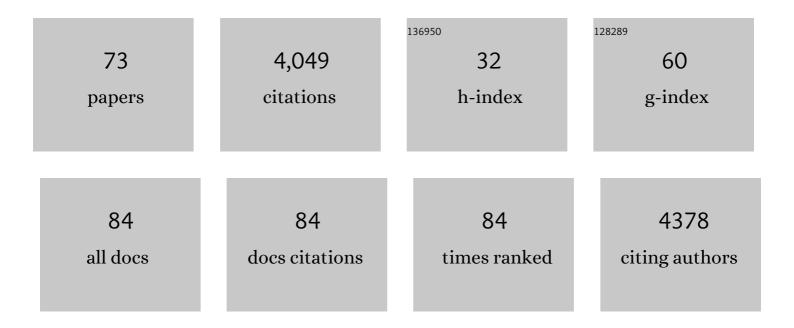
## Andreas Brachmann

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1427890/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Microbiome profiling reveals that <i>Pseudomonas</i> antagonises parasitic nodule colonisation of cheater rhizobia in <i>Lotus</i> . New Phytologist, 2022, 234, 242-255.	7.3	16
2	Fungal Communities of Eucalyptus grandis Leaves Are Influenced by the Insect Pest Leptocybe invasa. Frontiers in Microbiology, 2022, 13, 841621.	3.5	1
3	High-throughput sequencing analysis reveals genomic similarity in phenotypic heterogeneous Photorhabdus luminescens cell populations. Annals of Microbiology, 2022, 72, .	2.6	2
4	<i>In vivo</i> stabilization of endogenous chloroplast RNAs by customized artificial pentatricopeptide repeat proteins. Nucleic Acids Research, 2021, 49, 5985-5997.	14.5	14
5	mRNA Inventory of Extracellular Vesicles from Ustilago maydis. Journal of Fungi (Basel, Switzerland), 2021, 7, 562.	3.5	21
6	Microplastics accumulate fungal pathogens in terrestrial ecosystems. Scientific Reports, 2021, 11, 13214.	3.3	95
7	Meiotic recombination in the offspring of Microbotryum hybrids and its impact on pathogenicity. BMC Evolutionary Biology, 2020, 20, 123.	3.2	2
8	Candidatus Frankia nodulisporulans sp. nov., an Alnus glutinosa-infective Frankia species unable to grow in pure culture and able to sporulate in-planta. Systematic and Applied Microbiology, 2020, 43, 126134.	2.8	17
9	Genome-Wide Identification of Essential and Auxiliary Gene Sets for Magnetosome Biosynthesis in Magnetospirillum gryphiswaldense. MSystems, 2020, 5, .	3.8	14
10	Involvement of MexS and MexEF-OprN in Resistance to Toxic Ion Chelators in Pseudomonas putida KT2440. Microorganisms, 2020, 8, 1782.	3.6	5
11	A Novel Factor Essential for Unconventional Secretion of Chitinase Cts1. Frontiers in Microbiology, 2020, 11, 1529.	3.5	11
12	More Filtering on SNP Calling Does Not Remove Evidence of Inter-Nucleus Recombination in Dikaryotic Arbuscular Mycorrhizal Fungi. Frontiers in Plant Science, 2020, 11, 912.	3.6	6
13	Genetic Underpinnings of Host Manipulation by <i>Ophiocordyceps</i> as Revealed by Comparative Transcriptomics. G3: Genes, Genomes, Genetics, 2020, 10, 2275-2296.	1.8	33
14	Bradyrhizobium hipponense sp. nov., isolated from Lupinus angustifolius growing in the northern region of Tunisia. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5539-5550.	1.7	14
15	Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. Genome Biology and Evolution, 2019, 11, 2273-2291.	2.5	33
16	Phenotypic Heterogeneity of the Insect Pathogen Photorhabdus luminescens: Insights into the Fate of Secondary Cells. Applied and Environmental Microbiology, 2019, 85, .	3.1	16
17	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. New Phytologist, 2019, 222, 1474-1492.	7.3	11
18	An RNA Chaperone–Like Protein Plays Critical Roles in Chloroplast mRNA Stability and Translation in Arabidopsis and Maize. Plant Cell, 2019, 31, 1308-1327.	6.6	25

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19	Draft Genome Sequence of <i>Phyllobacterium endophythicum</i> mTS5, Isolated from <i>Lupinus micranthus</i> in Tunisia. Microbiology Resource Announcements, 2019, 8, .	0.6	0
20	PUMPKIN, the Sole Plastid UMP Kinase, Associates with Group II Introns and Alters Their Metabolism. Plant Physiology, 2019, 179, 248-264.	4.8	23
21	Transient leaf endophytes are the most active fungi in 1-year-old beech leaf litter. Fungal Diversity, 2018, 89, 237-251.	12.3	62
22	Complete genome of Rhizobium leguminosarum Norway, an ineffective Lotus micro-symbiont. Standards in Genomic Sciences, 2018, 13, 36.	1.5	17
23	Fungal guilds are evenly distributed along a vertical spruce forest soil profile while individual fungi show pronounced niche partitioning. Mycological Progress, 2018, 17, 925-939.	1.4	23
24	Single nucleus sequencing reveals evidence of inter-nucleus recombination in arbuscular mycorrhizal fungi. ELife, 2018, 7, .	6.0	51
25	Distinct sensitivity of fungal freshwater guilds to water quality. Mycological Progress, 2017, 16, 155-169.	1.4	24
26	Revisiting regulation of potassium homeostasis in <i>Escherichia coli</i> : the connection to phosphate limitation. MicrobiologyOpen, 2017, 6, e00438.	3.0	24
27	The Plant-Dependent Life Cycle of <i>Thecaphora thlaspeos</i> : A Smut Fungus Adapted to Brassicaceae. Molecular Plant-Microbe Interactions, 2017, 30, 271-282.	2.6	13
28	Ant-infecting Ophiocordyceps genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. Scientific Reports, 2017, 7, 12508.	3.3	52
29	Whole-Genome Sequences of 14 Strains of Bradyrhizobium canariense and 1 Strain of Bradyrhizobium japonicum Isolated from <i>Lupinus</i> spp. in Algeria. Genome Announcements, 2017, 5, .	0.8	5
30	PALE CRESS binds to plastid RNAs and facilitates the biogenesis of the 50S ribosomal subunit. Plant Journal, 2017, 92, 400-413.	5.7	26
31	Fungal Mating in the Most Widespread Plant Symbionts?. Trends in Plant Science, 2017, 22, 175-183.	8.8	62
32	Daily rhythms and enrichment patterns in the transcriptome of the behavior-manipulating parasite Ophiocordyceps kimflemingiae. PLoS ONE, 2017, 12, e0187170.	2.5	24
33	A quantitative hypermorphic CNGC allele confers ectopic calcium flux and impairs cellular development. ELife, 2017, 6, .	6.0	30
34	Diversity and Composition of the Leaf Mycobiome of Beech (Fagus sylvatica) Are Affected by Local Habitat Conditions and Leaf Biochemistry. PLoS ONE, 2016, 11, e0152878.	2.5	41
35	Identification and Initial Characterization of Prophages in Vibrio campbellii. PLoS ONE, 2016, 11, e0156010.	2.5	26
36	GintAMT3 – a Low-Affinity Ammonium Transporter of the Arbuscular Mycorrhizal Rhizophagus irregularis. Frontiers in Plant Science, 2016, 7, 679.	3.6	66

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37	Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. Nature Microbiology, 2016, 1, 16033.	13.3	137
38	The effector candidate repertoire of the arbuscular mycorrhizal fungus Rhizophagus clarus. BMC Genomics, 2016, 17, 101.	2.8	76
39	Overproduction of Magnetosomes by Genomic Amplification of Biosynthesis-Related Gene Clusters in a Magnetotactic Bacterium. Applied and Environmental Microbiology, 2016, 82, 3032-3041.	3.1	53
40	Singleâ€cell genomics of uncultivated deepâ€branching magnetotactic bacteria reveals a conserved set of magnetosome genes. Environmental Microbiology, 2016, 18, 21-37.	3.8	115
41	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. BMC Genomics, 2015, 16, 620.	2.8	107
42	Biosynthesis of magnetic nanostructures in a foreign organism by transfer of bacterial magnetosome gene clusters. Nature Nanotechnology, 2014, 9, 193-197.	31.5	198
43	Singleâ€cell genomics reveals potential for magnetite and greigite biomineralization in an uncultivated multicellular magnetotactic prokaryote. Environmental Microbiology Reports, 2014, 6, 524-531.	2.4	38
44	Characterization of Three Ammonium Transporters of the Glomeromycotan Fungus Geosiphon pyriformis. Eukaryotic Cell, 2013, 12, 1554-1562.	3.4	31
45	Two <i><scp>L</scp>otus japonicus</i> symbiosis mutants impaired at distinct steps of arbuscule development. Plant Journal, 2013, 75, 117-129.	5.7	15
46	A Set of Lotus japonicus Gifu x Lotus burttii Recombinant Inbred Lines Facilitates Map-based Cloning and QTL Mapping. DNA Research, 2012, 19, 317-323.	3.4	40
47	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. New Phytologist, 2012, 196, 561-573.	7.3	36
48	Kinesin-3 and dynein mediate microtubule-dependent co-transport of mRNPs and endosomes. Journal of Cell Science, 2012, 125, 2740-52.	2.0	140
49	Prion-Forming Ability of Ure2 of Yeasts Is Not Evolutionarily Conserved. Genetics, 2011, 188, 81-90.	2.9	30
50	Characterization of PvuRts1I endonuclease as a tool to investigate genomic 5–hydroxymethylcytosine. Nucleic Acids Research, 2011, 39, 5149-5156.	14.5	51
51	<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 Â. Plant Cell, 2010, 22, 2509-2526.	6.6	215
52	Sho1 and Msb2-Related Proteins Regulate Appressorium Development in the Smut Fungus <i>Ustilago maydis</i> Â Â. Plant Cell, 2010, 22, 2085-2101.	6.6	120
53	A Suite of <i>Lotus japonicus</i> Starch Mutants Reveals Both Conserved and Novel Features of Starch Metabolism Ä Ä. Plant Physiology, 2010, 154, 643-655.	4.8	63
54	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  Â. Plant Physiology, 2009, 151, 1281-1291.	4.8	89

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55	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  Â. Plant Physiology, 2009, 149, 1785-1796.	4.8	22
56	Tetracycline-regulated gene expression in the pathogen Ustilago maydis. Fungal Genetics and Biology, 2006, 43, 727-738.	2.1	51
57	Reporter assay systems for [URE3] detection and analysis. Methods, 2006, 39, 35-42.	3.8	26
58	The Most Widespread Symbiosis on Earth. PLoS Biology, 2006, 4, e239.	5.6	63
59	Genetic Suppressors of the Lotus japonicus har1-1 Hypernodulation Phenotype. Molecular Plant-Microbe Interactions, 2006, 19, 1082-1091.	2.6	45
60	Plant–fungal symbiosis en gros and en détail. New Phytologist, 2006, 171, 242-246.	7.3	12
61	Comparative analysis of a translocated copy of the trnK intron in carnivorous family Nepenthaceae. Molecular Phylogenetics and Evolution, 2006, 39, 478-490.	2.7	30
62	Prion generation in vitro: amyloid of Ure2p is infectious. EMBO Journal, 2005, 24, 3082-3092.	7.8	221
63	A reverse genetic approach for generating gene replacement mutants in Ustilago maydis. Molecular Genetics and Genomics, 2004, 272, 216-226.	2.1	157
64	Prion Genetics: New Rules for a New Kind of Gene. Annual Review of Genetics, 2004, 38, 681-707.	7.6	80
65	Prions: proteins as genes and infectious entities. Genes and Development, 2004, 18, 470-485.	5.9	76
66	Prions of Yeast Are Genes Made of Protein: Amyloids and Enzymes. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 489-496.	1.1	9
67	An unusual MAP kinase is required for efficient penetration of the plant surface by Ustilago maydis. EMBO Journal, 2003, 22, 2199-2210.	7.8	116
68	Heterologous transposition in Ustilago maydis. Molecular Genetics and Genomics, 2003, 269, 395-405.	2.1	8
69	Mating and Pathogenic Development of the Smut Fungus Ustilago maydis Are Regulated by One Mitogen-Activated Protein Kinase Cascade. Eukaryotic Cell, 2003, 2, 1187-1199.	3.4	138
70	Selection of Chloroplasts by Laser Microbeam Microdissection for Single-Chloroplast PCR. BioTechniques, 2003, 34, 1238-1243.	1.8	27
71	A homologue of the transcriptional repressor Ssn6p antagonizes cAMP signalling in Ustilago maydis. Molecular Microbiology, 2001, 40, 719-730.	2.5	130
72	Identification of genes in the bW/bE regulatory cascade in Ustilago maydis. Molecular Microbiology, 2001, 42, 1047-1063.	2.5	286

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73	Identification of a target gene for the bE-bW homeodomain protein complex in Ustilago maydis. Molecular Microbiology, 2000, 37, 54-66.	2.5	61