

Karl J Schmid

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

5,816
citations

147801

31
h-index

138484

58
g-index

81
all docs

81
docs citations

81
times ranked

8176
citing authors

#	ARTICLE	IF	CITATIONS
1	Physical geography, isolation by distance and environmental variables shape genomic variation of wild barley (<i>Hordeum vulgare</i> L. ssp. <i>spontaneum</i>) in the Southern Levant. <i>Heredity</i> , 2022, 128, 107-119.	2.6	10
2	Characterization of Flowering Time in Genebank Accessions of Grain Amaranths and Their Wild Relatives Reveals Signatures of Domestication and Local Adaptation. <i>Agronomy</i> , 2022, 12, 505.	3.0	3
3	Quinoa Diversity and Its Implications for Breeding. <i>Compendium of Plant Genomes</i> , 2021, , 107-118.	0.5	2
4	Breeding Amaranth for Biomass: Evaluating Dry Matter Content and Biomass Potential in Early and Late Maturing Genotypes. <i>Agronomy</i> , 2021, 11, 970.	3.0	3
5	Mineral-Ecological Cropping Systemsâ€”A New Approach to Improve Ecosystem Services by Farming without Chemical Synthetic Plant Protection. <i>Agronomy</i> , 2021, 11, 1710.	3.0	25
6	DeepCob: precise and high-throughput analysis of maize cob geometry using deep learning with an application in genebank phenomics. <i>Plant Methods</i> , 2021, 17, 91.	4.3	7
7	Genetic variation for tolerance to the downy mildew pathogen <i>Peronospora variabilis</i> in genetic resources of quinoa (<i>Chenopodium quinoa</i>). <i>BMC Plant Biology</i> , 2021, 21, 41.	3.6	26
8	Parallel Seed Color Adaptation during Multiple Domestication Attempts of an Ancient New World Grain. <i>Molecular Biology and Evolution</i> , 2020, 37, 1407-1419.	8.9	47
9	Hybrid transcriptome sequencing approach improved assembly and gene annotation in <i>Cynara cardunculus</i> (L.). <i>BMC Genomics</i> , 2020, 21, 317.	2.8	18
10	Combining focused identification of germplasm and core collection strategies to identify genebank accessions for central European soybean breeding. <i>Plant, Cell and Environment</i> , 2020, 43, 1421-1436.	5.7	18
11	Evolutionary genomics can improve prediction of speciesâ€™ responses to climate change. <i>Evolution Letters</i> , 2020, 4, 4-18.	3.3	190
12	Thermal plasticity of the circadian clock is under nuclear and cytoplasmic control in wild barley. <i>Plant, Cell and Environment</i> , 2019, 42, 3105-3120.	5.7	12
13	Microclimate predicts frost hardiness of alpine <i>Arabidopsis thaliana</i> populations better than elevation. <i>Ecology and Evolution</i> , 2019, 9, 13017-13029.	1.9	11
14	Genomic Prediction and Association Mapping of Curd-Related Traits in Gene Bank Accessions of Cauliflower. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 707-718.	1.8	29
15	Barley Domestication, Adaptation and Population Genomics. <i>Compendium of Plant Genomes</i> , 2018, , 317-336.	0.5	12
16	Comparative analysis of genetic diversity and differentiation of cauliflower (<i>Brassica oleracea</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	29
17	Genomic prediction ability for yield-related traits in German winter barley elite material. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1669-1683.	3.6	37
18	Transgenerational effects of mild heat in <i>Arabidopsis thaliana</i> show strong genotype specificity that is explained by climate at origin. <i>New Phytologist</i> , 2017, 215, 1221-1234.	7.3	48

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19	Genomic and phenotypic evidence for an incomplete domestication of South American grain amaranth (<i>Amaranthus caudatus</i>). <i>Molecular Ecology</i> , 2017, 26, 871-886.	3.9	43
20	Analysis of phylogenetic relationships and genome size evolution of the <i>Amaranthus</i> genus using GBS indicates the ancestors of an ancient crop. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 80-92.	2.7	95
21	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	5.7	238
22	Crossing Methods and Cultivation Conditions for Rapid Production of Segregating Populations in Three Grain Amaranth Species. <i>Frontiers in Plant Science</i> , 2016, 7, 816.	3.6	75
23	Genomic and phenotypic differentiation of <i>Arabidopsis thaliana</i> along altitudinal gradients in the North Italian Alps. <i>Molecular Ecology</i> , 2016, 25, 3574-3592.	3.9	47
24	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
25	Sequencing of the genus <i>Arabidopsis</i> identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	21.4	198
26	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	28.9	594
27	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	28.9	1,107
28	Transcriptomes of Plant Gametophytes Have a Higher Proportion of Rapidly Evolving and Young Genes than Sporophytes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1669-1678.	8.9	37
29	Genome-wide association studies in elite varieties of German winter barley using single-marker and haplotype-based methods. <i>Plant Breeding</i> , 2015, 134, 28-39.	1.9	59
30	Targeted re-sequencing of five Douglas-fir provenances reveals population structure and putative target genes of positive selection. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	20
31	RNA-Seq analysis identifies genes associated with differential reproductive success under drought-stress in accessions of wild barley <i>Hordeum spontaneum</i> . <i>BMC Plant Biology</i> , 2015, 15, 134.	3.6	62
32	Evaluation of cauliflower genebank accessions under organic and conventional cultivation in Southern Germany. <i>Euphytica</i> , 2015, 201, 389-400.	1.2	14
33	Uncovering Genes and Ploidy Involved in the High Diversity in Root Hair Density, Length and Response to Local Scarce Phosphate in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2015, 10, e0120604.	2.5	52
34	Transcriptome sequencing of two wild barley (<i>Hordeum spontaneum</i> L.) ecotypes differentially adapted to drought stress reveals ecotype-specific transcripts. <i>BMC Genomics</i> , 2014, 15, 995.	2.8	54
35	Genomic Selection in Barley Breeding. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , 367-378.	0.2	11
36	Water yam (<i>Dioscorea alata</i> L.) diversity pattern in Brazil: an analysis with SSR and morphological markers. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 611-624.	1.6	20

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37	Selection-Driven Evolution of Sex-Biased Genes Is Consistent with Sexual Selection in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 574-583.	8.9	61
38	Mutational Bias and Gene Conversion Affect the Intraspecific Nitrogen Stoichiometry of the <i>Arabidopsis thaliana</i> Transcriptome. <i>Molecular Biology and Evolution</i> , 2013, 30, 561-568.	8.9	11
39	A catalogue of putative unique transcripts from Douglas-fir (<i>Pseudotsuga menziesii</i>) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. <i>BMC Genomics</i> , 2012, 13, 673.	2.8	34
40	Islands and streams: clusters and gene flow in wild barley populations from the Levant. <i>Molecular Ecology</i> , 2012, 21, 1115-1129.	3.9	47
41	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	21.4	910
42	phenosim - A software to simulate phenotypes for testing in genome-wide association studies. <i>BMC Bioinformatics</i> , 2011, 12, 265.	2.6	18
43	Selection-Driven Divergence After Gene Duplication in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2011, 73, 153-165.	1.8	16
44	Deleterious amino acid polymorphisms in <i>Arabidopsis thaliana</i> and rice. <i>Theoretical and Applied Genetics</i> , 2010, 121, 157-168.	3.6	39
45	A phylogenetic approach to test for evidence of parental conflict or gene duplications associated with protein-encoding imprinted orthologous genes in placental mammals. <i>Mammalian Genome</i> , 2010, 21, 486-498.	2.2	27
46	Single feature polymorphism (SFP)-based selective sweep identification and association mapping of growth-related metabolic traits in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 188.	2.8	11
47	Multilocus Patterns of Nucleotide Diversity, Population Structure and Linkage Disequilibrium in <i>Boechera stricta</i> , a Wild Relative of <i>Arabidopsis</i> . <i>Genetics</i> , 2009, 181, 1021-1033.	2.9	54
48	The shrunken genome of <i>Arabidopsis thaliana</i> . <i>Plant Systematics and Evolution</i> , 2008, 273, 257-271.	0.9	35
49	The Trouble with Sliding Windows and the Selective Pressure in BRCA1. <i>PLoS ONE</i> , 2008, 3, e3746.	2.5	33
50	Fitness Effects Associated with the Major Flowering Time Gene FRIGIDA in <i>Arabidopsis thaliana</i> in the Field. <i>American Naturalist</i> , 2007, 169, E141-E157.	2.1	151
51	Positive darwinian selection at the imprinted MEDEA locus in plants. <i>Nature</i> , 2007, 448, 349-352.	27.8	144
52	Evidence for a large-scale population structure of <i>Arabidopsis thaliana</i> from genome-wide single nucleotide polymorphism markers. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1104-1114.	3.6	109
53	A Multilocus Sequence Survey in <i>Arabidopsis thaliana</i> Reveals a Genome-Wide Departure From a Neutral Model of DNA Sequence Polymorphism. <i>Genetics</i> , 2005, 169, 1601-1615.	2.9	188
54	Rapid Evolution of a Pollen-Specific Oleosin-Like Gene Family from <i>Arabidopsis thaliana</i> and Closely Related Species. <i>Molecular Biology and Evolution</i> , 2004, 21, 659-669.	8.9	55

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55	Large-Scale Identification and Analysis of Genome-Wide Single-Nucleotide Polymorphisms for Mapping in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2003, 13, 1250-1257.	5.5	184
56	The Evolutionary Analysis of "Orphans" From the <i>Drosophila</i> Genome Identifies Rapidly Diverging and Incorrectly Annotated Genes. <i>Genetics</i> , 2001, 159, 589-598.	2.9	64
57	A Comparison of Homologous Developmental Genes from <i>Drosophila</i> and <i>Tribolium</i> Reveals Major Differences in Length and Trinucleotide Repeat Content. <i>Journal of Molecular Evolution</i> , 1999, 49, 558-566.	1.8	13
58	The <i>Drosophila</i> gene 2A5 complements the defect in mitochondrial F1-ATPase assembly in yeast lacking the molecular chaperone Atp11p. <i>FEBS Letters</i> , 1999, 452, 305-308.	2.8	11
59	Large Number of Replacement Polymorphisms in Rapidly Evolving Genes of <i>Drosophila</i> : Implications for Genome-Wide Surveys of DNA Polymorphism. <i>Genetics</i> , 1999, 153, 1717-1729.	2.9	40
60	High-Density Mapping of Quantitative Trait Loci Controlling Agronomically Important Traits in Quinoa (<i>Chenopodium quinoa</i> Willd.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7
61	Genome-wide association study in quinoa reveals selection pattern typical for crops with a short breeding history. <i>ELife</i> , 0, 11, .	6.0	14