

Heiko Schoof

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

10,910
citations

218381

26
h-index

233125

45
g-index

51
all docs

51
docs citations

51
times ranked

12400
citing authors

#	ARTICLE	IF	CITATIONS
1	MuWU: Mutant-seq library analysis and annotation. <i>Bioinformatics</i> , 2022, 38, 837-838.	1.8	1
2	Single-parent expression complementation contributes to phenotypic heterosis in maize hybrids. <i>Plant Physiology</i> , 2022, , .	2.3	6
3	<i>ENHANCED GRAVITROPISM 2</i> encodes a STERILE ALPHA MOTIF-containing protein that controls root growth angle in barley and wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
4	Robust non-syntenic gene expression patterns in diverse maize hybrids during root development. <i>Journal of Experimental Botany</i> , 2020, 71, 865-876.	2.4	3
5	<i>BonnMu</i> : A Sequence-Indexed Resource of Transposon-Induced Maize Mutations for Functional Genomics Studies. <i>Plant Physiology</i> , 2020, 184, 620-631.	2.3	25
6	Transcriptome profiling at osmotic and ionic phases of salt stress response in bread wheat uncovers trait-specific candidate genes. <i>BMC Plant Biology</i> , 2020, 20, 428.	1.6	16
7	Transcriptome and Parasitome Analysis of Beet Cyst Nematode <i>Heterodera schachtii</i> . <i>Scientific Reports</i> , 2020, 10, 3315.	1.6	7
8	High light induces species specific changes in the membrane lipid composition of <i>Chlorella</i> . <i>Biochemical Journal</i> , 2020, 477, 2543-2559.	1.7	4
9	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
10	Single-Parent Expression Is a General Mechanism Driving Extensive Complementation of Non-syntenic Genes in Maize Hybrids. <i>Current Biology</i> , 2018, 28, 431-437.e4.	1.8	50
11	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. <i>Plant Physiology</i> , 2017, 173, 1247-1257.	2.3	36
12	Identification and characterization of a putative protein disulfide isomerase (HsPDI) as an alleged effector of <i>Heterodera schachtii</i> . <i>Scientific Reports</i> , 2017, 7, 13536.	1.6	27
13	<i>Heterodera schachtii</i> Tyrosinase-like protein - a novel nematode effector modulating plant hormone homeostasis. <i>Scientific Reports</i> , 2017, 7, 6874.	1.6	33
14	An improved procedure for isolation of high-quality RNA from nematode-infected <i>Arabidopsis</i> roots through laser capture microdissection. <i>Plant Methods</i> , 2016, 12, 25.	1.9	25
15	Structural insights into the function of the core-circadian factor TIMING OF CAB2 EXPRESSION 1 (TOC1). <i>Journal of Circadian Rhythms</i> , 2014, 6, 3.	2.9	16
16	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	9.4	731
17	Marker2sequence, mine your QTL regions for candidate genes. <i>Bioinformatics</i> , 2012, 28, 1921-1922.	1.8	8
18	Analysis of the <i>Arabidopsis</i> Shoot Meristem Transcriptome during Floral Transition Identifies Distinct Regulatory Patterns and a Leucine-Rich Repeat Protein That Promotes Flowering. <i>Plant Cell</i> , 2012, 24, 444-462.	3.1	178

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19	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
20	Natural variation of H3K27me3 distribution between two <i>Arabidopsis</i> accessions and its association with flanking transposable elements. <i>Genome Biology</i> , 2012, 13, R117.	13.9	34
21	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	13.7	1,166
22	An International Bioinformatics Infrastructure to Underpin the <i>Arabidopsis</i> Community. <i>Plant Cell</i> , 2010, 22, 2530-2536.	3.1	23
23	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	1.6	73
24	Control of perennial flowering and perenniality in <i>Arabis alpina</i> , a relative of <i>Arabidopsis thaliana</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2009, 153, S195-S196.	0.8	2
25	PEP1 regulates perennial flowering in <i>Arabis alpina</i> . <i>Nature</i> , 2009, 459, 423-427.	13.7	325
26	Integrating <i>ELF4</i> into the circadian system through combined structural and functional studies. <i>HFSP Journal</i> , 2009, 3, 350-366.	2.5	99
27	Protein function prediction and annotation in an integrated environment powered by web services (FAWE). <i>Bioinformatics</i> , 2008, 24, 2393-2394.	1.8	11
28	Interoperability with Moby 1.0-It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	3.2	91
29	MIPSPlantsDB-plant database resource for integrative and comparative plant genome research. <i>Nucleic Acids Research</i> , 2007, 35, D834-D840.	6.5	47
30	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
31	Comparative sequence analysis of <i>Solanum</i> and <i>Arabidopsis</i> in a hot spot for pathogen resistance on potato chromosome V reveals a patchwork of conserved and rapidly evolving genome segments. <i>BMC Genomics</i> , 2007, 8, 112.	1.2	38
32	MIPS Plant Genome Information Resources. , 2007, 406, 137-159.		6
33	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	3.3	286
34	BioMOBY Successfully Integrates Distributed Heterogeneous Bioinformatics Web Services. The <i>PlaNNet</i> Exemplar Case. <i>Plant Physiology</i> , 2005, 138, 5-17.	2.3	84
35	Munich Information Center for Protein Sequences Plant Genome Resources. A Framework for Integrative and Comparative Analyses. <i>Plant Physiology</i> , 2005, 138, 1301-1309.	2.3	13
36	PlantMarkers-a database of predicted molecular markers from plants. <i>Nucleic Acids Research</i> , 2004, 33, D628-D632.	6.5	40

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37	MIPS Arabidopsis thaliana Database (MAtdB): an integrated biological knowledge resource for plant genomics. <i>Nucleic Acids Research</i> , 2004, 32, 373D-376.	6.5	82
38	Conservation, diversification and expansion of C2H2 zinc finger proteins in the Arabidopsis thaliana genome. <i>BMC Genomics</i> , 2004, 5, 39.	1.2	355
39	The Arabidopsis Genome and Its Use in Cereal Genomics. , 2004, , 515-534.		0
40	Towards Interoperability in Genome Databases: The MAtdB (MIPSArabidopsis thalianaDatabase) Experience. <i>Comparative and Functional Genomics</i> , 2003, 4, 255-258.	2.0	8
41	Comparison of rice and Arabidopsis annotation. <i>Current Opinion in Plant Biology</i> , 2003, 6, 106-112.	3.5	27
42	MOsDB: an integrated information resource for rice genomics. <i>Nucleic Acids Research</i> , 2003, 31, 190-192.	6.5	27
43	MIPS Arabidopsisthaliana Database (MAtdB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93.	6.5	159
44	The Stem Cell Population of Arabidopsis Shoot Meristems Is Maintained by a Regulatory Loop between the CLAVATA and WUSCHEL Genes. <i>Cell</i> , 2000, 100, 635-644.	13.5	1,521
45	Role of the ZWILLE gene in the regulation of central shoot meristem cell fate during Arabidopsis embryogenesis. <i>EMBO Journal</i> , 1998, 17, 1799-1809.	3.5	342
46	Role of WUSCHEL in Regulating Stem Cell Fate in the Arabidopsis Shoot Meristem. <i>Cell</i> , 1998, 95, 805-815.	13.5	1,487
47	Maintaining the shoot meristem – the role of CLAVATA1. <i>Trends in Plant Science</i> , 1997, 2, 325-327.	4.3	20