

# Klaus Pillen

## List of Publications by Year in descending order

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120  
papers

5,437  
citations

81839

39  
h-index

95218

68  
g-index

127  
all docs

127  
docs citations

127  
times ranked

3999  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics and genetic regulation of leaf nutrient concentration in barley based on hyperspectral imaging and machine learning. <i>Plant Science</i> , 2022, 315, 111123.	1.7	15
2	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.	1.0	8
3	Association Mapping of Drought Tolerance Indices in Ethiopian Durum Wheat ( <i>Triticum turgidum</i> ssp.) Tj ETQq1 1 0.784314 18 BT /Over	1.7	18
4	The genetic diversity of Ethiopian barley genotypes in relation to their geographical origin. <i>PLoS ONE</i> , 2022, 17, e0260422.	1.1	11
5	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	5.8	44
6	Downy mildew resistance is genetically mediated by prophylactic production of phenylpropanoids in hop. <i>Plant, Cell and Environment</i> , 2021, 44, 323-338.	2.8	16
7	Genetic diversity of Ethiopian durum wheat landraces. <i>PLoS ONE</i> , 2021, 16, e0247016.	1.1	25
8	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.	1.1	5
9	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.	1.8	18
10	Genetic loci mediating circadian clock output plasticity and crop productivity under barley domestication. <i>New Phytologist</i> , 2021, 230, 1787-1801.	3.5	14
11	Importance of correcting genomic relationships in single-locus QTL mapping model with an advanced backcross population. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
12	Advances in Genomics-Based Breeding of Barley: Molecular Tools and Genomic Databases. <i>Agronomy</i> , 2021, 11, 894.	1.3	23
13	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.	2.4	12
14	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.	1.8	17
15	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.	2.8	4
16	Footprints of Selection Derived From Temporal Heterozygosity Patterns in a Barley Nested Association Mapping Population. <i>Frontiers in Plant Science</i> , 2021, 12, 764537.	1.7	0
17	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
18	Genomic Dissection of Peduncle Morphology in Barley through Nested Association Mapping. <i>Plants</i> , 2021, 10, 10.	1.6	5

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19	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.	1.0	4
20	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.	3.5	26
21	GenoTypeMapper: graphical genotyping on genetic and sequence-based maps. <i>Plant Methods</i> , 2020, 16, 123.	1.9	3
22	Identification of wild barley derived alleles associated with plant development in an Australian environment. <i>Euphytica</i> , 2020, 216, 1.	0.6	8
23	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.	1.2	10
24	Can metabolic prediction be an alternative to genomic prediction in barley?. <i>PLoS ONE</i> , 2020, 15, e0234052.	1.1	17
25	Evaluation of wild barley introgression lines for agronomic traits related to nitrogen fertilization. <i>Euphytica</i> , 2020, 216, 1.	0.6	8
26	Optimizing the procedure of grain nutrient predictions in barley via hyperspectral imaging. <i>PLoS ONE</i> , 2019, 14, e0224491.	1.1	15
27	Development of a bioassay to assess resistance to <i>Fusarium oxysporum</i> (Schlecht.) in asparagus ( <i>T. tetragynum</i> ) Tj ETQq1 1 0.784314 rgBT <sub>7</sub> /Overlo	0.5	7
28	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.	1.7	6
29	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.	0.6	7
30	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.	1.7	24
31	Barley yield formation under abiotic stress depends on the interplay between flowering time genes and environmental cues. <i>Scientific Reports</i> , 2019, 9, 6397.	1.6	71
32	Genome-wide association of barley plant growth under drought stress using a nested association mapping population. <i>BMC Plant Biology</i> , 2019, 19, 134.	1.6	73
33	“Wild barley serves as a source for biofortification of barley grains” <i>Plant Science</i> , 2019, 283, 83-94.	1.7	33
34	Whole-Genome Association Mapping and Genomic Prediction for Iron Concentration in Wheat Grains. <i>International Journal of Molecular Sciences</i> , 2019, 20, 76.	1.8	52
35	Nested association mapping in barley to identify extractable trait genes. <i>Burleigh Dodds Series in Agricultural Science</i> , 2019, , 451-474.	0.1	0
36	Changes in isovitexin-O-glycosylation during the development of young barley plants. <i>Phytochemistry</i> , 2018, 148, 11-20.	1.4	17

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37	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.	2.4	33
38	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.	2.4	18
39	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.	0.4	7
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.	1.2	43
41	Identifying Candidate Genes for Enhancing Grain Zn Concentration in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1313.	1.7	56
42	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.	2.3	28
43	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.	2.4	66
44	Genome-Wide Association Analysis of Grain Yield-Associated Traits in a Pan-European Barley Cultivar Collection. <i>Plant Genome</i> , 2018, 11, 170073.	1.6	78
45	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
46	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.	1.1	12
47	Estimating parent-specific QTL effects through cumulating linked identity-by-state SNP effects in multiparental populations. <i>Heredity</i> , 2017, 118, 477-485.	1.2	18
48	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.	1.0	11
49	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
50	Genome-Based Identification of Heterotic Patterns in Rice. <i>Rice</i> , 2017, 10, 22.	1.7	23
51	Growth curve registration for evaluating salinity tolerance in barley. <i>Plant Methods</i> , 2017, 13, 18.	1.9	29
52	Combining genome-wide prediction and a phenology model to simulate heading date in spring barley. <i>Field Crops Research</i> , 2017, 202, 84-93.	2.3	8
53	Genetic Architecture of Anther Extrusion in Spring and Winter Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 754.	1.7	53
54	Genome-Wide Association Study of Calcium Accumulation in Grains of European Wheat Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 1797.	1.7	78

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55	QTL controlling grain filling under terminal drought stress in a set of wild barley introgression lines. PLoS ONE, 2017, 12, e0185983.	1.1	29
56	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. PLoS ONE, 2017, 12, e0186803.	1.1	42
57	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.	1.1	9
58	Exotic QTL improve grain quality in the tri-parental wheat population SW84. PLoS ONE, 2017, 12, e0179851.	1.1	11
59	Genetic and physical mapping of anther extrusion in elite European winter wheat. PLoS ONE, 2017, 12, e0187744.	1.1	17
60	Genome-Wide Association Mapping of Anther Extrusion in Hexaploid Spring Wheat. PLoS ONE, 2016, 11, e0155494.	1.1	23
61	Yield-related salinity tolerance traits identified in a nested association mapping (NAM) population of wild barley. Scientific Reports, 2016, 6, 32586.	1.6	118
62	Genomic Prediction of Barley Hybrid Performance. Plant Genome, 2016, 9, plantgenome2016.02.0016.	1.6	35
63	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.	2.4	82
64	Editorial: Recent Advances in Flowering Time Control. Frontiers in Plant Science, 2016, 7, 2011.	1.7	26
65	Quantitative Trait Loci and Inter-Organ Partitioning for Essential Metal and Toxic Analogue Accumulation in Barley. PLoS ONE, 2016, 11, e0153392.	1.1	22
66	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
67	Genetic analysis and detection of new QTL alleles for <i>S</i> ptoria tritici blotch resistance using two advanced backcross wheat populations. Plant Breeding, 2015, 134, 514-519.	1.0	16
68	Modelling the genetic architecture of flowering time control in barley through nested association mapping. BMC Genomics, 2015, 16, 290.	1.2	192
69	Wild barley introgression lines revealed novel QTL alleles for root and related shoot traits in the cultivated barley ( <i>Hordeum vulgare</i> L.). BMC Genetics, 2014, 15, 107.	2.7	79
70	Evolutionary Conserved Function of Barley and Arabidopsis 3-KETOACYL-CoA SYNTHASES in Providing Wax Signals for Germination of Powdery Mildew Fungi <i>A. A.</i> Plant Physiology, 2014, 166, 1621-1633.	2.3	76
71	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.	1.8	41
72	Genetic and environmental effects on the occurrence of speltoids in winter wheat cultivars. Plant Breeding, 2014, 133, 442-447.	1.0	3

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73	Evaluation of juvenile drought stress tolerance and genotyping by sequencing with wild barley introgression lines. <i>Molecular Breeding</i> , 2014, 34, 1475-1495.	1.0	36
74	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.	1.0	42
75	High-Throughput Phenotyping to Detect Drought Tolerance QTL in Wild Barley Introgression Lines. <i>PLoS ONE</i> , 2014, 9, e97047.	1.1	262
76	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.	1.8	14
77	Detection of exotic QTLs controlling nitrogen stress tolerance among wild barley introgression lines. <i>Euphytica</i> , 2013, 189, 67-88.	0.6	22
78	Inheritance of field resistance to <i>Septoria tritici</i> blotch in the wheat doubled-haploid population Solitár—Mazurka. <i>Euphytica</i> , 2013, 194, 161-176.	0.6	11
79	Structural and Temporal Variation in Genetic Diversity of European Spring Two-Row Barley Cultivars and Association Mapping of Quantitative Traits. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0007.	1.6	95
80	Vision-Based 3D-Reconstruction of Barley Plants. <i>Lecture Notes in Computer Science</i> , 2013, , 406-415.	1.0	0
81	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.	1.0	14
82	Identification of proteins associated with malting quality in a subset of wild barley introgression lines. <i>Proteomics</i> , 2012, 12, 2843-2851.	1.3	23
83	AB-QTL analysis reveals new alleles associated to proline accumulation and leaf wilting under drought stress conditions in barley ( <i>Hordeum vulgare</i> L.). <i>BMC Genetics</i> , 2012, 13, 61.	2.7	80
84	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
85	Discrimination of alleles and copy numbers at the Q locus in hexaploid wheat using quantitative pyrosequencing. <i>Euphytica</i> , 2012, 186, 207-218.	0.6	5
86	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.	1.0	28
87	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.	0.6	28
88	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.	0.8	72
89	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. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1559-1574.	1.8	103
90	Detection of epistatic interactions between exotic alleles introgressed from wild barley ( <i>H. vulgare</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	40

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91	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.	1.0	21
92	Identification and verification of QTLs for agronomic traits using wild barley introgression lines. <i>Theoretical and Applied Genetics</i> , 2009, 118, 483-497.	1.8	83
93	Detection and verification of malting quality QTLs using wild barley introgression lines. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1411-1427.	1.8	50
94	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.	1.8	26
95	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.	1.0	59
96	Mapping of the leaf rust resistance gene Lr38 on wheat chromosome arm 6DL using SSR markers. <i>Euphytica</i> , 2008, 162, 457-466.	0.6	49
97	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.	1.8	44
98	Selecting a set of wild barley introgression lines and verification of QTL effects for resistance to powdery mildew and leaf rust. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1093-1106.	1.8	101
99	Postulation of Seedling Leaf Rust Resistance Genes in Selected Ethiopian and German Bread Wheat Cultivars. <i>Crop Science</i> , 2008, 48, 507-516.	0.8	29
100	AB-QTL analysis in winter wheat: I. Synthetic hexaploid wheat ( <i>T. turgidum</i> ssp. <i>dicoccoides</i> × <i>Â</i> — <i>Â</i> T.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Applied Genetics</i> , 2007, 115, 683-695.	1.8	120
101	Molecular Diversity in <i>Puccinia triticina</i> Isolates from Ethiopia and Germany. <i>Journal of Phytopathology</i> , 2006, 154, 701-710.	0.5	19
102	AB-QTL analysis in spring barley: II. Detection of favourable exotic alleles for agronomic traits introgressed from wild barley ( <i>H. vulgare</i> ssp. <i>spontaneum</i> ). <i>Theoretical and Applied Genetics</i> , 2006, 112, 1221-1231.	1.8	143
103	AB-QTL analysis in spring barley. I. Detection of resistance genes against powdery mildew, leaf rust and scald introgressed from wild barley. <i>Theoretical and Applied Genetics</i> , 2005, 111, 583-590.	1.8	117
104	Mixed modelling for QTL × environment interaction analysis. <i>Euphytica</i> , 2004, 137, 147-153.	0.6	22
105	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.	1.8	73
106	Development of candidate introgression lines using an exotic barley accession ( <i>Hordeum vulgare</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Theoretical and Applied Genetics</i> , 2004, 108, 1591-1601.	1.8	115
107	Advanced backcross QTL analysis in barley ( <i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2003, 107, 340-352.	1.8	233
108	Mapping new EMBL-derived barley microsatellites and their use in differentiating German barley cultivars. <i>Theoretical and Applied Genetics</i> , 2000, 101, 652-660.	1.8	121

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109	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.	1.3	10
110	Rapid and reliable screening of a tomato YAC library exclusively based on PCR. <i>Plant Molecular Biology Reporter</i> , 1996, 14, 58-67.	1.0	6
111	Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. <i>Molecular Genetics and Genomics</i> , 1996, 251, 526-531.	2.4	46
112	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.	1.8	19
113	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.	1.8	5
114	Telomere-homologous sequences occur near the centromeres of many tomato chromosomes. <i>Molecular Genetics and Genomics</i> , 1996, 251, 526.	2.4	5
115	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
116	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.	1.8	67
117	Phylogenetic relationships between cultivated and wild species of the genus <i>Beta</i> revealed by DNA fingerprinting?. <i>Theoretical and Applied Genetics</i> , 1993, 86, 449-457.	1.8	93
118	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.	1.0	77
119	A linkage map of sugar beet ( <i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 1992, 84, 129-135.	1.8	106
120	Construction of an RFLP map of barley. <i>Theoretical and Applied Genetics</i> , 1991, 83, 250-256.	1.8	542