Jens Keilwagen

List of Publications by Year
in descending order

63 papers	7,046 citations	218677 26 h-index	123424 61 g-index
73 all docs	73 docs citations	73 times ranked	9814 citing authors

#	Article	IF	Citations
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
2	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
3	Critical assessment of automated flow cytometry data analysis techniques. Nature Methods, 2013, 10, 228-238.	19.0	509
4	Using intron position conservation for homology-based gene prediction. Nucleic Acids Research, 2016, 44, e89-e89.	14.5	449
5	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	17.5	341
6	PRROC: computing and visualizing precision-recall and receiver operating characteristic curves in R. Bioinformatics, 2015, 31, 2595-2597.	4.1	288
7	Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. BMC Bioinformatics, 2018, 19, 189.	2.6	192
8	GeMoMa: Homology-Based Gene Prediction Utilizing Intron Position Conservation and RNA-seq Data. Methods in Molecular Biology, 2019, 1962, 161-177.	0.9	165
9	Toward the identification and regulation of the Arabidopsis thaliana ABI3 regulon. Nucleic Acids Research, 2012, 40, 8240-8254.	14.5	145
10	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	21.4	138
11	Elongation‐related functions of LEAFY COTYLEDON1 during the development of *Arabidopsis thaliana*. Plant Journal, 2012, 71, 427-442.	5.7	133
12	Area under Precision-Recall Curves for Weighted and Unweighted Data. PLoS ONE, 2014, 9, e92209.	2.5	131
13	Accurate prediction of cell type-specific transcription factor binding. Genome Biology, 2019, 20, 9.	8.8	82
14	Detection and Identification of Genome Editing in Plants: Challenges and Opportunities. Frontiers in Plant Science, 2019, 10, 236.	3.6	81
15	Which Factors Affect the Occurrence of Off-Target Effects Caused by the Use of CRISPR/Cas: A Systematic Review in Plants. Frontiers in Plant Science, 2020, 11, 574959.	3.6	76
16	DiffLogo: a comparative visualization of sequence motifs. BMC Bioinformatics, 2015, 16, 387.	2.6	71
17	The Terpene Synthase Gene Family of Carrot (Daucus carota L.): Identification of QTLs and Candidate Genes Associated with Terpenoid Volatile Compounds. Frontiers in Plant Science, 2017, 8, 1930.	3.6	68
18	Varying levels of complexity in transcription factor binding motifs. Nucleic Acids Research, 2015, 43, e119-e119.	14.5	66

#	ARTICLE	IF	CITATIONS
19	Highly efficient multiplex editing: oneâ€shot generation of 8Ã— <i>Nicotiana benthamiana</i> and 12Ã— Arabidopsis mutants. Plant Journal, 2021, 106, 8-22.	5.7	65
20	Separating the wheat from the chaff â€" a strategy to utilize plant genetic resources from ex situ genebanks. Scientific Reports, 2014, 4, 5231.	3.3	51
21	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog (Canis lupus) Tj ETQq1 1 0.784314 rgBT	6.4	47
22	Genetic architecture and temporal patterns of biomass accumulation in spring barley revealed by image analysis. BMC Plant Biology, 2017, 17, 137.	3.6	45
23	De-Novo Discovery of Differentially Abundant Transcription Factor Binding Sites Including Their Positional Preference. PLoS Computational Biology, 2011, 7, e1001070.	3.2	44
24	A general approach for discriminative de novo motif discovery from high-throughput data. Nucleic Acids Research, 2013, 41, e197-e197.	14.5	44
25	Baculovirus Kimura two-parameter species demarcation criterion is confirmed by the distances of 38 core gene nucleotide sequences. Journal of General Virology, 2018, 99, 1307-1320.	2.9	40
26	A chromosomeâ€scale assembly of the model desiccation tolerant grass <i>Oropetium thomaeum</i>. Plant Direct, 2018, 2, e00096.	1.9	39
27	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
28	Comparison Between Core Set Selection Methods Using Different Illumina Marker Platforms: A Case Study of Assessment of Diversity in Wheat. Frontiers in Plant Science, 2020, 11, 1040.	3.6	31
29	Towards map-based cloning of FB_Mfu10: identification of a receptor-like kinase candidate gene underlying the Malus fusca fire blight resistance locus on linkage group 10. Molecular Breeding, 2018, 38, 106.	2.1	28
30	Mineralocorticoid receptor interaction with SP1 generates a new response element for pathophysiologically relevant gene expression. Nucleic Acids Research, 2013, 41, 8045-8060.	14.5	27
31	Exact algorithms and heuristics for the Quadratic Traveling Salesman Problem with an application in bioinformatics. Discrete Applied Mathematics, 2014, 166, 97-114.	0.9	26
32	Genetic diversity and population structure in Beninese pigeon pea [Cajanus cajan (L.) Huth] landraces collection revealed by SSR and genome wide SNP markers. Genetic Resources and Crop Evolution, 2020, 67, 191-208.	1.6	26
33	On the Value of Intra-Motif Dependencies of Human Insulator Protein CTCF. PLoS ONE, 2014, 9, e85629.	2.5	26
34	Chromosomal Passports Provide New Insights into Diffusion of Emmer Wheat. PLoS ONE, 2015, 10, e0128556.	2.5	23
35	Detecting major introgressions in wheat and their putative origins using coverage analysis. Scientific Reports, 2022, 12, 1908.	3.3	23
36	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. Frontiers in Plant Science, 2019, 10, 1133.	3.6	22

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37	Chromosome-length genome assembly and structural variations of the primal Basenji dog (Canis lupus) Tj ETQq1 1 0.784314 rgBT /Ov	2.8	22
38	Transposable elements and introgression introduce genetic variation in the invasive ant *Cardiocondyla obscurior*. Molecular Ecology, 2021, 30, 6211-6228.	3.9	20
39	Construction of a dense genetic map of the Malus fusca fire blight resistant accession MAL0045 using tunable genotyping-by-sequencing SNPs and microsatellites. Scientific Reports, 2020, 10, 16358.	3.3	17
40	Leveraging the Use of Historical Data Gathered During Seed Regeneration of an ex Situ Genebank Collection of Wheat. Frontiers in Plant Science, 2018, 9, 609.	3.6	15
41	High Resolution Mapping of RphMBR1012 Conferring Resistance to Puccinia hordei in Barley (Hordeum) Tj ETQq1 1 0.784314 rgBT /Ov	3.6	14
42	The draft chromosome-level genome assembly of tetraploid ground cherry (Prunus fruticosa Pall.) from long reads. Genomics, 2021, 113, 4173-4183.	2.9	14
43	The Australian dingo is an early offshoot of modern breed dogs. Science Advances, 2022, 8, eabm5944.	10.3	14
44	Statistical test for tolerability of effects of an antifungal biocontrol strain on fungal communities in three arable soils. Microbial Biotechnology, 2017, 10, 434-449.	4.2	13
45	Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. Scientific Data, 2019, 6, 137.	5.3	13
46	Genome wide association study of frost tolerance in wheat. Scientific Reports, 2022, 12, 5275.	3.3	13
47	Development of barley introgression lines carrying the leaf rust resistance genes *Rph1* to *Rph15*. Crop Science, 2020, 60, 282-302.	1.8	11
48	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. Plant Genome, 2015, 8, eplantgenome2015.06.0045.	2.8	10
49	Apples and oranges: avoiding different priors in Bayesian DNA sequence analysis. BMC Bioinformatics, 2010, 11, 149.	2.6	9
50	MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations. Genome Biology, 2009, 10, R46.	9.6	8
51	Utilizing gene pair orientations for HMM-based analysis of promoter array ChIP-chip data. Bioinformatics, 2009, 25, 2118-2125.	4.1	7
52	Transfer of the Dominant Virus Resistance Gene AV-1pro From Asparagus prostratus to Chromosome 2 of Garden Asparagus A. officinalis L.. Frontiers in Plant Science, 2021, 12, 809069.	3.6	6
53	Computational Recognition of RNA Splice Sites by Exact Algorithms for the Quadratic Traveling Salesman Problem. Computation, 2015, 3, 285-298.	2.0	5
54	Mapping of the Waxy Bloom Gene in 'Black Jewel' in a Parental Linkage Map of 'Black Jewel' × 'Glen Ample' (Rubus) Interspecific Population. Agronomy, 2020, 10, 1579.	3.0	5

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55	Comparative genomics reveals low levels of inter- and intraspecies diversity in the causal agents of dwarf and common bunt of wheat and hint at conspecificity of Tilletia caries and T. laevis. IMA Fungus, 2022, 13, .	3.8	5
56	Unifying generative and discriminative learning principles. BMC Bioinformatics, 2010, 11, 98.	2.6	4
57	DepLogo: visualizing sequence dependencies in R. Bioinformatics, 2019, 35, 4812-4814.	4.1	4
58	On genetic diversity in caraway: Genotyping of a large germplasm collection. PLoS ONE, 2020, 15, e0244666.	2.5	3
59	No Evidence of Unexpected Transgenic Insertions in T1190 â€" A Transgenic Apple Used in Rapid Cycle Breeding â€" Following Whole Genome Sequencing. Frontiers in Plant Science, 2021, 12, 715737.	3.6	2
60	Probabilistic Approaches to Transcription Factor Binding Site Prediction. Methods in Molecular Biology, 2010, 674, 97-119.	0.9	2
61	DISPOM: A DISCRIMINATIVE DE-NOVO MOTIF DISCOVERY TOOL BASED ON THE JSTACS LIBRARY. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340006.	0.8	1
62	The Gene and Repetitive Element Landscape of the Rye Genome. Compendium of Plant Genomes, 2021, , 117-133.	0.5	0
63	ZÃ¼chtungsmethodische AnsÃ¤tze zur Verbesserung der Trockenstresstoleranz am Beispiel der MÃ¶hre. , 0, , .		0