

Jens Keilwagen

List of Publications by Year in descending order

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Version: 2024-02-01

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
19	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog (<i>Canis lupus</i>) Tj ETQq1 1 0.784314 rgBT /O	6.4	47
20	On genetic diversity in caraway: Genotyping of a large germplasm collection. PLoS ONE, 2020, 15, e0244666.	2.5	3
21	Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. Scientific Data, 2019, 6, 137.	5.3	13
22	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. Frontiers in Plant Science, 2019, 10, 1133.	3.6	22
23	High Resolution Mapping of RphMBR1012 Conferring Resistance to Puccinia hordei in Barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314 rgBT /O	3.6	14
24	DepLogo: visualizing sequence dependencies in R. Bioinformatics, 2019, 35, 4812-4814.	4.1	4
25	GeMoMa: Homology-Based Gene Prediction Utilizing Intron Position Conservation and RNA-seq Data. Methods in Molecular Biology, 2019, 1962, 161-177.	0.9	165
26	Detection and Identification of Genome Editing in Plants: Challenges and Opportunities. Frontiers in Plant Science, 2019, 10, 236.	3.6	81
27	Accurate prediction of cell type-specific transcription factor binding. Genome Biology, 2019, 20, 9.	8.8	82
28	A chromosome-scale assembly of the model desiccation tolerant grass <i>Oropetium thomaeum</i> . Plant Direct, 2018, 2, e00096.	1.9	39
29	Towards map-based cloning of FB_Mfu10: identification of a receptor-like kinase candidate gene underlying the <i>Malus fusca</i> fire blight resistance locus on linkage group 10. Molecular Breeding, 2018, 38, 106.	2.1	28
30	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. BMC Genomics, 2018, 19, 409.	2.8	31
31	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
32	Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. BMC Bioinformatics, 2018, 19, 189.	2.6	192
33	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
34	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
35	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
36	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

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37	The Terpene Synthase Gene Family of Carrot (<i>Daucus carota</i> L.): Identification of QTLs and Candidate Genes Associated with Terpenoid Volatile Compounds. <i>Frontiers in Plant Science</i> , 2017, 8, 1930.	3.6	68
38	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
39	Using intron position conservation for homology-based gene prediction. <i>Nucleic Acids Research</i> , 2016, 44, e89-e89.	14.5	449
40	DiffLogo: a comparative visualization of sequence motifs. <i>BMC Bioinformatics</i> , 2015, 16, 387.	2.6	71
41	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.06.0045.	2.8	10
42	Chromosomal Passports Provide New Insights into Diffusion of Emmer Wheat. <i>PLoS ONE</i> , 2015, 10, e0128556.	2.5	23
43	Computational Recognition of RNA Splice Sites by Exact Algorithms for the Quadratic Traveling Salesman Problem. <i>Computation</i> , 2015, 3, 285-298.	2.0	5
44	Varying levels of complexity in transcription factor binding motifs. <i>Nucleic Acids Research</i> , 2015, 43, e119-e119.	14.5	66
45	PRROC: computing and visualizing precision-recall and receiver operating characteristic curves in R. <i>Bioinformatics</i> , 2015, 31, 2595-2597.	4.1	288
46	Exact algorithms and heuristics for the Quadratic Traveling Salesman Problem with an application in bioinformatics. <i>Discrete Applied Mathematics</i> , 2014, 166, 97-114.	0.9	26
47	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
48	On the Value of Intra-Motif Dependencies of Human Insulator Protein CTCF. <i>PLoS ONE</i> , 2014, 9, e85629.	2.5	26
49	Area under Precision-Recall Curves for Weighted and Unweighted Data. <i>PLoS ONE</i> , 2014, 9, e92209.	2.5	131
50	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	17.5	341
51	Critical assessment of automated flow cytometry data analysis techniques. <i>Nature Methods</i> , 2013, 10, 228-238.	19.0	509
52	Mineralocorticoid receptor interaction with SP1 generates a new response element for pathophysiological relevant gene expression. <i>Nucleic Acids Research</i> , 2013, 41, 8045-8060.	14.5	27
53	A general approach for discriminative de novo motif discovery from high-throughput data. <i>Nucleic Acids Research</i> , 2013, 41, e197-e197.	14.5	44
54	DISPOM: A DISCRIMINATIVE DE-NOVO MOTIF DISCOVERY TOOL BASED ON THE JSTACS LIBRARY. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340006.	0.8	1

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55	Toward the identification and regulation of the Arabidopsis thaliana ABI3 regulon. Nucleic Acids Research, 2012, 40, 8240-8254.	14.5	145
56	Elongation-related functions of LEAFY COTYLEDON1 during the development of Arabidopsis thaliana. Plant Journal, 2012, 71, 427-442.	5.7	133
57	De-Novo Discovery of Differentially Abundant Transcription Factor Binding Sites Including Their Positional Preference. PLoS Computational Biology, 2011, 7, e1001070.	3.2	44
58	Apples and oranges: avoiding different priors in Bayesian DNA sequence analysis. BMC Bioinformatics, 2010, 11, 149.	2.6	9
59	Unifying generative and discriminative learning principles. BMC Bioinformatics, 2010, 11, 98.	2.6	4
60	Probabilistic Approaches to Transcription Factor Binding Site Prediction. Methods in Molecular Biology, 2010, 674, 97-119.	0.9	2
61	Utilizing gene pair orientations for HMM-based analysis of promoter array CHIP-chip data. Bioinformatics, 2009, 25, 2118-2125.	4.1	7
62	MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations. Genome Biology, 2009, 10, R46.	9.6	8
63	Züchtungsmethodische Ansätze zur Verbesserung der Trockenstresstoleranz am Beispiel der Mähre. , O, , .		0