Klaus Pillen

List of Publications by Year
in descending order

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120 papers	5,437 citations	81900 39 h-index	95266 68 g-index

127 all docs	127 docs citations	127 times ranked	3999 citing authors

#	Article	IF	Citations
1	Construction of an RFLP map of barley. Theoretical and Applied Genetics, 1991, 83, 250-256.	3.6	542
2	High-Throughput Phenotyping to Detect Drought Tolerance QTL in Wild Barley Introgression Lines. PLoS ONE, 2014, 9, e97047.	2.5	262
3	Advanced backcross QTL analysis in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2003, 107, 340-352.	3.6	233
4	Modelling the genetic architecture of flowering time control in barley through nested association mapping. BMC Genomics, 2015, 16, 290.	2.8	192
5	AB-QTL analysis in spring barley: II. Detection of favourable exotic alleles for agronomic traits introgressed from wild barley (H. vulgare ssp. spontaneum). Theoretical and Applied Genetics, 2006, 112, 1221-1231.	3.6	143
6	Mapping new EMBL-derived barley microsatellites and their use in differentiating German barley cultivars. Theoretical and Applied Genetics, 2000, 101, 652-660.	3.6	121
7	AB-QTL analysis in winter wheat: I. Synthetic hexaploid wheat (T. turgidum ssp. dicoccoidesÂ Ã—ÂT.) Tj ETQq1 1 0.784314 rgBT /Over Applied Genetics, 2007, 115, 683-695.	3.6	120
8	Yield-related salinity tolerance traits identified in a nested association mapping (NAM) population of wild barley. Scientific Reports, 2016, 6, 32586.	3.3	118
9	AB-QTL analysis in spring barley. I. Detection of resistance genes against powdery mildew, leaf rust and scald introgressed from wild barley. Theoretical and Applied Genetics, 2005, 111, 583-590.	3.6	117
10	Development of candidate introgression lines using an exotic barley accession (Hordeum vulgare ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	115
11	A linkage map of sugar beet (Beta vulgaris L.). Theoretical and Applied Genetics, 1992, 84, 129-135.	3.6	106
12	Association of barley photoperiod and vernalization genes with QTLs for flowering time and agronomic traits in a BC2DH population and a set of wild barley introgression lines. Theoretical and Applied Genetics, 2010, 120, 1559-1574.	3.6	103
13	Selecting a set of wild barley introgression lines and verification of QTL effects for resistance to powdery mildew and leaf rust. Theoretical and Applied Genetics, 2008, 117, 1093-1106.	3.6	101
14	Structural and Temporal Variation in Genetic Diversity of European Spring Twoâ€Row Barley Cultivars and Association Mapping of Quantitative Traits. Plant Genome, 2013, 6, plantgenome2013.03.0007.	2.8	95
15	Phylogenetic relationships between cultivated and wild species of the genusBeta revealed by DNA ?fingerprinting?. Theoretical and Applied Genetics, 1993, 86, 449-457.	3.6	93
16	Identification and verification of QTLs for agronomic traits using wild barley introgression lines. Theoretical and Applied Genetics, 2009, 118, 483-497.	3.6	83
17	Genomic dissection of plant development and its impact on thousand grain weight in barley through nested association mapping. Journal of Experimental Botany, 2016, 67, 2507-2518.	4.8	82
18	AB-QTL analysis reveals new alleles associated to proline accumulation and leaf wilting under drought stress conditions in barley (Hordeum vulgareL.). BMC Genetics, 2012, 13, 61.	2.7	80

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19	Wild barley introgression lines revealed novel QTL alleles for root and related shoot traits in the cultivated barley (Hordeum vulgareL.). BMC Genetics, 2014, 15, 107.	2.7	79
20	Genome-Wide Association Study of Calcium Accumulation in Grains of European Wheat Cultivars. Frontiers in Plant Science, 2017, 8, 1797.	3.6	78
21	Genomeâ€Wide Association Analysis of Grain Yieldâ€Associated Traits in a Panâ€European Barley Cultivar Collection. Plant Genome, 2018, 11, 170073.	2.8	78
22	An Extended Linkage Map of Sugar Beet (Beta vulgaris L.) Including Nine Putative Lethal Genes and the Restorer Gene X. Plant Breeding, 1993, 111, 265-272.	1.9	77
23	Evolutionary Conserved Function of Barley and Arabidopsis 3-KETOACYL-CoA SYNTHASES in Providing Wax Signals for Germination of Powdery Mildew Fungi Â Â. Plant Physiology, 2014, 166, 1621-1633.	4.8	76
24	Comparative AB-QTL analysis in barley using a single exotic donor of Hordeum vulgare ssp. spontaneum.. Theoretical and Applied Genetics, 2004, 108, 1591-1601.	3.6	73
25	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
26	High-Resolution Genotyping of Wild Barley Introgression Lines and Fine-Mapping of the Threshability Locus thresh-1 Using the Illumina GoldenGate Assay. G3: Genes, Genomes, Genetics, 2011, 1, 187-196.	1.8	72
27	Barley yield formation under abiotic stress depends on the interplay between flowering time genes and environmental cues. Scientific Reports, 2019, 9, 6397.	3.3	71
28	Identification of RFLP markers closely linked to the bolting gene B and their significance for the study of the annual habit in beets (Beta vulgaris L.). Theoretical and Applied Genetics, 1994, 88, 852-858.	3.6	67
29	Genome-wide association of yield traits in a nested association mapping population of barley reveals new gene diversity for future breeding. Journal of Experimental Botany, 2018, 69, 3811-3822.	4.8	66
30	AB-QTL analysis in spring barley: III. Identification of exotic alleles for the improvement of malting quality in spring barley (H. vulgare ssp. spontaneum). Molecular Breeding, 2008, 21, 81-93.	2.1	59
31	Identifying Candidate Genes for Enhancing Grain Zn Concentration in Wheat. Frontiers in Plant Science, 2018, 9, 1313.	3.6	56
32	Molecular genetic analysis of theripening-inhibitor andnon-ripening loci of tomato: A first step in genetic map-based cloning of fruit ripening genes. Molecular Genetics and Genomics, 1995, 248, 195-206.	2.4	55
33	Genetic Architecture of Anther Extrusion in Spring and Winter Wheat. Frontiers in Plant Science, 2017, 8, 754.	3.6	53
34	Whole-Genome Association Mapping and Genomic Prediction for Iron Concentration in Wheat Grains. International Journal of Molecular Sciences, 2019, 20, 76.	4.1	52
35	Detection and verification of malting quality QTLs using wild barley introgression lines. Theoretical and Applied Genetics, 2009, 118, 1411-1427.	3.6	50
36	Mapping of the leaf rust resistance gene Lr38 on wheat chromosome arm 6DL using SSR markers. Euphytica, 2008, 162, 457-466.	1.2	49

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37	Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. Molecular Genetics and Genomics, 1996, 251, 526-531.	2.4	46
38	AB-QTL analysis in winter wheat: II. Genetic analysis of seedling and field resistance against leaf rust in a wheat advanced backcross population. Theoretical and Applied Genetics, 2008, 116, 1095-1104.	3.6	44
39	Identifying plant genes shaping microbiota composition in the barley rhizosphere. Nature Communications, 2022, 13, .	12.8	44
40	Adaptive selection of founder segments and epistatic control of plant height in the MAGIC winter wheat population WM-800. BMC Genomics, 2018, 19, 559.	2.8	43
41	Detection and validation of novel QTL for shoot and root traits in barley (Hordeum vulgare L.). Molecular Breeding, 2014, 34, 1373-1387.	2.1	42
42	A nested association mapping population identifies multiple small effect QTL conferring resistance against net blotch (Pyrenophora teres f. teres) in wild barley. PLoS ONE, 2017, 12, e0186803.	2.5	42
43	Detection of nitrogen deficiency QTL in juvenile wild barley introgression linesgrowing in a hydroponic system. BMC Genetics, 2012, 13, 88.	2.7	41
44	A first step toward the development of a barley NAM population and its utilization to detect QTLs conferring leaf rust seedling resistance. Theoretical and Applied Genetics, 2014, 127, 1513-1525.	3.6	41
45	Detection of epistatic interactions between exotic alleles introgressed from wild barley (H. vulgare) Tj ETQq1 1 0.784314 rgBT /Overlo	3.6	40
46	Evaluation of juvenile drought stress tolerance and genotyping by sequencing with wild barley introgression lines. Molecular Breeding, 2014, 34, 1475-1495.	2.1	36
47	Genomic Prediction of Barley Hybrid Performance. Plant Genome, 2016, 9, plantgenome2016.02.0016.	2.8	35
48	Contrasting genetic regulation of plant development in wild barley grown in two European environments revealed by nested association mapping. Journal of Experimental Botany, 2018, 69, 1517-1531.	4.8	33
49	â€œWild barley serves as a source for biofortification of barley grainsâ€• Plant Science, 2019, 283, 83-94.	3.6	33
50	Association genetics studies on frost tolerance in wheat (Triticum aestivum L.) reveal new highly conserved amino acid substitutions in CBF-A3, CBF-A15, VRN3 and PPD1 genes. BMC Genomics, 2018, 19, 409.	2.8	31
51	Postulation of Seedling Leaf Rust Resistance Genes in Selected Ethiopian and German Bread Wheat Cultivars. Crop Science, 2008, 48, 507-516.	1.8	29
52	Growth curve registration for evaluating salinity tolerance in barley. Plant Methods, 2017, 13, 18.	4.3	29
53	QTL controlling grain filling under terminal drought stress in a set of wild barley introgression lines. PLoS ONE, 2017, 12, e0185983.	2.5	29
54	Advanced-backcross QTL analysis in spring barley: IV. Localization of QTLÂÃ—Ânitrogen interaction effects for yield-related traits. Euphytica, 2011, 177, 223-239.	1.2	28

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55	Validation for rootâ€related quantitative trait locus effects of wild origin in the cultivated background of barley (Hordeum vulgare L.). Plant Breeding, 2012, 131, 392-398.	1.9	28
56	An Ancestral Allele of Pyrroline-5-carboxylate synthase1 Promotes Proline Accumulation and Drought Adaptation in Cultivated Barley. Plant Physiology, 2018, 178, 771-782.	4.8	28
57	Advanced backcross-QTL analysis in spring barley (H.Âvulgare ssp. spontaneum) comparing a REML versus a Bayesian model in multi-environmental field trials. Theoretical and Applied Genetics, 2009, 119, 105-123.	3.6	26
58	Editorial: Recent Advances in Flowering Time Control. Frontiers in Plant Science, 2016, 7, 2011.	3.6	26
59	Natural variation in meiotic recombination rate shapes introgression patterns in intraspecific hybrids between wild and domesticated barley. New Phytologist, 2020, 228, 1852-1863.	7.3	26
60	Genetic diversity of Ethiopian durum wheat landraces. PLoS ONE, 2021, 16, e0247016.	2.5	25
61	Genetic dissection of grain elements predicted by hyperspectral imaging associated with yield-related traits in a wild barley NAM population. Plant Science, 2019, 285, 151-164.	3.6	24
62	Identification of proteins associated with malting quality in a subset of wild barley introgression lines. Proteomics, 2012, 12, 2843-2851.	2.2	23
63	Genome-Wide Association Mapping of Anther Extrusion in Hexaploid Spring Wheat. PLoS ONE, 2016, 11, e0155494.	2.5	23
64	Genome-Based Identification of Heterotic Patterns in Rice. Rice, 2017, 10, 22.	4.0	23
65	Advances in Genomics-Based Breeding of Barley: Molecular Tools and Genomic Databases. Agronomy, 2021, 11, 894.	3.0	23
66	Mixed modelling for QTL Ã— environment interaction analysis. Euphytica, 2004, 137, 147-153.	1.2	22
67	Detection of exotic QTLs controlling nitrogen stress tolerance among wild barley introgression lines. Euphytica, 2013, 189, 67-88.	1.2	22
68	Quantitative Trait Loci and Inter-Organ Partitioning for Essential Metal and Toxic Analogue Accumulation in Barley. PLoS ONE, 2016, 11, e0153392.	2.5	22
69	Stability parameter and genotype mean estimates for drought stress effects on root and shoot growth of wild barley pre-introgression lines. Molecular Breeding, 2010, 26, 583-593.	2.1	21
70	Construction of a high-resolution genetic map and YAC-contigs in the tomato Tm-2a region. Theoretical and Applied Genetics, 1996, 93-93, 228-233.	3.6	19
71	Molecular Diversity in Puccinia triticina Isolates from Ethiopia and Germany. Journal of Phytopathology, 2006, 154, 701-710.	1.0	19
72	Estimating parent-specific QTL effects through cumulating linked identity-by-state SNP effects in multiparental populations. Heredity, 2017, 118, 477-485.	2.6	18

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73	Genome scan identifies flowering-independent effects of barley HsDry2.2 locus on yield traits under water deficit. Journal of Experimental Botany, 2018, 69, 1765-1779.	4.8	18
74	Discovery and fine mapping of Rph28: a new gene conferring resistance to Puccinia hordei from wild barley. Theoretical and Applied Genetics, 2021, 134, 2167-2179.	3.6	18
75	Genotypic and phenotypic changes in wild barley (Hordeum vulgare subsp. spontaneum) during a period of climate change in Jordan. Genetic Resources and Crop Evolution, 2017, 64, 1295-1312.	1.6	17
76	Changes in isovitexin-O-glycosylation during the development of young barley plants. Phytochemistry, 2018, 148, 11-20.	2.9	17
77	Can metabolic prediction be an alternative to genomic prediction in barley?. PLoS ONE, 2020, 15, e0234052.	2.5	17
78	Evaluation of RGB and Multispectral Unmanned Aerial Vehicle (UAV) Imagery for High-Throughput Phenotyping and Yield Prediction in Barley Breeding. Remote Sensing, 2021, 13, 2670.	4.0	17
79	Genetic and physical mapping of anther extrusion in elite European winter wheat. PLoS ONE, 2017, 12, e0187744.	2.5	17
80	Genetic analysis and detection of new <scp>QTL</scp> alleles for <scp>S</scp>eptoria tritici blotch resistance using two advanced backcross wheat populations. Plant Breeding, 2015, 134, 514-519.	1.9	16
81	Downy mildew resistance is genetically mediated by prophylactic production of phenylpropanoids in hop. Plant, Cell and Environment, 2021, 44, 323-338.	5.7	16
82	Optimizing the procedure of grain nutrient predictions in barley via hyperspectral imaging. PLoS ONE, 2019, 14, e0224491.	2.5	15
83	Dynamics and genetic regulation of leaf nutrient concentration in barley based on hyperspectral imaging and machine learning. Plant Science, 2022, 315, 111123.	3.6	15
84	Advanced backcross quantitative trait locus analysis in winter wheat: Dissection of stripe rust seedling resistance and identification of favorable exotic alleles originated from a primary hexaploid wheat (Triticum turgidum ssp. dicoccoidesÂÃ—ÂAegilops tauschii). Molecular Breeding, 2012, 30, 1219-1229.	2.1	14
85	Copy number variation of chromosome 5A and its association with Q gene expression, morphological aberrations, and agronomic performance of winter wheat cultivars. Theoretical and Applied Genetics, 2013, 126, 3049-3063.	3.6	14
86	Genetic loci mediating circadian clock output plasticity and crop productivity under barley domestication. New Phytologist, 2021, 230, 1787-1801.	7.3	14
87	Geography of Genetic Structure in Barley Wild Relative Hordeum vulgare subsp. spontaneum in Jordan. PLoS ONE, 2016, 11, e0160745.	2.5	13
88	Toward identification of a putative candidate gene for nutrient mineral accumulation in wheat grains for human nutrition purposes. Journal of Experimental Botany, 2021, 72, 6305-6318.	4.8	12
89	Identification of QTL conferring resistance to stripe rust (Puccinia striiformis f. sp. hordei) and leaf rust (Puccinia hordei) in barley using nested association mapping (NAM). PLoS ONE, 2018, 13, e0191666.	2.5	12
90	Inheritance of field resistance to Septoria tritici blotch in the wheat doubled-haploid population SolitÃrÂÃ—ÂMazurka. Euphytica, 2013, 194, 161-176.	1.2	11

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91	Genetic regulation of growth and nutrient content under phosphorus deficiency in the wild barley introgression library S42IL. Plant Breeding, 2017, 136, 892-907.	1.9	11
92	Exotic QTL improve grain quality in the tri-parental wheat population SW84. PLoS ONE, 2017, 12, e0179851.	2.5	11
93	The genetic diversity of Ethiopian barley genotypes in relation to their geographical origin. PLoS ONE, 2022, 17, e0260422.	2.5	11
94	Genetic mapping of genes for twelve nuclear-encoded polypeptides associated with the thylakoid membranes inBeta vulgarisL. FEBS Letters, 1996, 395, 58-62.	2.8	10
95	Identification of QTLs conferring resistance to scald (Rhynchosporium commune) in the barley nested association mapping population HEB-25. BMC Genomics, 2020, 21, 837.	2.8	10
96	Association Mapping of Drought Tolerance Indices in Ethiopian Durum Wheat (Triticum turgidum ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	10
97	A donor-specific QTL, exhibiting allelic variation for leaf sheath hairiness in a nested association mapping population, is located on barley chromosome 4H. PLoS ONE, 2017, 12, e0189446.	2.5	9
98	Combining genome-wide prediction and a phenology model to simulate heading date in spring barley. Field Crops Research, 2017, 202, 84-93.	5.1	8
99	Identification of wild barley derived alleles associated with plant development in an Australian environment. Euphytica, 2020, 216, 1.	1.2	8
100	Evaluation of wild barley introgression lines for agronomic traits related to nitrogen fertilization. Euphytica, 2020, 216, 1.	1.2	8
101	Genomic dissection reveals QTLs for grain biomass and correlated traits under drought stress in Ethiopian durum wheat (<i>Triticum turgidum ssp<i>. <i>durum<i>). Plant Breeding, 2022, 141, 338-354.	1.9	8
102	Changes in barley (Hordeum vulgare L. subsp. vulgare) genetic diversity and structure in Jordan over a period of 31 years. Plant Genetic Resources: Characterisation and Utilisation, 2018, 16, 112-126.	0.8	7
103	Development of a bioassay to assess resistance to Fusarium oxysporum (Schlecht.) in asparagus () Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	7
104	Mapping of quantitative trait loci (QTL) for resistance against Zymoseptoria tritici in the winter spelt wheat accession HTRI1410 (Triticum aestivum subsp. spelta). Euphytica, 2019, 215, 1.	1.2	7
105	Rapid and reliable screening of a tomato YAC library exclusively based on PCR. Plant Molecular Biology Reporter, 1996, 14, 58-67.	1.8	6
106	Genetic Analysis and Transfer of Favorable Exotic QTL Alleles for Grain Yield Across D Genome Using Two Advanced Backcross Wheat Populations. Frontiers in Plant Science, 2019, 10, 711.	3.6	6
107	Discrimination of alleles and copy numbers at the Q locus in hexaploid wheat using quantitative pyrosequencing. Euphytica, 2012, 186, 207-218.	1.2	5
108	Genome-wide association study on metabolite accumulation in a wild barley NAM population reveals natural variation in sugar metabolism. PLoS ONE, 2021, 16, e0246510.	2.5	5

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109	Construction of a high-resolution genetic map and YAC-contigs in the tomato Tm-2a region. Theoretical and Applied Genetics, 1996, 93, 228-233.	3.6	5
110	Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. Molecular Genetics and Genomics, 1996, 251, 526.	2.4	5
111	Genomic Dissection of Peduncle Morphology in Barley through Nested Association Mapping. Plants, 2021, 10, 10.	3.5	5
112	Proof of concept to unmask the breeding value of genetic resources of barley (Hordeum vulgare) with a hybrid strategy. Plant Breeding, 2020, 139, 536-549.	1.9	4
113	Lr21 diversity unveils footprints of wheat evolution and its new role in broadâ€spectrum leaf rust resistance. Plant, Cell and Environment, 2021, 44, 3445-3458.	5.7	4
114	Detection and Verification of QTL for Salinity Tolerance at Germination and Seedling Stages Using Wild Barley Introgression Lines. Plants, 2021, 10, 2246.	3.5	4
115	Genetic and environmental effects on the occurrence of speltoids in winter wheat cultivars. Plant Breeding, 2014, 133, 442-447.	1.9	3
116	GenoTypeMapper: graphical genotyping on genetic and sequence-based maps. Plant Methods, 2020, 16, 123.	4.3	3
117	Importance of correcting genomic relationships in single-locus QTL mapping model with an advanced backcross population. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	0
118	Footprints of Selection Derived From Temporal Heterozygosity Patterns in a Barley Nested Association Mapping Population. Frontiers in Plant Science, 2021, 12, 764537.	3.6	0
119	Vision-Based 3D-Reconstruction of Barley Plants. Lecture Notes in Computer Science, 2013, , 406-415.	1.3	0
120	Nested association mapping in barley to identify extractable trait genes. Burleigh Dodds Series in Agricultural Science, 2019, , 451-474.	0.2	0