

Andreas Brachmann

List of Publications by Year in descending order

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73
papers

4,049
citations

136950

32
h-index

128289

60
g-index

84
all docs

84
docs citations

84
times ranked

4378
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of genes in the bW/bE regulatory cascade in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2001, 42, 1047-1063.	2.5	286
2	Prion generation in vitro: amyloid of Ure2p is infectious. <i>EMBO Journal</i> , 2005, 24, 3082-3092.	7.8	221
3	<i>NENA</i> , a <i>Lotus japonicus</i> Homolog of <i>Sec13</i> , Is Required for Rhizodermal Infection by Arbuscular Mycorrhiza Fungi and Rhizobia but Dispensable for Cortical Endosymbiotic Development. <i>Plant Cell</i> , 2010, 22, 2509-2526.	6.6	215
4	Biosynthesis of magnetic nanostructures in a foreign organism by transfer of bacterial magnetosome gene clusters. <i>Nature Nanotechnology</i> , 2014, 9, 193-197.	31.5	198
5	A reverse genetic approach for generating gene replacement mutants in <i>Ustilago maydis</i> . <i>Molecular Genetics and Genomics</i> , 2004, 272, 216-226.	2.1	157
6	Kinesin-3 and dynein mediate microtubule-dependent co-transport of mRNPs and endosomes. <i>Journal of Cell Science</i> , 2012, 125, 2740-52.	2.0	140
7	Mating and Pathogenic Development of the Smut Fungus <i>Ustilago maydis</i> Are Regulated by One Mitogen-Activated Protein Kinase Cascade. <i>Eukaryotic Cell</i> , 2003, 2, 1187-1199.	3.4	138
8	Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. <i>Nature Microbiology</i> , 2016, 1, 16033.	13.3	137
9	A homologue of the transcriptional repressor Ssn6p antagonizes cAMP signalling in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2001, 40, 719-730.	2.5	130
10	Sho1 and Msb2-Related Proteins Regulate Appressorium Development in the Smut Fungus <i>Ustilago maydis</i> . <i>Plant Cell</i> , 2010, 22, 2085-2101.	6.6	120
11	An unusual MAP kinase is required for efficient penetration of the plant surface by <i>Ustilago maydis</i> . <i>EMBO Journal</i> , 2003, 22, 2199-2210.	7.8	116
12	Single-cell genomics of uncultivated deep-sea branching magnetotactic bacteria reveals a conserved set of magnetosome genes. <i>Environmental Microbiology</i> , 2016, 18, 21-37.	3.8	115
13	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. <i>BMC Genomics</i> , 2015, 16, 620.	2.8	107
14	Microplastics accumulate fungal pathogens in terrestrial ecosystems. <i>Scientific Reports</i> , 2021, 11, 13214.	3.3	95
15	TILLING in <i>Lotus japonicus</i> Identified Large Allelic Series for Symbiosis Genes and Revealed a Bias in Functionally Defective Ethyl Methanesulfonate Alleles toward Glycine Replacements. <i>Plant Physiology</i> , 2009, 151, 1281-1291.	4.8	89
16	Prion Genetics: New Rules for a New Kind of Gene. <i>Annual Review of Genetics</i> , 2004, 38, 681-707.	7.6	80
17	Prions: proteins as genes and infectious entities. <i>Genes and Development</i> , 2004, 18, 470-485.	5.9	76
18	The effector candidate repertoire of the arbuscular mycorrhizal fungus <i>Rhizophagus clarus</i> . <i>BMC Genomics</i> , 2016, 17, 101.	2.8	76

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19	GintAMT3 – a Low-Affinity Ammonium Transporter of the Arbuscular Mycorrhizal Rhizophagus irregularis. <i>Frontiers in Plant Science</i> , 2016, 7, 679.	3.6	66
20	The Most Widespread Symbiosis on Earth. <i>PLoS Biology</i> , 2006, 4, e239.	5.6	63
21	A Suite of <i>Lotus japonicus</i> Starch Mutants Reveals Both Conserved and Novel Features of Starch Metabolism. <i>Plant Physiology</i> , 2010, 154, 643-655.	4.8	63
22	Fungal Mating in the Most Widespread Plant Symbionts?. <i>Trends in Plant Science</i> , 2017, 22, 175-183.	8.8	62
23	Transient leaf endophytes are the most active fungi in 1-year-old beech leaf litter. <i>Fungal Diversity</i> , 2018, 89, 237-251.	12.3	62
24	Identification of a target gene for the bE-bW homeodomain protein complex in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2000, 37, 54-66.	2.5	61
25	Overproduction of Magnetosomes by Genomic Amplification of Biosynthesis-Related Gene Clusters in a Magnetotactic Bacterium. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3032-3041.	3.1	53
26	Ant-infecting <i>Ophiocordyceps</i> genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. <i>Scientific Reports</i> , 2017, 7, 12508.	3.3	52
27	Tetracycline-regulated gene expression in the pathogen <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 727-738.	2.1	51
28	Characterization of PvuRtsII endonuclease as a tool to investigate genomic 5-hydroxymethylcytosine. <i>Nucleic Acids Research</i> , 2011, 39, 5149-5156.	14.5	51
29	Single nucleus sequencing reveals evidence of inter-nucleus recombination in arbuscular mycorrhizal fungi. <i>ELife</i> , 2018, 7, .	6.0	51
30	Genetic Suppressors of the <i>Lotus japonicus</i> har1-1 Hypernodulation Phenotype. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1082-1091.	2.6	45
31	Diversity and Composition of the Leaf Mycobiome of Beech (<i>Fagus sylvatica</i>) Are Affected by Local Habitat Conditions and Leaf Biochemistry. <i>PLoS ONE</i> , 2016, 11, e0152878.	2.5	41
32	A Set of <i>Lotus japonicus</i> Gifu x <i>Lotus burttii</i> Recombinant Inbred Lines Facilitates Map-based Cloning and QTL Mapping. <i>DNA Research</i> , 2012, 19, 317-323.	3.4	40
33	Single-cell genomics reveals potential for magnetite and greigite biomineralization in an uncultivated multicellular magnetotactic prokaryote. <i>Environmental Microbiology Reports</i> , 2014, 6, 524-531.	2.4	38
34	Polymorphic infection and organogenesis patterns induced by a <i>Rhizobium leguminosarum</i> isolate from <i>Lotus</i> root nodules are determined by the host genotype. <i>New Phytologist</i> , 2012, 196, 561-573.	7.3	36
35	Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. <i>Genome Biology and Evolution</i> , 2019, 11, 2273-2291.	2.5	33
36	Genetic Underpinnings of Host Manipulation by <i>Ophiocordyceps</i> as Revealed by Comparative Transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2275-2296.	1.8	33

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37	Characterization of Three Ammonium Transporters of the Glomeromycotan Fungus <i>Geosiphon pyriformis</i> . <i>Eukaryotic Cell</i> , 2013, 12, 1554-1562.	3.4	31
38	Comparative analysis of a translocated copy of the <i>trnK</i> intron in carnivorous family <i>Nepenthaceae</i> . <i>Molecular Phylogenetics and Evolution</i> , 2006, 39, 478-490.	2.7	30
39	Prion-Forming Ability of <i>Ure2</i> of Yeasts Is Not Evolutionarily Conserved. <i>Genetics</i> , 2011, 188, 81-90.	2.9	30
40	A quantitative hypermorphic CNGC allele confers ectopic calcium flux and impairs cellular development. <i>ELife</i> , 2017, 6, .	6.0	30
41	Selection of Chloroplasts by Laser Microbeam Microdissection for Single-Chloroplast PCR. <i>BioTechniques</i> , 2003, 34, 1238-1243.	1.8	27
42	Reporter assay systems for [URE3] detection and analysis. <i>Methods</i> , 2006, 39, 35-42.	3.8	26
43	Identification and Initial Characterization of Prophages in <i>Vibrio campbellii</i> . <i>PLoS ONE</i> , 2016, 11, e0156010.	2.5	26
44	PALE CRESS binds to plastid RNAs and facilitates the biogenesis of the 50S ribosomal subunit. <i>Plant Journal</i> , 2017, 92, 400-413.	5.7	26
45	An RNA Chaperone-Like Protein Plays Critical Roles in Chloroplast mRNA Stability and Translation in <i>Arabidopsis</i> and <i>Maize</i> . <i>Plant Cell</i> , 2019, 31, 1308-1327.	6.6	25
46	Distinct sensitivity of fungal freshwater guilds to water quality. <i>Mycological Progress</i> , 2017, 16, 155-169.	1.4	24
47	Revisiting regulation of potassium homeostasis in <i>Escherichia coli</i> : the connection to phosphate limitation. <i>MicrobiologyOpen</i> , 2017, 6, e00438.	3.0	24
48	Daily rhythms and enrichment patterns in the transcriptome of the behavior-manipulating parasite <i>Ophiocordyceps kimflamingiae</i> . <i>PLoS ONE</i> , 2017, 12, e0187170.	2.5	24
49	Fungal guilds are evenly distributed along a vertical spruce forest soil profile while individual fungi show pronounced niche partitioning. <i>Mycological Progress</i> , 2018, 17, 925-939.	1.4	23
50	PUMPKIN, the Sole Plastid UMP Kinase, Associates with Group II Introns and Alters Their Metabolism. <i>Plant Physiology</i> , 2019, 179, 248-264.	4.8	23
51	The Temperature-Sensitive <i>brush</i> Mutant of the Legume <i>Lotus japonicus</i> Reveals a Link between Root Development and Nodule Infection by Rhizobia. <i>Plant Physiology</i> , 2009, 149, 1785-1796.	4.8	22
52	mRNA Inventory of Extracellular Vesicles from <i>Ustilago maydis</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 562.	3.5	21
53	Complete genome of <i>Rhizobium leguminosarum</i> Norway, an ineffective <i>Lotus</i> micro-symbiont. <i>Standards in Genomic Sciences</i> , 2018, 13, 36.	1.5	17
54	Candidatus <i>Frankia nodulisporulans</i> sp. nov., an <i>Alnus glutinosa</i> -infective <i>Frankia</i> species unable to grow in pure culture and able to sporulate in-plant. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126134.	2.8	17

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55	Phenotypic Heterogeneity of the Insect Pathogen <i>Photorhabdus luminescens</i> : Insights into the Fate of Secondary Cells. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	16
56	Microbiome profiling reveals that <i>Pseudomonas</i> antagonises parasitic nodule colonisation of cheater rhizobia in <i>Lotus</i> . <i>New Phytologist</i> , 2022, 234, 242-255.	7.3	16
57	Two <i>Lotus japonicus</i> symbiosis mutants impaired at distinct steps of arbuscule development. <i>Plant Journal</i> , 2013, 75, 117-129.	5.7	15
58	Genome-Wide Identification of Essential and Auxiliary Gene Sets for Magnetosome Biosynthesis in <i>Magnetospirillum gryphiswaldense</i> . <i>MSystems</i> , 2020, 5, .	3.8	14
59	<i>In vivo</i> stabilization of endogenous chloroplast RNAs by customized artificial pentatricopeptide repeat proteins. <i>Nucleic Acids Research</i> , 2021, 49, 5985-5997.	14.5	14
60	<i>Bradyrhizobium hipponense</i> sp. nov., isolated from <i>Lupinus angustifolius</i> growing in the northern region of Tunisia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5539-5550.	1.7	14
61	The Plant-Dependent Life Cycle of <i>Thecaphora thlaspeos</i> : A Smut Fungus Adapted to Brassicaceae. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 271-282.	2.6	13
62	Plant-fungal symbiosis en gros and en détail. <i>New Phytologist</i> , 2006, 171, 242-246.	7.3	12
63	Smut infection of perennial hosts: the genome and the transcriptome of the Brassicaceae smut fungus <i>Thecaphora thlaspeos</i> reveal functionally conserved and novel effectors. <i>New Phytologist</i> , 2019, 222, 1474-1492.	7.3	11
64	A Novel Factor Essential for Unconventional Secretion of Chitinase Cts1. <i>Frontiers in Microbiology</i> , 2020, 11, 1529.	3.5	11
65	Prions of Yeast Are Genes Made of Protein: Amyloids and Enzymes. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2004, 69, 489-496.	1.1	9
66	Heterologous transposition in <i>Ustilago maydis</i> . <i>Molecular Genetics and Genomics</i> , 2003, 269, 395-405.	2.1	8
67	More Filtering on SNP Calling Does Not Remove Evidence of Inter-Nucleus Recombination in Dikaryotic Arbuscular Mycorrhizal Fungi. <i>Frontiers in Plant Science</i> , 2020, 11, 912.	3.6	6
68	Whole-Genome Sequences of 14 Strains of <i>Bradyrhizobium canariense</i> and 1 Strain of <i>Bradyrhizobium japonicum</i> Isolated from <i>Lupinus</i> spp. in Algeria. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
69	Involvement of MexS and MexEF-OprN in Resistance to Toxic Ion Chelators in <i>Pseudomonas putida</i> KT2440. <i>Microorganisms</i> , 2020, 8, 1782.	3.6	5
70	Meiotic recombination in the offspring of <i>Microbotryum</i> hybrids and its impact on pathogenicity. <i>BMC Evolutionary Biology</i> , 2020, 20, 123.	3.2	2
71	High-throughput sequencing analysis reveals genomic similarity in phenotypic heterogeneous <i>Photorhabdus luminescens</i> cell populations. <i>Annals of Microbiology</i> , 2022, 72, .	2.6	2
72	Fungal Communities of <i>Eucalyptus grandis</i> Leaves Are Influenced by the Insect Pest <i>Leptocybe invasa</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 841621.	3.5	1

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73	Draft Genome Sequence of <i>Phyllobacterium endophyticum</i> mTS5, Isolated from <i>Lupinus micranthus</i> in Tunisia. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0