

# Klaus Pillen

## List of Publications by Year in descending order

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Version: 2024-02-01

120  
papers

5,437  
citations

81889

39  
h-index

95259

68  
g-index

127  
all docs

127  
docs citations

127  
times ranked

3999  
citing authors



#	ARTICLE	IF	CITATIONS
19	Wild barley introgression lines revealed novel QTL alleles for root and related shoot traits in the cultivated barley ( <i>Hordeum vulgare</i> L.). <i>BMC Genetics</i> , 2014, 15, 107.	2.7	79
20	Genome-Wide Association Study of Calcium Accumulation in Grains of European Wheat Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 1797.	3.6	78
21	Genome-Wide Association Analysis of Grain Yield-Associated Traits in a Pan-European Barley Cultivar Collection. <i>Plant Genome</i> , 2018, 11, 170073.	2.8	78
22	An Extended Linkage Map of Sugar Beet ( <i>Beta vulgaris</i> L.) Including Nine Putative Lethal Genes and the Restorer Gene X. <i>Plant Breeding</i> , 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. <i>Plant Physiology</i> , 2014, 166, 1621-1633.	4.8	76
24	Comparative AB-QTL analysis in barley using a single exotic donor of <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> .. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1591-1601.	3.6	73
25	Genome-wide association of barley plant growth under drought stress using a nested association mapping population. <i>BMC Plant Biology</i> , 2019, 19, 134.	3.6	73
26	High-Resolution Genotyping of Wild Barley Introgression Lines and Fine-Mapping of the Threshability Locus <i>thresh-1</i> Using the Illumina GoldenGate Assay. <i>G3: Genes, Genomes, Genetics</i> , 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. <i>Scientific Reports</i> , 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 ( <i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 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. <i>Journal of Experimental Botany</i> , 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 ( <i>H. vulgare</i> ssp. <i>spontaneum</i> ). <i>Molecular Breeding</i> , 2008, 21, 81-93.	2.1	59
31	Identifying Candidate Genes for Enhancing Grain Zn Concentration in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1313.	3.6	56
32	Molecular genetic analysis of the ripening-inhibitor and non-ripening loci of tomato: A first step in genetic map-based cloning of fruit ripening genes. <i>Molecular Genetics and Genomics</i> , 1995, 248, 195-206.	2.4	55
33	Genetic Architecture of Anther Extrusion in Spring and Winter Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 754.	3.6	53
34	Whole-Genome Association Mapping and Genomic Prediction for Iron Concentration in Wheat Grains. <i>International Journal of Molecular Sciences</i> , 2019, 20, 76.	4.1	52
35	Detection and verification of malting quality QTLs using wild barley introgression lines. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1411-1427.	3.6	50
36	Mapping of the leaf rust resistance gene Lr38 on wheat chromosome arm 6DL using SSR markers. <i>Euphytica</i> , 2008, 162, 457-466.	1.2	49

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37	Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. <i>Molecular Genetics and Genomics</i> , 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. <i>Theoretical and Applied Genetics</i> , 2008, 116, 1095-1104.	3.6	44
39	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 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. <i>BMC Genomics</i> , 2018, 19, 559.	2.8	43
41	Detection and validation of novel QTL for shoot and root traits in barley ( <i>Hordeum vulgare</i> L.). <i>Molecular Breeding</i> , 2014, 34, 1373-1387.	2.1	42
42	A nested association mapping population identifies multiple small effect QTL conferring resistance against net blotch ( <i>Pyrenophora teres</i> f. <i>teres</i> ) in wild barley. <i>PLoS ONE</i> , 2017, 12, e0186803.	2.5	42
43	Detection of nitrogen deficiency QTL in juvenile wild barley introgression lines growing in a hydroponic system. <i>BMC Genetics</i> , 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. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1513-1525.	3.6	41
45	Detection of epistatic interactions between exotic alleles introgressed from wild barley ( <i>H. vulgare</i> ) Tj ETQq1 1 0.784314 rgBT / Overl	3.6	40
46	Evaluation of juvenile drought stress tolerance and genotyping by sequencing with wild barley introgression lines. <i>Molecular Breeding</i> , 2014, 34, 1475-1495.	2.1	36
47	Genomic Prediction of Barley Hybrid Performance. <i>Plant Genome</i> , 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. <i>Journal of Experimental Botany</i> , 2018, 69, 1517-1531.	4.8	33
49	Wild barley serves as a source for biofortification of barley grains. <i>Plant Science</i> , 2019, 283, 83-94.	3.6	33
50	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.	2.8	31
51	Postulation of Seedling Leaf Rust Resistance Genes in Selected Ethiopian and German Bread Wheat Cultivars. <i>Crop Science</i> , 2008, 48, 507-516.	1.8	29
52	Growth curve registration for evaluating salinity tolerance in barley. <i>Plant Methods</i> , 2017, 13, 18.	4.3	29
53	QTL controlling grain filling under terminal drought stress in a set of wild barley introgression lines. <i>PLoS ONE</i> , 2017, 12, e0185983.	2.5	29
54	Advanced-backcross QTL analysis in spring barley: IV. Localization of QTL—Nitrogen interaction effects for yield-related traits. <i>Euphytica</i> , 2011, 177, 223-239.	1.2	28

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55	Validation for root-related quantitative trait locus effects of wild origin in the cultivated background of barley ( <i>Hordeum vulgare</i> L.). <i>Plant Breeding</i> , 2012, 131, 392-398.	1.9	28
56	An Ancestral Allele of <i>Pyrroline-5-carboxylate synthase1</i> Promotes Proline Accumulation and Drought Adaptation in Cultivated Barley. <i>Plant Physiology</i> , 2018, 178, 771-782.	4.8	28
57	Advanced backcross-QTL analysis in spring barley ( <i>H. vulgare</i> ssp. <i>spontaneum</i> ) comparing a REML versus a Bayesian model in multi-environmental field trials. <i>Theoretical and Applied Genetics</i> , 2009, 119, 105-123.	3.6	26
58	Editorial: Recent Advances in Flowering Time Control. <i>Frontiers in Plant Science</i> , 2016, 7, 2011.	3.6	26
59	Natural variation in meiotic recombination rate shapes introgression patterns in intraspecific hybrids between wild and domesticated barley. <i>New Phytologist</i> , 2020, 228, 1852-1863.	7.3	26
60	Genetic diversity of Ethiopian durum wheat landraces. <i>PLoS ONE</i> , 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. <i>Plant Science</i> , 2019, 285, 151-164.	3.6	24
62	Identification of proteins associated with malting quality in a subset of wild barley introgression lines. <i>Proteomics</i> , 2012, 12, 2843-2851.	2.2	23
63	Genome-Wide Association Mapping of Anther Extrusion in Hexaploid Spring Wheat. <i>PLoS ONE</i> , 2016, 11, e0155494.	2.5	23
64	Genome-Based Identification of Heterotic Patterns in Rice. <i>Rice</i> , 2017, 10, 22.	4.0	23
65	Advances in Genomics-Based Breeding of Barley: Molecular Tools and Genomic Databases. <i>Agronomy</i> , 2021, 11, 894.	3.0	23
66	Mixed modelling for QTL × environment interaction analysis. <i>Euphytica</i> , 2004, 137, 147-153.	1.2	22
67	Detection of exotic QTLs controlling nitrogen stress tolerance among wild barley introgression lines. <i>Euphytica</i> , 2013, 189, 67-88.	1.2	22
68	Quantitative Trait Loci and Inter-Organ Partitioning for Essential Metal and Toxic Analogue Accumulation in Barley. <i>PLoS ONE</i> , 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. <i>Molecular Breeding</i> , 2010, 26, 583-593.	2.1	21
70	Construction of a high-resolution genetic map and YAC-contigs in the tomato Tm-2a region. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 228-233.	3.6	19
71	Molecular Diversity in <i>Puccinia triticina</i> Isolates from Ethiopia and Germany. <i>Journal of Phytopathology</i> , 2006, 154, 701-710.	1.0	19
72	Estimating parent-specific QTL effects through cumulating linked identity-by-state SNP effects in multiparental populations. <i>Heredity</i> , 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. <i>Journal of Experimental Botany</i> , 2018, 69, 1765-1779.	4.8	18
74	Discovery and fine mapping of Rph28: a new gene conferring resistance to <i>Puccinia hordei</i> from wild barley. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2167-2179.	3.6	18
75	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.	1.6	17
76	Changes in isovitexin-O-glycosylation during the development of young barley plants. <i>Phytochemistry</i> , 2018, 148, 11-20.	2.9	17
77	Can metabolic prediction be an alternative to genomic prediction in barley?. <i>PLoS ONE</i> , 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. <i>Remote Sensing</i> , 2021, 13, 2670.	4.0	17
79	Genetic and physical mapping of anther extrusion in elite European winter wheat. <i>PLoS ONE</i> , 2017, 12, e0187744.	2.5	17
80	Genetic analysis and detection of new QTL alleles for <i>Sceptoria tritici</i> blotch resistance using two advanced backcross wheat populations. <i>Plant Breeding</i> , 2015, 134, 514-519.	1.9	16
81	Downy mildew resistance is genetically mediated by prophylactic production of phenylpropanoids in hop. <i>Plant, Cell and Environment</i> , 2021, 44, 323-338.	5.7	16
82	Optimizing the procedure of grain nutrient predictions in barley via hyperspectral imaging. <i>PLoS ONE</i> , 2019, 14, e0224491.	2.5	15
83	Dynamics and genetic regulation of leaf nutrient concentration in barley based on hyperspectral imaging and machine learning. <i>Plant Science</i> , 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 ( <i>Triticum turgidum</i> ssp. <i>dicoccoides</i> — <i>Aegilops tauschii</i> ). <i>Molecular Breeding</i> , 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. <i>Theoretical and Applied Genetics</i> , 2013, 126, 3049-3063.	3.6	14
86	Genetic loci mediating circadian clock output plasticity and crop productivity under barley domestication. <i>New Phytologist</i> , 2021, 230, 1787-1801.	7.3	14
87	Geography of Genetic Structure in Barley Wild Relative <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> in Jordan. <i>PLoS ONE</i> , 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. <i>Journal of Experimental Botany</i> , 2021, 72, 6305-6318.	4.8	12
89	Identification of QTL conferring resistance to stripe rust ( <i>Puccinia striiformis</i> f. sp. <i>hordei</i> ) and leaf rust ( <i>Puccinia hordei</i> ) in barley using nested association mapping (NAM). <i>PLoS ONE</i> , 2018, 13, e0191666.	2.5	12
90	Inheritance of field resistance to <i>Septoria tritici</i> blotch in the wheat doubled-haploid population Solit—Mazurka. <i>Euphytica</i> , 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. <i>Plant Breeding</i> , 2017, 136, 892-907.	1.9	11
92	Exotic QTL improve grain quality in the tri-parental wheat population SW84. <i>PLoS ONE</i> , 2017, 12, e0179851.	2.5	11
93	The genetic diversity of Ethiopian barley genotypes in relation to their geographical origin. <i>PLoS ONE</i> , 2022, 17, e0260422.	2.5	11
94	Genetic mapping of genes for twelve nuclear-encoded polypeptides associated with the thylakoid membranes in <i>Beta vulgaris</i> L. <i>FEBS Letters</i> , 1996, 395, 58-62.	2.8	10
95	Identification of QTLs conferring resistance to scald ( <i>Rhynchosporium commune</i> ) in the barley nested association mapping population HEB-25. <i>BMC Genomics</i> , 2020, 21, 837.	2.8	10
96	Association Mapping of Drought Tolerance Indices in Ethiopian Durum Wheat ( <i>Triticum turgidum</i> 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. <i>PLoS ONE</i> , 2017, 12, e0189446.	2.5	9
98	Combining genome-wide prediction and a phenology model to simulate heading date in spring barley. <i>Field Crops Research</i> , 2017, 202, 84-93.	5.1	8
99	Identification of wild barley derived alleles associated with plant development in an Australian environment. <i>Euphytica</i> , 2020, 216, 1.	1.2	8
100	Evaluation of wild barley introgression lines for agronomic traits related to nitrogen fertilization. <i>Euphytica</i> , 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</i> ssp. <i>durum</i> ). <i>Plant Breeding</i> , 2022, 141, 338-354.	1.9	8
102	Changes in barley ( <i>Hordeum vulgare</i> L. subsp. <i>vulgare</i> ) genetic diversity and structure in Jordan over a period of 31 years. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 112-126.	0.8	7
103	Development of a bioassay to assess resistance to <i>Fusarium oxysporum</i> (Schlecht.) in asparagus ( <i>)</i> Tj ETQq1 1 0.784314 rgBT <sub>7</sub> /Overlock	1.0	7
104	Mapping of quantitative trait loci (QTL) for resistance against <i>Zymoseptoria tritici</i> in the winter spelt wheat accession HTRI1410 ( <i>Triticum aestivum</i> subsp. <i>spelta</i> ). <i>Euphytica</i> , 2019, 215, 1.	1.2	7
105	Rapid and reliable screening of a tomato YAC library exclusively based on PCR. <i>Plant Molecular Biology Reporter</i> , 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. <i>Frontiers in Plant Science</i> , 2019, 10, 711.	3.6	6
107	Discrimination of alleles and copy numbers at the Q locus in hexaploid wheat using quantitative pyrosequencing. <i>Euphytica</i> , 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. <i>PLoS ONE</i> , 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. <i>Theoretical and Applied Genetics</i> , 1996, 93, 228-233.	3.6	5
110	Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. <i>Molecular Genetics and Genomics</i> , 1996, 251, 526.	2.4	5
111	Genomic Dissection of Peduncle Morphology in Barley through Nested Association Mapping. <i>Plants</i> , 2021, 10, 10.	3.5	5
112	Proof of concept to unmask the breeding value of genetic resources of barley ( <i>Hordeum vulgare</i> ) with a hybrid strategy. <i>Plant Breeding</i> , 2020, 139, 536-549.	1.9	4
113	Lr21 diversity unveils footprints of wheat evolution and its new role in broad-spectrum leaf rust resistance. <i>Plant, Cell and Environment</i> , 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. <i>Plants</i> , 2021, 10, 2246.	3.5	4
115	Genetic and environmental effects on the occurrence of speltoids in winter wheat cultivars. <i>Plant Breeding</i> , 2014, 133, 442-447.	1.9	3
116	GenoTypeMapper: graphical genotyping on genetic and sequence-based maps. <i>Plant Methods</i> , 2020, 16, 123.	4.3	3
117	Importance of correcting genomic relationships in single-locus QTL mapping model with an advanced backcross population. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
118	Footprints of Selection Derived From Temporal Heterozygosity Patterns in a Barley Nested Association Mapping Population. <i>Frontiers in Plant Science</i> , 2021, 12, 764537.	3.6	0
119	Vision-Based 3D-Reconstruction of Barley Plants. <i>Lecture Notes in Computer Science</i> , 2013, , 406-415.	1.3	0
120	Nested association mapping in barley to identify extractable trait genes. <i>Burleigh Dodds Series in Agricultural Science</i> , 2019, , 451-474.	0.2	0