

Norman Warthmann

List of Publications by Year in descending order

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33
papers

7,554
citations

236925

25
h-index

414414

32
g-index

36
all docs

36
docs citations

36
times ranked

10274
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly Specific Gene Silencing by Artificial MicroRNAs in Arabidopsis. <i>Plant Cell</i> , 2006, 18, 1121-1133.	6.6	1,207
2	The Rate and Molecular Spectrum of Spontaneous Mutations in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2010, 327, 92-94.	12.6	1,004
3	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	12.6	689
4	Export of FT Protein from Phloem Companion Cells Is Sufficient for Floral Induction in Arabidopsis. <i>Current Biology</i> , 2007, 17, 1055-1060.	3.9	554
5	Autoimmune Response as a Mechanism for a Dobzhansky-Muller-Type Incompatibility Syndrome in Plants. <i>PLoS Biology</i> , 2007, 5, e236.	5.6	489
6	Sequencing of natural strains of <i>Arabidopsis thaliana</i> with short reads. <i>Genome Research</i> , 2008, 18, 2024-2033.	5.5	442
7	Sequence and Expression Differences Underlie Functional Specialization of Arabidopsis MicroRNAs miR159 and miR319. <i>Developmental Cell</i> , 2007, 13, 115-125.	7.0	399
8	The Scale of Population Structure in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000843.	3.5	338
9	Highly Specific Gene Silencing by Artificial miRNAs in Rice. <i>PLoS ONE</i> , 2008, 3, e1829.	2.5	295
10	Reference-guided assembly of four diverse <i>Arabidopsis thaliana</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10249-10254.	7.1	237
11	Simultaneous alignment of short reads against multiple genomes. <i>Genome Biology</i> , 2009, 10, R98.	9.6	215
12	The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2006, 38, 711-715.	21.4	191
13	Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2460-2465.	7.1	174
14	Local-Scale Patterns of Genetic Variability, Outcrossing, and Spatial Structure in Natural Stands of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000890.	3.5	172
15	Genome expansion of <i>Arabis alpina</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
16	The recombination landscape in <i>Arabidopsis thaliana</i> F2 populations. <i>Heredity</i> , 2012, 108, 447-455.	2.6	155
17	A Promiscuous Intermediate Underlies the Evolution of LEAFY DNA Binding Specificity. <i>Science</i> , 2014, 343, 645-648.	12.6	117
18	Cis-regulatory Changes at FLOWERING LOCUS T Mediate Natural Variation in Flowering Responses of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009, 183, 723-732.	2.9	109

#	ARTICLE	IF	CITATIONS
19	QTL Mapping in New Arabidopsis thaliana Advanced Intercross-Recombinant Inbred Lines. PLoS ONE, 2009, 4, e4318.	2.5	92
20	Major-Effect Alleles at Relatively Few Loci Underlie Distinct Vernalization and Flowering Variation in Arabidopsis Accessions. PLoS ONE, 2011, 6, e19949.	2.5	76
21	Do longer root hairs improve phosphorus uptake? Testing the hypothesis with transgenic <i>Brachypodium distachyon</i> lines overexpressing endogenous <i>RSL</i> genes. New Phytologist, 2018, 217, 1654-1666.	7.3	68
22	High habitat-specificity in fungal communities in oligo-mesotrophic, temperate Lake Stechlin (North-East Germany). MycoKeys, 0, 16, 17-44.	1.9	68
23	Comparative Analysis of the MIR319a MicroRNA Locus in Arabidopsis and Related Brassicaceae. Molecular Biology and Evolution, 2008, 25, 892-902.	8.9	67
24	Directed Gene Silencing with Artificial MicroRNAs. Methods in Molecular Biology, 2010, 592, 71-88.	0.9	53
25	MSQT for choosing SNP assays from multiple DNA alignments. Bioinformatics, 2007, 23, 2784-2787.	4.1	41
26	kWIP: The k-mer weighted inner product, a de novo estimator of genetic similarity. PLoS Computational Biology, 2017, 13, e1005727.	3.2	39
27	Genomic breeding for food, environment and livelihoods. Food Security, 2015, 7, 375-382.	5.3	23
28	ESTs and EST-linked polymorphisms for genetic mapping and phylogenetic reconstruction in the guppy, <i>Poecilia reticulata</i> . BMC Genomics, 2007, 8, 269.	2.8	21
29	Analysis of DNAs associated with coconut foliar decay disease implicates a unique single-stranded DNA virus representing a new taxon. Scientific Reports, 2018, 8, 5698.	3.3	19
30	Global Diversity of the <i>Brachypodium</i> Species Complex as a Resource for Genome-Wide Association Studies Demonstrated for Agronomic Traits in Response to Climate. Genetics, 2019, 211, 317-331.	2.9	17
31	DNA metabarcoding of unfractionated water samples relates phyto-, zoo- and bacterioplankton dynamics and reveals a single taxon bacterial bloom. Environmental Microbiology Reports, 2017, 9, 383-388.	2.4	13
32	Artificial MicroRNAs for Specific Gene Silencing in Rice. Methods in Molecular Biology, 2013, 956, 131-149.	0.9	5
33	Response to Comment on "A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity". Science, 2015, 347, 621-621.	12.6	4