

Bruno Huettel

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

7,989
citations

126858

33
h-index

91828

69
g-index

75
all docs

75
docs citations

75
times ranked

10563
citing authors

#	ARTICLE	IF	CITATIONS
1	A chromosome scale tomato genome built from complementary PacBio and Nanopore sequences alone reveals extensive linkage drag during breeding. <i>Plant Journal</i> , 2022, 110, 572-588.	2.8	29
2	The megabase-scale crossover landscape is largely independent of sequence divergence. <i>Nature Communications</i> , 2022, 13, .	5.8	25
3	Anaerobic endosymbiont generates energy for ciliate host by denitrification. <i>Nature</i> , 2021, 591, 445-450.	13.7	53
4	Two high-quality <i>de novo</i> genomes from single ethanol-preserved specimens of tiny metazoans (Collembola). <i>GigaScience</i> , 2021, 10, .	3.3	17
5	Genetic Diversity of <i>Botrytis cinerea</i> Revealed by Multilocus Sequencing, and Identification of <i>B. cinerea</i> Populations Showing Genetic Isolation and Distinct Host Adaptation. <i>Frontiers in Plant Science</i> , 2021, 12, 663027.	1.7	24
6	Aiming off the target: recycling target capture sequencing reads for investigating repetitive DNA. <i>Annals of Botany</i> , 2021, 128, 835-848.	1.4	13
7	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. <i>PeerJ</i> , 2021, 9, e11721.	0.9	14
8	Plastome evolution in the <i>Caesalpinia</i> group (Leguminosae) and its application in phylogenomics and populations genetics. <i>Planta</i> , 2021, 254, 27.	1.6	9
9	<i>Sphingomonas aliaeris</i> sp. nov., a new species isolated from pork steak packed under modified atmosphere. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	13
10	Identification and initial characterization of a new pair of sibling sRNAs of <i>Neisseria gonorrhoeae</i> involved in type IV pilus biogenesis. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	1
11	The temperature-regulated DEAD-box RNA helicase CrhR interactome: autoregulation and photosynthesis-related transcripts. <i>Journal of Experimental Botany</i> , 2021, , .	2.4	7
12	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021, 113, 3666-3680.	1.3	17
13	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. <i>Nature Communications</i> , 2021, 12, 7227.	5.8	58
14	Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar 'Börner'™. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
15	The sugar transporter SWEET10 acts downstream of FLOWERING LOCUS T during floral transition of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 53.	1.6	59
16	<i>Arthrobacter bussei</i> sp. nov., a pink-coloured organism isolated from cheese made of cow's milk. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3027-3036.	0.8	18
17	Gamete binning: chromosome-level and haplotype-resolved genome assembly enabled by high-throughput single-cell sequencing of gamete genomes. <i>Genome Biology</i> , 2020, 21, 306.	3.8	44
18	Interplay and Targetome of the Two Conserved Cyanobacterial sRNAs Yfr1 and Yfr2 in <i>Prochlorococcus</i> MED4. <i>Scientific Reports</i> , 2019, 9, 14331.	1.6	10

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19	Evolutionary convergence or homology? Comparative cytogenomics of Caesalpinia group species (Leguminosae) reveals diversification in the pericentromeric heterochromatic composition. <i>Planta</i> , 2019, 250, 2173-2186.	1.6	17
20	Linked-read sequencing of gametes allows efficient genome-wide analysis of meiotic recombination. <i>Nature Communications</i> , 2019, 10, 4310.	5.8	41
21	Development and characterization of eleven microsatellite loci for the tropical understory tree <i>Paypayrola blanchetiana</i> Tul. (Violaceae). <i>Molecular Biology Reports</i> , 2019, 46, 2529-2532.	1.0	2
22	Sulfur-Oxidizing Symbionts without Canonical Genes for Autotrophic CO ₂ Fixation. <i>MBio</i> , 2019, 10, .	1.8	29
23	A chromosome-level sequence assembly reveals the structure of the <i>Arabidopsis thaliana</i> Nd-1 genome and its gene set. <i>PLoS ONE</i> , 2019, 14, e0216233.	1.1	40
24	Development of ten microsatellite markers for <i>Alibertia edulis</i> (Rubiaceae), a Brazilian savanna tree species. <i>Molecular Biology Reports</i> , 2019, 46, 4593-4597.	1.0	3
25	Initial Studies on Cucumber Transcriptome Analysis under Silicon Treatment. <i>Silicon</i> , 2019, 11, 2365-2369.	1.8	9
26	Identification of the DNA methyltransferases establishing the methylome of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>DNA Research</i> , 2018, 25, 343-352.	1.5	38
27	Benefit from decline: the primary transcriptome of <i>Alteromonas macleodii</i> str. Te101 during <i>Trichodesmium</i> demise. <i>ISME Journal</i> , 2018, 12, 981-996.	4.4	30
28	Single molecule real time sequencing in ADTKD-MUC1 allows complete assembly of the VNTR and exact positioning of causative mutations. <i>Scientific Reports</i> , 2018, 8, 4170.	1.6	40
29	Is there foul play in the leaf pocket? The metagenome of floating fern <i>Azolla</i> reveals endophytes that do not fix N ₂ but may denitrify. <i>New Phytologist</i> , 2018, 217, 453-466.	3.5	42
30	Global impacts of chromosomal imbalance on gene expression in <i>Arabidopsis</i> and other taxa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11321-E11330.	3.3	51
31	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	4.7	391
32	Development of 15 nuclear microsatellite markers in <i>Deuterocohnia</i> (Pitcairnioideae; Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 222 T	0.8	3
33	Improving and correcting the contiguity of long-read genome assemblies of three plant species using optical mapping and chromosome conformation capture data. <i>Genome Research</i> , 2017, 27, 778-786.	2.4	155
34	Specificity in diversity: single origin of a widespread ciliate-bacteria symbiosis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170764.	1.2	34
35	Flowering Time Gene Variation in Brassica Species Shows Evolutionary Principles. <i>Frontiers in Plant Science</i> , 2017, 8, 1742.	1.7	33
36	Methylation Markers for the Identification of Body Fluids and Tissues from Forensic Trace Evidence. <i>PLoS ONE</i> , 2016, 11, e0147973.	1.1	62

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37	Microsatellites from <i>Fosterella christophii</i> (Bromeliaceae) by de novo transcriptome sequencing on the Pacific Biosciences RS platform. <i>Applications in Plant Sciences</i> , 2016, 4, 1500084.	0.8	3
38	Transcriptomic profiling of <i>Arabidopsis</i> gene expression in response to varying micronutrient zinc supply. <i>Genomics Data</i> , 2016, 7, 256-258.	1.3	17
39	cDNA Library Enrichment of Full Length Transcripts for SMRT Long Read Sequencing. <i>PLoS ONE</i> , 2016, 11, e0157779.	1.1	51
40	<i>Staphylococcus aureus</i> Exploits a Non-ribosomal Cyclic Dipeptide to Modulate Survival within Epithelial Cells and Phagocytes. <i>PLoS Pathogens</i> , 2016, 12, e1005857.	2.1	48
41	Differentiation of <i>Candidatus</i> <i>Phytoplasma cynodontis</i> ™ Based on 16S rRNA and <i>groEL</i> Genes and Identification of a New Subgroup, 16SrXIV-C. <i>Plant Disease</i> , 2015, 99, 1578-1583.	0.7	22
42	The <i>GL</i> <i>CDF</i> module of <i>Arabidopsis</i> affects freezing tolerance and growth as well as flowering. <i>Plant Journal</i> , 2015, 81, 695-706.	2.8	104
43	SWP73 Subunits of <i>Arabidopsis</i> SWI/SNF Chromatin Remodeling Complexes Play Distinct Roles in Leaf and Flower Development. <i>Plant Cell</i> , 2015, 27, 1889-1906.	3.1	42
44	Genome-wide expression profiling and phenotypic evaluation of European maize inbreds at seedling stage in response to heat stress. <i>BMC Genomics</i> , 2015, 16, 123.	1.2	83
45	Functional overlap of the <i>Arabidopsis</i> leaf and root microbiota. <i>Nature</i> , 2015, 528, 364-369.	13.7	1,062
46	Capturing sequence variation among flowering-time regulatory gene homologs in the allopolyploid crop species <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 404.	1.7	91
47	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. <i>Frontiers in Plant Science</i> , 2014, 5, 377.	1.7	21
48	Trait-directed de novo population transcriptome dissects genetic regulation of a balanced polymorphism in phosphorus nutrition/arsenate tolerance in a wild grass, <i>Holcus lanatus</i> . <i>New Phytologist</i> , 2014, 201, 144-154.	3.5	6
49	Development of 15 nuclear microsatellite markers in the genus <i>Dyckia</i> (Pitcairnioideae; Bromeliaceae) using 454 pyrosequencing. <i>Conservation Genetics Resources</i> , 2013, 5, 81-84.	0.4	10
50	The Genome of the Alga-Associated Marine Flavobacterium <i>Formosa agariphila</i> KMM 3901 Reveals a Broad Potential for Degradation of Algal Polysaccharides. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6813-6822.	1.4	222
51	The genomic landscape of meiotic crossovers and gene conversions in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 2013, 2, e01426.	2.8	197
52	A set of plastid microsatellite loci for the genus <i>Dyckia</i> (Bromeliaceae) derived from 454 pyrosequencing. <i>American Journal of Botany</i> , 2012, 99, e470-e473.	0.8	10
53	Spread of a Distinct <i>Stx2</i> -Encoding Phage Prototype among <i>Escherichia coli</i> O104:H4 Strains from Outbreaks in Germany, Norway, and Georgia. <i>Journal of Virology</i> , 2012, 86, 10444-10455.	1.5	39
54	Development of microsatellite markers in <i>Fosterella rusbyi</i> (Bromeliaceae) using 454 pyrosequencing. <i>American Journal of Botany</i> , 2012, 99, e160-e163.	0.8	19

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55	Plasma Membrane Calcium ATPases Are Important Components of Receptor-Mediated Signaling in Plant Immune Responses and Development. <i>Plant Physiology</i> , 2012, 159, 798-809.	2.3	112
56	CDKF;1 and CDKD Protein Kinases Regulate Phosphorylation of Serine Residues in the C-Terminal Domain of Arabidopsis RNA Polymerase II. <i>Plant Cell</i> , 2012, 24, 1626-1642.	3.1	70
57	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. <i>Nature</i> , 2012, 488, 91-95.	13.7	2,127
58	RNA-directed DNA methylation and plant development require an IWR1-type transcription factor. <i>EMBO Reports</i> , 2010, 11, 65-71.	2.0	77
59	<i>Arabidopsis thaliana</i> transcription factors bZIP19 and bZIP23 regulate the adaptation to zinc deficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10296-10301.	3.3	334
60	RNA-mediated chromatin-based silencing in plants. <i>Current Opinion in Cell Biology</i> , 2009, 21, 367-376.	2.6	503
61	A structural-maintenance-of-chromosomes hinge domain-containing protein is required for RNA-directed DNA methylation. <i>Nature Genetics</i> , 2008, 40, 670-675.	9.4	180
62	Effects of Aneuploidy on Genome Structure, Expression, and Interphase Organization in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000226.	1.5	96
63	Targets of RNA-directed DNA methylation. <i>Current Opinion in Plant Biology</i> , 2007, 10, 512-519.	3.5	209
64	Endogenous targets of RNA-directed DNA methylation and Pol IV in Arabidopsis. <i>EMBO Journal</i> , 2006, 25, 2828-2836.	3.5	246
65	Atypical RNA polymerase subunits required for RNA-directed DNA methylation. <i>Nature Genetics</i> , 2005, 37, 761-765.	9.4	385
66	Use of Two-Color Fluorescence-Tagged Transgenes to Study Interphase Chromosomes in Living Plants. <i>Plant Physiology</i> , 2005, 139, 1586-1596.	2.3	79
67	A PCR-based assay to detect En/Spm-like transposon sequences in plants. <i>Chromosome Research</i> , 2001, 9, 591-605.	1.0	27
68	The potential of microsatellites for hybridization- and polymerase chain reaction-based DNA fingerprinting of chickpea (<i>Cicer arietinum</i> L.) and related species. <i>Electrophoresis</i> , 1995, 16, 1755-1761.	1.3	37