

# Benjamin Kilian

## List of Publications by Year in descending order

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96  
papers

7,172  
citations

71102

41  
h-index

66911

78  
g-index

101  
all docs

101  
docs citations

101  
times ranked

6859  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic diversity, distribution and domestication history of the neglected GGAtAt gene pool of wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 755-776.	3.6	20
2	Reap the crop wild relatives for breeding future crops. <i>Trends in Biotechnology</i> , 2022, 40, 412-431.	9.3	122
3	Detecting major introgressions in wheat and their putative origins using coverage analysis. <i>Scientific Reports</i> , 2022, 12, 1908.	3.3	23
4	Reaping the Potential of Wild <i>Cajanus</i> Species through Pre-Breeding for Improving Resistance to Pod Borer, <i>Helicoverpa armigera</i> , in Cultivated Pigeonpea ( <i>Cajanus cajan</i> (L.) Millsp.). <i>Biology</i> , 2022, 11, 485.	2.8	3
5	The grain quality of wheat wild relatives in the evolutionary context. <i>Theoretical and Applied Genetics</i> , 2022, 135, 4029-4048.	3.6	13
6	Photoperiod Insensitivity in Pigeonpea Introgression Lines Derived from Wild <i>Cajanus</i> Species. <i>Agronomy</i> , 2022, 12, 1370.	3.0	1
7	Adapting Agriculture to Climate Change: A Synopsis of Coordinated National Crop Wild Relative Seed Collecting Programs across Five Continents. <i>Plants</i> , 2022, 11, 1840.	3.5	12
8	Characterization and pre-breeding of diverse alfalfa wild relatives originating from drought-stressed environments. <i>Crop Science</i> , 2021, 61, 69-88.	1.8	21
9	Phenotypic response of farmer-selected CWR-derived rice lines to salt stress in the Mekong Delta. <i>Crop Science</i> , 2021, 61, 201-218.	1.8	10
10	Harnessing wild relatives of pearl millet for germplasm enhancement: Challenges and opportunities. <i>Crop Science</i> , 2021, 61, 177-200.	1.8	22
11	<i>Crop Science</i> special issue: Adapting agriculture to climate change: A walk on the wild side. <i>Crop Science</i> , 2021, 61, 32-36.	1.8	54
12	Participatory selection of CWR-derived salt-tolerant rice lines adapted to the coastal zone of the Mekong Delta. <i>Crop Science</i> , 2021, 61, 277-288.	1.8	6
13	From bits to bites: Advancement of the Germinate platform to support prebreeding informatics for crop wild relatives. <i>Crop Science</i> , 2021, 61, 1538-1566.	1.8	26
14	Wheat genomics and breeding: bridging the gap.. , 2021, 2021, .		9
15	Development of High Yielding Cowpea [ <i>Vigna unguiculata</i> (L.) Walp.] Lines with Improved Quality Seeds through Mutation and Pedigree Selection Methods. <i>Horticulturae</i> , 2021, 7, 271.	2.8	4
16	Evaluation of a Set of <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> Accessions for $\beta$ -Glucans and Microelement Contents. <i>Agriculture (Switzerland)</i> , 2021, 11, 950.	3.1	7
17	Introducing Beneficial Alleles from Plant Genetic Resources into the Wheat Germplasm. <i>Biology</i> , 2021, 10, 982.	2.8	46
18	Genome-wide sequence information reveals recurrent hybridization among diploid wheat wild relatives. <i>Plant Journal</i> , 2020, 102, 493-506.	5.7	40

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19	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	12.8	129
20	Concomitant phytonutrient and transcriptome analysis of mature fruit and leaf tissues of tomato ( <i>Solanum lycopersicum</i> L. cv. Oregon Spring) grown using organic and conventional fertilizer. <i>PLoS ONE</i> , 2020, 15, e0227429.	2.5	14
21	Segmental duplications are hot spots of copy number variants affecting barley gene content. <i>Plant Journal</i> , 2020, 103, 1073-1088.	5.7	6
22	Title is missing!. , 2020, 15, e0227429.		0
23	Title is missing!. , 2020, 15, e0227429.		0
24	Title is missing!. , 2020, 15, e0227429.		0
25	Title is missing!. , 2020, 15, e0227429.		0
26	Title is missing!. , 2020, 15, e0227429.		0
27	Title is missing!. , 2020, 15, e0227429.		0
28	Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. <i>Scientific Data</i> , 2019, 6, 137.	5.3	13
29	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	3.6	22
30	Non-Invasive Phenotyping Reveals Genomic Regions Involved in Pre-Anthesis Drought Tolerance and Recovery in Spring Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 1307.	3.6	16
31	Shoot sodium exclusion in salt stressed barley ( <i>Hordeum vulgare</i> L.) is determined by allele specific increased expression of HKT1;5. <i>Journal of Plant Physiology</i> , 2019, 241, 153029.	3.5	26
32	Exome sequences and multi-€environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	5.7	50
33	Genome-wide association mapping in a diverse spring barley collection reveals the presence of QTL hotspots and candidate genes for root and shoot architecture traits at seedling stage. <i>BMC Plant Biology</i> , 2019, 19, 216.	3.6	40
34	Genetic Dissection of Root System Architectural Traits in Spring Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 400.	3.6	58
35	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	21.4	230
36	The highly divergent Jekyll genes, required for sexual reproduction, are lineage specific for the related grass tribes Triticeae and Bromeae. <i>Plant Journal</i> , 2019, 98, 961-974.	5.7	7

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37	A tiered approach to genome-wide association analysis for the adherence of hulls to the caryopsis of barley seeds reveals footprints of selection. <i>BMC Plant Biology</i> , 2019, 19, 95.	3.6	10
38	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	21.4	576
39	Mirza (HacÄ±zade) CÅŕkgÅŕl (1897â€“1981): the great explorer of wheat genetic resources in Turkey. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 693-711.	1.6	10
40	Genomeâ€Wide Association Analysis of Grain Yieldâ€Associated Traits in a Panâ€European Barley Cultivar Collection. <i>Plant Genome</i> , 2018, 11, 170073.	2.8	78
41	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.	3.6	15
42	Barley Domestication, Adaptation and Population Genomics. <i>Compendium of Plant Genomes</i> , 2018, , 317-336.	0.5	12
43	Geographical and environmental determinants of the genetic structure of wild barley in southeastern Anatolia. <i>PLoS ONE</i> , 2018, 13, e0192386.	2.5	6
44	Sequence diversification in recessive alleles of two host factor genes suggests adaptive selection for bymovirus resistance in cultivated barley from East Asia. <i>Theoretical and Applied Genetics</i> , 2017, 130, 331-344.	3.6	21
45	Natural diversity of inflorescence architecture traces cryptic domestication genes in barley ( <i>Hordeum vulgare</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 843-853.	1.6	11
46	Past and Future Use of Wild Relatives in Crop Breeding. <i>Crop Science</i> , 2017, 57, 1070-1082.	1.8	446
47	Evaluation of multiple approaches to identify genome-wide polymorphisms in closely related genotypes of sweet cherry ( <i>Prunus avium</i> L.). <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 290-298.	4.1	10
48	Growth response of 98 barley ( <i>Hordeum vulgare</i> L.) genotypes to elevated CO <sub>2</sub> and identification of related quantitative trait loci using genomeâ€wide association studies. <i>Plant Breeding</i> , 2017, 136, 483-497.	1.9	15
49	Introgressiomics: a new approach for using crop wild relatives in breeding for adaptation to climate change. <i>Euphytica</i> , 2017, 213, 1.	1.2	154
50	Dated tribe-wide whole chloroplast genome phylogeny indicates recurrent hybridizations within Triticeae. <i>BMC Evolutionary Biology</i> , 2017, 17, 141.	3.2	78
51	Genetic architecture and temporal patterns of biomass accumulation in spring barley revealed by image analysis. <i>BMC Plant Biology</i> , 2017, 17, 137.	3.6	45
52	On the Origin of the Non-brittle Rachis Trait of Domesticated Einkorn Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 2031.	3.6	58
53	Molecular cytogenetic characterization of <i>Triticum timopheevii</i> chromosomes provides new insight on genome evolution of <i>T. zhukovskyi</i> . <i>Plant Systematics and Evolution</i> , 2016, 302, 943-956.	0.9	33
54	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	21.4	259

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55	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	21.4	122
56	The grain Hardness locus characterized in a diverse wheat panel ( <i>Triticum aestivum</i> L.) adapted to the central part of the Fertile Crescent: genetic diversity, haplotype structure, and phylogeny. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1259-1275.	2.1	8
57	Chromosomal Passports Provide New Insights into Diffusion of Emmer Wheat. <i>PLoS ONE</i> , 2015, 10, e0128556.	2.5	23
58	Inter-primer binding site retrotransposon and inter-simple sequence repeat diversity among wild <i>Lens</i> species. <i>Biochemical Systematics and Ecology</i> , 2015, 58, 162-168.	1.3	30
59	Diversity of germination and seedling traits in a spring barley ( <i>Hordeum vulgare</i> L.) collection under drought simulated conditions. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 275-292.	1.6	32
60	Dissecting spatiotemporal biomass accumulation in barley under different water regimes using high-throughput image analysis. <i>Plant, Cell and Environment</i> , 2015, 38, 1980-1996.	5.7	76
61	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	28.9	265
62	Modelling the genetic architecture of flowering time control in barley through nested association mapping. <i>BMC Genomics</i> , 2015, 16, 290.	2.8	192
63	Dissecting the Phenotypic Components of Crop Plant Growth and Drought Responses Based on High-Throughput Image Analysis. <i>Plant Cell</i> , 2015, 26, 4636-4655.	6.6	329
64	Genetic Linkage Map of Anatolian Durum Wheat Derived from a Cross of Kunderu-1149 × Cham1. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 209-220.	1.8	22
65	Discovery of genes affecting resistance of barley to adapted and non-adapted powdery mildew fungi. <i>Genome Biology</i> , 2014, 15, 518.	8.8	52
66	PROTEIN DISULFIDE ISOMERASE LIKE 5-1 is a susceptibility factor to plant viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2104-2109.	7.1	85
67	Evolutionary History of Wild Barley ( <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> ) Analyzed Using Multilocus Sequence Data and Paleodistribution Modeling. <i>Genome Biology and Evolution</i> , 2014, 6, 685-702.	2.5	64
68	Mapping-by-Sequencing Identifies HvPHYTOCHROME C as a Candidate Gene for the early maturity 5 Locus Modulating the Circadian Clock and Photoperiodic Flowering in Barley. <i>Genetics</i> , 2014, 198, 383-396.	2.9	102
69	Elisabeth Schiemann (1881–1972): a pioneer of crop plant research, with special reference to cereal phylogeny. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 89-106.	1.6	4
70	A Distorted Circadian Clock Causes Early Flowering and Temperature-Dependent Variation in Spike Development in the Eps-3A Mutant of Einkorn Wheat. <i>Genetics</i> , 2014, 196, 1253-1261.	2.9	88
71	Genetic structure and eco-geographical adaptation of garlic landraces ( <i>Allium sativum</i> L.) in Iran. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 1565-1580.	1.6	12
72	Separating the wheat from the chaff – a strategy to utilize plant genetic resources from ex situ genebanks. <i>Scientific Reports</i> , 2014, 4, 5231.	3.3	51

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73	Sequencing of Chloroplast Genomes from Wheat, Barley, Rye and Their Relatives Provides a Detailed Insight into the Evolution of the Triticeae Tribe. PLoS ONE, 2014, 9, e85761.	2.5	190
74	Genetic Dissection of Photoperiod Response Based on GWAS of Pre-Anthesis Phase Duration in Spring Barley. PLoS ONE, 2014, 9, e113120.	2.5	105
75	Genetic Diversity and Population Structure in a Legacy Collection of Spring Barley Landraces Adapted to a Wide Range of Climates. PLoS ONE, 2014, 9, e116164.	2.5	61
76	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. Plant Journal, 2013, 76, 494-505.	5.7	260
77	iPBS-Retrotransposons-based genetic diversity and relationship among wild annual Cicer species. Journal of Plant Biochemistry and Biotechnology, 2013, 22, 453-466.	1.7	56
78	Comparative analysis of genome composition in Triticeae reveals strong variation in transposable element dynamics and nucleotide diversity. Plant Journal, 2013, 73, 347-356.	5.7	43
79	Association mapping of salt tolerance in barley ( <i>Hordeum vulgare</i> L.). Theoretical and Applied Genetics, 2013, 126, 2335-2351.	3.6	124
80	Structural and Temporal Variation in Genetic Diversity of European Spring Two-Row Barley Cultivars and Association Mapping of Quantitative Traits. Plant Genome, 2013, 6, plantgenome2013.03.0007.	2.8	95
81	Genome-wide association studies for agronomical traits in a world wide spring barley collection. BMC Plant Biology, 2012, 12, 16.	3.6	341
82	Natural variation in a homolog of Antirrhinum CENTRORADIALIS contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genetics, 2012, 44, 1388-1392.	21.4	477
83	NGS technologies for analyzing germplasm diversity in genebanks*. Briefings in Functional Genomics, 2012, 11, 38-50.	2.7	140
84	Diversity of Macro- and Micronutrients in the Seeds of Lentil Landraces. Scientific World Journal, The, 2012, 2012, 1-9.	2.1	61
85	Diversity Assessment of Turkish Maize Landraces Based on Fluorescent Labelled SSR Markers. Plant Molecular Biology Reporter, 2012, 30, 261-274.	1.8	53
86	Heterotic Trait Locus (HTL) Mapping Identifies Intra-Locus Interactions That Underlie Reproductive Hybrid Vigor in Sorghum bicolor. PLoS ONE, 2012, 7, e38993.	2.5	29
87	Aegilops. , 2011, , 1-76.		89
88	Geographic distribution and domestication of wild emmer wheat ( <i>Triticum dicoccoides</i> ). Genetic Resources and Crop Evolution, 2011, 58, 11-53.	1.6	140
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. Theoretical and Applied Genetics, 2010, 120, 1559-1574.	3.6	103
90	Nutritional and physicochemical variation in Turkish kabuli chickpea ( <i>Cicer arietinum</i> L.) landraces. Euphytica, 2010, 175, 237-249.	1.2	49

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91	Testing of rye-specific markers located on 1RS chromosome and distribution of 1AL.RS and 1BL.RS translocations in Turkish wheat ( <i>Triticum aestivum</i> L., <i>T. durum</i> Desf.) varieties and landraces. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 119-129.	1.6	24
92	Genome size variation in diploid and tetraploid wild wheats. <i>AoB PLANTS</i> , 2010, 2010, plq015.	2.3	27
93	Genetic Diversity, Evolution and Domestication of Wheat and Barley in the Fertile Crescent. , 2010, , 137-166.		29
94	A catalogue of <i>Triticum monococcum</i> genes encoding toxic and immunogenic peptides for celiac disease patients. <i>Molecular Genetics and Genomics</i> , 2009, 281, 289-300.	2.1	56
95	Domestication of the Triticeae in the Fertile Crescent. , 2009, , 81-119.		49
96	Haplotype structure at seven barley genes: relevance to gene pool bottlenecks, phylogeny of ear type and site of barley domestication. <i>Molecular Genetics and Genomics</i> , 2006, 276, 230-241.	2.1	114