wheat (<i>scp>T</scp>riticum aestivum </i> <scp>L</scp>.) and rye (<i>scp>S</scp>eale cereale </i> <scp>L</scp>.): a new look at an old phenomenon. Plant Biology, 2015, 17, 320-326.</i></i>	1.8	10
89	Genome-wide association mapping and biochemical markers reveal that seed ageing and longevity are intricately affected by genetic background and developmental and environmental conditions in barley. Plant, Cell and Environment, 2015, 38, 1011-1022.	2.8	95
90	Effect of <i>scp>VRN</scp>â€1</i> and <i>scp>PPD</scp>â€D1</i> genes on heading time in European bread wheat cultivars. Plant Breeding, 2015, 134, 49-55.</i></i>	1.0	34

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91	Assessing genetic diversity of Egyptian hexaploid wheat (<i>Triticum aestivum</i> L.) using microsatellite markers. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 377-385.	0.8	22
92	A novel noninvasive procedure for high-throughput screening of major seed traits. <i>Plant Biotechnology Journal</i> , 2015, 13, 188-199.	4.1	29
93	Enlargement of the Genetic Diversity for Grain Quality in Bread Wheat Through Alien Introgression. , 2015, , 287-292.		1
94	Longevity of <i>Nicotiana</i> seeds conserved at low temperatures in ex situ genebanks. <i>Seed Science and Technology</i> , 2014, 42, 355-362.	0.6	9
95	Wheat Rht-1 Dwarfs Exhibit Better Photosynthetic Response to Water Deficit at Seedling Stage Compared to the Wild Type. <i>Journal of Agronomy and Crop Science</i> , 2014, 200, 434-443.	1.7	22
96	Salinity Stress in Roots of Contrasting Barley Genotypes Reveals Time-Distinct and Genotype-Specific Patterns for Defined Proteins. <i>Molecular Plant</i> , 2014, 7, 336-355.	3.9	51
97	Changes in Water Status, Membrane Stability and Antioxidant Capacity of Wheat Seedlings Carrying Different Rht-1 Dwarfing Alleles under Drought Stress. <i>Journal of Agronomy and Crop Science</i> , 2014, 200, 83-91.	1.7	22
98	The genetic basis of durum wheat germination and seedling growth under osmotic stress. <i>Biologia Plantarum</i> , 2014, 58, 681-688.	1.9	17
99	Genome wide association mapping to identify aluminium tolerance loci in bread wheat. <i>Euphytica</i> , 2014, 198, 401-411.	0.6	16
100	Separating the wheat from the chaff – a strategy to utilize plant genetic resources from ex situ genebanks. <i>Scientific Reports</i> , 2014, 4, 5231.	1.6	51
101	The antioxidant enzymes activity in leaves of inter-varietal substitution lines of wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2455-2465.	1.0	12
102	Discovery of loci determining pre-harvest sprouting and dormancy in wheat and barley applying segregation and association mapping. <i>Biologia Plantarum</i> , 2013, 57, 663-674.	1.9	24
103	Genetic variation for secondary seed dormancy and seed longevity in a set of black-seeded European winter oilseed rape cultivars. <i>Plant Breeding</i> , 2013, 132, 174-179.	1.0	26
104	A Noninvasive Platform for Imaging and Quantifying Oil Storage in Submillimeter Tobacco Seed. <i>Plant Physiology</i> , 2013, 161, 583-593.	2.3	33
105	Effects of Rht dwarfing alleles on wheat seed vigour after controlled deterioration. <i>Crop and Pasture Science</i> , 2013, 64, 857.	0.7	9
106	Population Structure of <i>Mycosphaerella graminicola</i> and Location of Genes for Resistance to the Pathogen: Recent Advances in Argentina. <i>International Journal of Agronomy</i> , 2012, 2012, 1-7.	0.5	9
107	The D genome carries a gene determining purple grain colour in wheat. <i>Cereal Research Communications</i> , 2012, 40, 334-341.	0.8	44
108	Molecular markers in management of ex situ PGR – A case study. <i>Journal of Biosciences</i> , 2012, 37, 871-877.	0.5	16

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109	Mapping wheat powdery mildew resistance derived from <i>Aegilops markgrafii</i> . Plant Genetic Resources: Characterisation and Utilisation, 2012, 10, 137-140.	0.4	11
110	An association mapping analysis of dormancy and pre-harvest sprouting in wheat. Euphytica, 2012, 188, 409-417.	0.6	42
111	QTL analysis for thousand-grain weight under terminal drought stress in bread wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 50	0.6	50
112	Genetic studies of seed longevity in hexaploid wheat using segregation and association mapping approaches. Euphytica, 2012, 186, 1-13.	0.6	70
113	Could EST-based markers be used for the marker-assisted selection of drought tolerant barley (Hordeum vulgare) lines?. Euphytica, 2011, 178, 373-391.	0.6	16
114	Comparative molecular marker-based genetic mapping of flavanone 3-hydroxylase genes in wheat, rye and barley. Euphytica, 2011, 179, 333-341.	0.6	23
115	Genome-wide association mapping: a case study in bread wheat (Triticum aestivum L.). Molecular Breeding, 2011, 27, 37-58.	1.0	278
116	Leaf dehydroascorbate reductase and catalase activity is associated with soil drought tolerance in bread wheat. Acta Physiologiae Plantarum, 2011, 33, 2169-2177.	1.0	26
117	Haplotyping, linkage mapping and expression analysis of barley genes regulated by terminal drought stress influencing seed quality. BMC Plant Biology, 2011, 11, 1.	1.6	214
118	The allelic state at the major semi-dwarfing genes in a panel of Turkish bread wheat cultivars and landraces. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 423-429.	0.4	15
119	Seed longevity in oilseed rape (<i>Brassica napus</i> L.) – genetic variation and QTL mapping. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 260-263.	0.4	52
120	Variability of Rc (red coleoptile) alleles in wheat and wheat-alien genetic stock collections. Cereal Research Communications, 2011, 39, 465-474.	0.8	22
121	Functional diversity at the Rc (red coleoptile) gene in bread wheat. Molecular Breeding, 2010, 25, 125-132.	1.0	28
122	Mapping quantitative resistance to septoria tritici blotch in spelt wheat. European Journal of Plant Pathology, 2010, 128, 317-324.	0.8	22
123	Genetic mapping within the wheat D genome reveals QTL for germination, seed vigour and longevity, and early seedling growth. Euphytica, 2010, 171, 129.	0.6	82
124	Mapping genes controlling anthocyanin pigmentation on the glume and pericarp in tetraploid wheat (Triticum durum L.). Euphytica, 2010, 171, 65-69.	0.6	51
125	Embryo lethality in wheat – “rye hybrids” mode of inheritance and the identification of a complementary gene in wheat. Euphytica, 2010, 176, 191-198.	0.6	7
126	EST-SSR based estimates on functional genetic variation in a barley (Hordeum vulgare L.) collection from Egypt. Genetic Resources and Crop Evolution, 2010, 57, 515-521.	0.8	13

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127	Population structures of genebank accessions of <i>Salvia officinalis</i> L. (Lamiaceae) revealed by high resolution melting analysis. <i>Biochemical Systematics and Ecology</i> , 2010, 38, 178-186.	0.6	23
128	Variability of the essential oil composition in the sage collection of the Genebank Gatersleben: a new viridiflorol chemotype. <i>Flavour and Fragrance Journal</i> , 2010, 25, 75-82.	1.2	23
129	Interspecies and intergenus transferability of barley and wheat Dâ€genome microsatellite markers. <i>Annals of Applied Biology</i> , 2010, 156, 347-356.	1.3	20
130	Comparative analysis of the grain proteome fraction in barley genotypes with contrasting salinity tolerance during germination. <i>Plant, Cell and Environment</i> , 2010, 33, 211-222.	2.8	102
131	Microsatellite mapping of a leaf rust resistance gene transferred to common wheat from <i>Triticum timopheevii</i> . <i>Cereal Research Communications</i> , 2010, 38, 211-219.	0.8	15
132	The longevity of crop seeds stored under ambient conditions. <i>Seed Science Research</i> , 2010, 20, 1-12.	0.8	135
133	Investigation of Antioxidant and Rosmarinic Acid Variation in the Sage Collection of the Genebank in Gatersleben. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 3813-3819.	2.4	71
134	Clustering anthocyanin pigmentation genes in wheat group 7 chromosomes. <i>Cereal Research Communications</i> , 2009, 37, 391-398.	0.8	31
135	Glume coloration in wheat: Allelism test, consensus mapping and its association with specific microsatellite allele. <i>Cereal Research Communications</i> , 2009, 37, 37-43.	0.8	12
136	Mapping of loci affecting copper tolerance in wheatâ€The possible impact of the vernalization gene <i>Vrn-A1</i> . <i>Environmental and Experimental Botany</i> , 2009, 65, 369-375.	2.0	14
137	A new gene controlling the flowering response to photoperiod in wheat. <i>Euphytica</i> , 2009, 165, 579-585.	0.6	28
138	Molecular mapping of quantitative trait loci (QTLs) controlling aluminium tolerance in bread wheat. <i>Euphytica</i> , 2009, 166, 283-290.	0.6	42
139	Seed conservation in ex situ genebanksâ€genetic studies on longevity in barley. <i>Euphytica</i> , 2009, 170, 5-14.	0.6	74
140	Variation in salt tolerance within a Georgian wheat germplasm collection. <i>Genetic Resources and Crop Evolution</i> , 2009, 56, 1125-1130.	0.8	28
141	Microsatellite mapping of genes that determine supernumerary spikelets in wheat (<i>T.Âaestivum</i>) and rye (<i>S.Âcereale</i>). <i>Theoretical and Applied Genetics</i> , 2009, 119, 867-874.	1.8	39
142	Salt stress-induced alterations in the root proteome of barley genotypes with contrasting response towards salinity. <i>Journal of Experimental Botany</i> , 2009, 60, 3545-3557.	2.4	191
143	A QTL analysis of aluminium tolerance in barley, using gene-based markers. <i>Cereal Research Communications</i> , 2009, 37, 531-540.	0.8	22
144	Molecular mapping of genomic regions associated with wheat seedling growth under osmotic stress. <i>Biologia Plantarum</i> , 2008, 52, 259-266.	1.9	73

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145	Mapping quantitative trait loci for growth responses to exogenously applied stress induced hormones in wheat. <i>Euphytica</i> , 2008, 164, 719-727.	0.6	11
146	Fine mapping of the region on wheat chromosome 7D controlling grain weight. <i>Functional and Integrative Genomics</i> , 2008, 8, 79-86.	1.4	101
147	Validation and utilisation of <i>Rht</i> dwarfing gene specific. <i>Cereal Research Communications</i> , 2008, 36, 235-246.	0.8	10
148	Evaluation of Drought-Related Traits and Screening Methods at Different Developmental Stages in Spring Barley. <i>Journal of Agronomy and Crop Science</i> , 2008, 194, 334-342.	1.7	73
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164	Microsatellite mapping of complementary genes for purple grain colour in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	62
165	More precise map position and origin of a durable non-specific adult plant disease resistance against stripe rust (<i>Puccinia striiformis</i>) in wheat. <i>Euphytica</i> , 2006, 153, 1-10.	0.6	33
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167	Development and QTL assessment of <i>Triticum aestivum</i> "Aegilops tauschii" introgression lines. <i>Theoretical and Applied Genetics</i> , 2006, 112, 634-647.	1.8	77
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182	Identification of microsatellite markers for a leaf rust resistance gene introgressed into common wheat from <i>Triticum timopheevii</i> . <i>Plant Breeding</i> , 2004, 123, 93-95.	1.0	14
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