

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	Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. Nature, 2012, 488, 91-95.	13.7	2,127
2	Functional overlap of the Arabidopsis leaf and root microbiota. Nature, 2015, 528, 364-369.	13.7	1,062
3	RNA-mediated chromatin-based silencing in plants. Current Opinion in Cell Biology, 2009, 21, 367-376.	2.6	503
4	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. Nature Plants, 2018, 4, 460-472.	4.7	391
5	Atypical RNA polymerase subunits required for RNA-directed DNA methylation. Nature Genetics, 2005, 37, 761-765.	9.4	385
6	<i>Arabidopsis thaliana</i> transcription factors bZIP19 and bZIP23 regulate the adaptation to zinc deficiency. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10296-10301.	3.3	334
7	Endogenous targets of RNA-directed DNA methylation and Pol IV in Arabidopsis. EMBO Journal, 2006, 25, 2828-2836.	3.5	246
8	The Genome of the Alga-Associated Marine Flavobacterium Formosa agariphila KMM 3901 ^T Reveals a Broad Potential for Degradation of Algal Polysaccharides. Applied and Environmental Microbiology, 2013, 79, 6813-6822.	1.4	222
9	Targets of RNA-directed DNA methylation. Current Opinion in Plant Biology, 2007, 10, 512-519.	3.5	209
10	The genomic landscape of meiotic crossovers and gene conversions in Arabidopsis thaliana. ELife, 2013, 2, e01426.	2.8	197
11	A structural-maintenance-of-chromosomes hinge domain-containing protein is required for RNA-directed DNA methylation. Nature Genetics, 2008, 40, 670-675.	9.4	180
12	Improving and correcting the contiguity of long-read genome assemblies of three plant species using optical mapping and chromosome conformation capture data. Genome Research, 2017, 27, 778-786.	2.4	155
13	Plasma Membrane Calcium ATPases Are Important Components of Receptor-Mediated Signaling in Plant Immune Responses and Development. Plant Physiology, 2012, 159, 798-809.	2.3	112
14	The <i>GL</i> <i>CDF</i> module of Arabidopsis affects freezing tolerance and growth as well as flowering. Plant Journal, 2015, 81, 695-706.	2.8	104
15	Effects of Aneuploidy on Genome Structure, Expression, and Interphase Organization in Arabidopsis thaliana. PLoS Genetics, 2008, 4, e1000226.	1.5	96
16	Capturing sequence variation among flowering-time regulatory gene homologs in the allopolyploid crop species Brassica napus. Frontiers in Plant Science, 2014, 5, 404.	1.7	91
17	Genome-wide expression profiling and phenotypic evaluation of European maize inbreds at seedling stage in response to heat stress. BMC Genomics, 2015, 16, 123.	1.2	83
18	Use of Two-Color Fluorescence-Tagged Transgenes to Study Interphase Chromosomes in Living Plants. Plant Physiology, 2005, 139, 1586-1596.	2.3	79

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19	RNA-directed DNA methylation and plant development require an IWR1-type transcription factor. <i>EMBO Reports</i> , 2010, 11, 65-71.	2.0	77
20	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
21	Methylation Markers for the Identification of Body Fluids and Tissues from Forensic Trace Evidence. <i>PLoS ONE</i> , 2016, 11, e0147973.	1.1	62
22	The sugar transporter SWEET10 acts downstream of FLOWERING LOCUS T during floral transition of Arabidopsis thaliana. <i>BMC Plant Biology</i> , 2020, 20, 53.	1.6	59
23	Genetic determinants of endophytism in the Arabidopsis root mycobiome. <i>Nature Communications</i> , 2021, 12, 7227.	5.8	58
24	Anaerobic endosymbiont generates energy for ciliate host by denitrification. <i>Nature</i> , 2021, 591, 445-450.	13.7	53
25	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
26	cDNA Library Enrichment of Full Length Transcripts for SMRT Long Read Sequencing. <i>PLoS ONE</i> , 2016, 11, e0157779.	1.1	51
27	Staphylococcus aureus Exploits a Non-ribosomal Cyclic Dipeptide to Modulate Survival within Epithelial Cells and Phagocytes. <i>PLoS Pathogens</i> , 2016, 12, e1005857.	2.1	48
28	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
29	SWP73 Subunits of Arabidopsis SWI/SNF Chromatin Remodeling Complexes Play Distinct Roles in Leaf and Flower Development. <i>Plant Cell</i> , 2015, 27, 1889-1906.	3.1	42
30	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
31	Linked-read sequencing of gametes allows efficient genome-wide analysis of meiotic recombination. <i>Nature Communications</i> , 2019, 10, 4310.	5.8	41
32	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
33	A chromosome-level sequence assembly reveals the structure of the Arabidopsis thaliana Nd-1 genome and its gene set. <i>PLoS ONE</i> , 2019, 14, e0216233.	1.1	40
34	Spread of a Distinct Stx2-Encoding Phage Prototype among Escherichia coli O104:H4 Strains from Outbreaks in Germany, Norway, and Georgia. <i>Journal of Virology</i> , 2012, 86, 10444-10455.	1.5	39
35	Identification of the DNA methyltransferases establishing the methylome of the cyanobacterium Synechocystis sp. PCC 6803. <i>DNA Research</i> , 2018, 25, 343-352.	1.5	38
36	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

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37	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
38	Flowering Time Gene Variation in Brassica Species Shows Evolutionary Principles. <i>Frontiers in Plant Science</i> , 2017, 8, 1742.	1.7	33
39	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
40	Sulfur-Oxidizing Symbionts without Canonical Genes for Autotrophic CO ₂ Fixation. <i>MBio</i> , 2019, 10, .	1.8	29
41	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
42	A PCR-based assay to detect En/Spm-like transposon sequences in plants. <i>Chromosome Research</i> , 2001, 9, 591-605.	1.0	27
43	The megabase-scale crossover landscape is largely independent of sequence divergence. <i>Nature Communications</i> , 2022, 13, .	5.8	25
44	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
45	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
46	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. <i>Frontiers in Plant Science</i> , 2014, 5, 377.	1.7	21
47	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
48	<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
49	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
50	Evolutionary convergence or homology? Comparative cytogenomics of <i>Caesalpinia</i> group species (Leguminosae) reveals diversification in the pericentromeric heterochromatic composition. <i>Planta</i> , 2019, 250, 2173-2186.	1.6	17
51	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
52	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021, 113, 3666-3680.	1.3	17
53	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. <i>PeerJ</i> , 2021, 9, e11721.	0.9	14
54	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

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55	Spingomonas aliaeris sp. nov., a new species isolated from pork steak packed under modified atmosphere. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	13
56	A set of plastid microsatellite loci for the genus Dyckia (Bromeliaceae) derived from 454 pyrosequencing. American Journal of Botany, 2012, 99, e470-e473.	0.8	10
57	Development of 15 nuclear microsatellite markers in the genus Dyckia (Pitcairnioideae; Bromeliaceae) using 454 pyrosequencing. Conservation Genetics Resources, 2013, 5, 81-84.	0.4	10
58	Interplay and Targetome of the Two Conserved Cyanobacterial sRNAs Yfr1 and Yfr2 in Prochlorococcus MED4. Scientific Reports, 2019, 9, 14331.	1.6	10
59	Initial Studies on Cucumber Transcriptome Analysis under Silicon Treatment. Silicon, 2019, 11, 2365-2369.	1.8	9
60	Plastome evolution in the Caesalpinia group (Leguminosae) and its application in phylogenomics and populations genetics. Planta, 2021, 254, 27.	1.6	9
61	The temperature-regulated DEAD-box RNA helicase CrhR interactome: autoregulation and photosynthesis-related transcripts. Journal of Experimental Botany, 2021, , .	2.4	7
62	Traitâ€directed de novo population transcriptome dissects genetic regulation of a balanced polymorphism in phosphorus nutrition/arsenate tolerance in a wild grass, Helianthus lanatus. New Phytologist, 2014, 201, 144-154.	3.5	6
63	Microsatellites from <i>Fosterella christophii</i> (Bromeliaceae) by de novo transcriptome sequencing on the Pacific Biosciences RS platform. Applications in Plant Sciences, 2016, 4, 1500084.	0.8	3
64	Development of 15 nuclear microsatellite markers in <i>Deuterocohnia</i> (Pitcairnioideae;) Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 382 T	0.8	3
65	Development of ten microsatellite markers for Alibertia edulis (Rubiaceae), a Brazilian savanna tree species. Molecular Biology Reports, 2019, 46, 4593-4597.	1.0	3
66	Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar â€BÃrmerâ€™™. Microbiology Resource Announcements, 2020, 9, .	0.3	3
67	Development and characterization of eleven microsatellite loci for the tropical understory tree Paypayrola blanchetiana Tul. (Violaceae). Molecular Biology Reports, 2019, 46, 2529-2532.	1.0	2
68	Identification and initial characterization of a new pair of sibling sRNAs of Neisseria gonorrhoeae involved in type IV pilus biogenesis. Microbiology (United Kingdom), 2021, 167, .	0.7	1