

Magnus Nordborg

List of Publications by Year in descending order

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127
papers

23,933
citations

15880

67
h-index

18944

123
g-index

158
all docs

158
docs citations

158
times ranked

22663
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Genetic Heterogeneity in Adaptive Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 4822-4831.	3.5	27
2	Revisiting a GWAS peak in <i>Arabidopsis thaliana</i> reveals possible confounding by genetic heterogeneity. <i>Heredity</i> , 2021, 127, 245-252.	1.2	8
3	Gradual evolution of allopolyploidy in <i>Arabidopsis suecica</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 1367-1381.	3.4	64
4	AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2020, 48, D1063-D1068.	6.5	44
5	Response to \AA reappraisal of the phylogenetic placement of the <i>Aquilegia</i> whole-genome duplication. <i>Genome Biology</i> , 2020, 21, 297.	3.8	5
6	Adaptive reduction of male gamete number in the selfing plant <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2020, 11, 2885.	5.8	27
7	<i>Arabidopsis</i> shoot stem cells display dynamic transcription and $\text{\textless scp>DNA</scp>}$ methylation patterns. <i>EMBO Journal</i> , 2020, 39, e103667.	3.5	55
8	Transgenerational effects of inter-ploidy cross direction on reproduction and F2 seed development of <i>Arabidopsis thaliana</i> F1 hybrid triploids. <i>Plant Reproduction</i> , 2019, 32, 275-289.	1.3	5
9	Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2019, 15, e1008492.	1.5	68
10	The <i>Aquilegia</i> genome reveals a hybrid origin of core eudicots. <i>Genome Biology</i> , 2019, 20, 256.	3.8	38
11	Why structure matters. <i>ELife</i> , 2019, 8, .	2.8	107
12	Title is missing!. , 2019, 15, e1008492.		0
13	Title is missing!. , 2019, 15, e1008492.		0
14	Title is missing!. , 2019, 15, e1008492.		0
15	Title is missing!. , 2019, 15, e1008492.		0
16	The AraGWAS Catalog: a curated and standardized <i>Arabidopsis thaliana</i> GWAS catalog. <i>Nucleic Acids Research</i> , 2018, 46, D1150-D1156.	6.5	83
17	Eco-Metabolomics and Metabolic Modeling: Making the Leap From Model Systems in the Lab to Native Populations in the Field. <i>Frontiers in Plant Science</i> , 2018, 9, 1556.	1.7	28
18	GWAS with Heterogeneous Data: Estimating the Fraction of Phenotypic Variation Mediated by Gene Expression Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3059-3068.	0.8	28

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19	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, .	2.8	120
20	Genome sequencing reveals the origin of the allotetraploid <i>Arabidopsis suecica</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw299.	3.5	73
21	Unstable Inheritance of 45S rRNA Genes in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1201-1209.	0.8	43
22	Genomic Rearrangements in <i>Arabidopsis</i> Considered as Quantitative Traits. <i>Genetics</i> , 2017, 205, 1425-1441.	1.2	21
23	On the post-glacial spread of human commensal <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2017, 8, 14458.	5.8	83
24	AraPheno: a public database for <i>Arabidopsis thaliana</i> phenotypes. <i>Nucleic Acids Research</i> , 2017, 45, D1054-D1059.	6.5	91
25	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017, 49, 1705-1713.	9.4	107
26	Verification of <i>Arabidopsis</i> stock collections using SNPmatch, a tool for genotyping high-plexed samples. <i>Scientific Data</i> , 2017, 4, 170184.	2.4	26
27	Patterns of Polymorphism at the Self-Incompatibility Locus in 1,083 <i>Arabidopsis thaliana</i> Genomes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1878-1889.	3.5	48
28	The maternal environment interacts with genetic variation in regulating seed dormancy in Swedish <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2017, 12, e0190242.	1.1	24
29	Epistatic and allelic interactions control expression of ribosomal RNA gene clusters in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2017, 18, 75.	3.8	36
30	50 years of <i>Arabidopsis</i> research: highlights and future directions. <i>New Phytologist</i> , 2016, 209, 921-944.	3.5	186
31	Germline replications and somatic mutation accumulation are independent of vegetative life span in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12226-12231.	3.3	83
32	The genetic architecture of freezing tolerance varies across the range of <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2016, 39, 2570-2579.	2.8	41
33	Molecular, genetic and evolutionary analysis of a paracentric inversion in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 159-178.	2.8	81
34	Sequencing of the genus <i>Arabidopsis</i> identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	9.4	198
35	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	13.5	594
36	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	13.5	1,107

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37	A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , 2016, 28, 606-609.	3.1	31
38	Limited Contribution of DNA Methylation Variation to Expression Regulation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2016, 12, e1006141.	1.5	94
39	Multiple alleles at a single locus control seed dormancy in Swedish <i>Arabidopsis</i> . <i>ELife</i> , 2016, 5, .	2.8	57
40	"Missing" G x E Variation Controls Flowering Time in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2015, 11, e1005597.	1.5	87
41	Genetic Architecture of Natural Variation of Telomere Length in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2015, 199, 625-635.	1.2	26
42	The Spontaneous Mutation Rate in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Genetics</i> , 2015, 201, 737-744.	1.2	127
43	Population Genomics for Understanding Adaptation in Wild Plant Species. <i>Annual Review of Genetics</i> , 2015, 49, 315-338.	3.2	94
44	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
45	DNA methylation in <i>Arabidopsis</i> has a genetic basis and shows evidence of local adaptation. <i>ELife</i> , 2015, 4, e05255.	2.8	457
46	Keeping It Local: Evidence for Positive Selection in Swedish <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 3026-3039.	3.5	70
47	Multiple <i>FLC</i> haplotypes defined by independent <i>cis</i> -regulatory variation underpin life history diversity in <i>Arabidopsis thaliana</i> . <i>Genes and Development</i> , 2014, 28, 1635-1640.	2.7	122
48	Genome-wide association study of <i>Arabidopsis thaliana</i> leaf microbial community. <i>Nature Communications</i> , 2014, 5, 5320.	5.8	322
49	Towards the discovery of novel genetic component involved in stress resistance in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2014, 201, 810-824.	3.5	12
50	The nature of confounding in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2013, 14, 1-2.	7.7	169
51	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	9.4	374
52	GWAPP: A Web Application for Genome-Wide Association Mapping in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 24, 4793-4805.	3.1	162
53	Genetic Architecture of Skin and Eye Color in an African-European Admixed Population. <i>PLoS Genetics</i> , 2013, 9, e1003372.	1.5	137
54	JAWAMix5: an out-of-core HDF5-based java implementation of whole-genome association studies using mixed models. <i>Bioinformatics</i> , 2013, 29, 1220-1222.	1.8	15

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55	Massive genomic variation and strong selection in <i>Arabidopsis thaliana</i> lines from Sweden. <i>Nature Genetics</i> , 2013, 45, 884-890.	9.4	371
56	Co-Variation between Seed Dormancy, Growth Rate and Flowering Time Changes with Latitude in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2013, 8, e61075.	1.1	130
57	Genome-Wide Association Studies Identify Heavy Metal ATPase3 as the Primary Determinant of Natural Variation in Leaf Cadmium in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2012, 8, e1002923.	1.5	224
58	Genome-wide patterns of genetic variation in worldwide <i>Arabidopsis thaliana</i> accessions from the RegMap panel. <i>Nature Genetics</i> , 2012, 44, 212-216.	9.4	476
59	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. <i>Nature Genetics</i> , 2012, 44, 1066-1071.	9.4	380
60	An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. <i>Nature Genetics</i> , 2012, 44, 825-830.	9.4	884
61	A comparison of population types used for QTL mapping in <i>Arabidopsis thaliana</i> . <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 185-188.	0.4	17
62	PoolHap: Inferring Haplotype Frequencies from Pooled Samples by Next Generation Sequencing. <i>PLoS ONE</i> , 2011, 6, e15292.	1.1	38
63	Analysis and visualization of <i>Arabidopsis thaliana</i> GWAS using web 2.0 technologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar014-bar014.	1.4	8
64	Source verification of misidentified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , 2011, 67, 554-566.	2.8	63
65	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	9.4	814
66	High-Resolution Analysis of Parent-of-Origin Allelic Expression in the <i>Arabidopsis</i> Endosperm. <i>PLoS Genetics</i> , 2011, 7, e1002126.	1.5	237
67	Major-Effect Alleles at Relatively Few Loci Underlie Distinct Vernalization and Flowering Variation in <i>Arabidopsis</i> Accessions. <i>PLoS ONE</i> , 2011, 6, e19949.	1.1	76
68	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	13.7	1,651
69	Natural allelic variation underlying a major fitness trade-off in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2010, 465, 632-636.	13.7	378
70	Genetic Variation at Nuclear Loci Fails to Distinguish Two Morphologically Distinct Species of <i>Aquilegia</i> . <i>PLoS ONE</i> , 2010, 5, e8655.	1.1	23
71	Genome-wide survey of <i>Arabidopsis</i> natural variation in downy mildew resistance using combined association and linkage mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10302-10307.	3.3	120
72	Linkage and Association Mapping of <i>Arabidopsis thaliana</i> Flowering Time in Nature. <i>PLoS Genetics</i> , 2010, 6, e1000940.	1.5	415

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73	A Coastal Cline in Sodium Accumulation in <i>Arabidopsis thaliana</i> Is Driven by Natural Variation of the Sodium Transporter AtHKT1;1. <i>PLoS Genetics</i> , 2010, 6, e1001193.	1.5	317
74	The Scale of Population Structure in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000843.	1.5	338
75	Conditions Under Which Genome-Wide Association Studies Will be Positively Misleading. <i>Genetics</i> , 2010, 186, 1045-1052.	1.2	178
76	Association mapping of local climate-sensitive quantitative trait loci in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21199-21204.	3.3	278
77	Next-generation genetics in plants. <i>Nature</i> , 2008, 456, 720-723.	13.7	409
78	The Impact of <i>Arabidopsis</i> on Human Health: Diversifying Our Portfolio. <i>Cell</i> , 2008, 133, 939-943.	13.5	101
79	Selection on Amino Acid Substitutions in <i>Arabidopsis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1375-1383.	3.5	71
80	Evolution and Control of Imprinted FWA Genes in the Genus <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2008, 4, e1000048.	1.5	111
81	Exploring Population Genetic Models With Recombination Using Efficient Forward-Time Simulations. <i>Genetics</i> , 2008, 178, 2417-2427.	1.2	48
82	Strong Signature of Natural Selection within an FHIT Intron Implicated in Prostate Cancer Risk. <i>PLoS ONE</i> , 2008, 3, e3533.	1.1	13
83	Genome-wide patterns of single-feature polymorphism in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12057-12062.	3.3	157
84	An <i>Arabidopsis</i> Example of Association Mapping in Structured Samples. <i>PLoS Genetics</i> , 2007, 3, e4.	1.5	625
85	A Single IGF1 Allele Is a Major Determinant of Small Size in Dogs. <i>Science</i> , 2007, 316, 112-115.	6.0	587
86	The Evolution of Selfing in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 1070-1072.	6.0	160
87	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	6.0	689
88	Genome-wide association mapping using mixed-models: application to GAW15 Problem 3. <i>BMC Proceedings</i> , 2007, 1, S164.	1.8	4
89	Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2007, 39, 1151-1155.	9.4	497
90	A Unique Recent Origin of the Allotetraploid Species <i>Arabidopsis suecica</i> : Evidence from Nuclear DNA Markers. <i>Molecular Biology and Evolution</i> , 2006, 23, 1217-1231.	3.5	119

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91	Variation in the epigenetic silencing of FLC contributes to natural variation in Arabidopsis vernalization response. <i>Genes and Development</i> , 2006, 20, 3079-3083.	2.7	200
92	Relative Influences of Crossing Over and Gene Conversion on the Pattern of Linkage Disequilibrium in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2006, 172, 2441-2448.	1.2	26
93	A General Population-Genetic Model for the Production by Population Structure of Spurious Genotype-Phenotype Associations in Discrete, Admixed or Spatially Distributed Populations. <i>Genetics</i> , 2006, 173, 1665-1678.	1.2	55
94	Estimating Recombination Rates From Single-Nucleotide Polymorphisms Using Summary Statistics. <i>Genetics</i> , 2006, 174, 1517-1528.	1.2	28
95	Association Mapping With Single-Feature Polymorphisms. <i>Genetics</i> , 2006, 173, 1125-1133.	1.2	31
96	A Nonparametric Test Reveals Selection for Rapid Flowering in the Arabidopsis Genome. <i>PLoS Biology</i> , 2006, 4, e137.	2.6	118
97	The Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005, 3, e196.	2.6	895
98	Genome-Wide Association Mapping in <i>Arabidopsis</i> Identifies Previously Known Flowering Time and Pathogen Resistance Genes. <i>PLoS Genetics</i> , 2005, 1, e60.	1.5	378
99	Natural Variation in <i>Arabidopsis</i> . How Do We Find the Causal Genes?. <i>Plant Physiology</i> , 2005, 138, 567-568.	2.3	88
100	Role of FRIGIDA and FLOWERING LOCUS C in Determining Variation in Flowering Time of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 138, 1163-1173.	2.3	383
101	Genome-wide association mapping in <i>Arabidopsis thaliana</i> identifies previously known genes responsible for variation in flowering time and pathogen resistance. <i>PLoS Genetics</i> , 2005, preprint, e60.	1.5	3
102	Haplotype Structure and Phenotypic Associations in the Chromosomal Regions Surrounding Two <i>Arabidopsis thaliana</i> Flowering Time Loci. Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY781906, AY785055.. <i>Genetics</i> , 2004, 168, 1627-1638.	1.2	67
103	The Probability and Chromosomal Extent of trans-specific Polymorphism. <i>Genetics</i> , 2004, 168, 2363-2372.	1.2	67
104	Adjust quality scores from alignment and improve sequencing accuracy. <i>Nucleic Acids Research</i> , 2004, 32, 5183-5191.	6.5	33
105	Estimating the Rate of Gene Conversion on Human Chromosome 21. <i>American Journal of Human Genetics</i> , 2004, 75, 386-397.	2.6	42
106	Hot and Cold Spots of Recombination in the Human Genome: the Reason We Should Find Them and How This Can Be Achieved. <i>American Journal of Human Genetics</i> , 2003, 73, 5-16.	2.6	99
107	The Pattern of Polymorphism on Human Chromosome 21. <i>Genome Research</i> , 2003, 13, 1158-1168.	2.4	35
108	The Impact of Genomics on the Study of Natural Variation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2003, 132, 718-725.	2.3	113

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109	The Genealogy of Sequences Containing Multiple Sites Subject to Strong Selection in a Subdivided Population. <i>Genetics</i> , 2003, 163, 1201-1213.	1.2	51
110	The Extent of Linkage Disequilibrium and Haplotype Sharing Around a Polymorphic Site. <i>Genetics</i> , 2003, 165, 437-444.	1.2	22
111	Recombination or Mutational Hot Spots in Human mtDNA?. <i>Molecular Biology and Evolution</i> , 2002, 19, 1122-1127.	3.5	51
112	Haplotype Block Structure and Its Applications to Association Studies: Power and Study Designs. <i>American Journal of Human Genetics</i> , 2002, 71, 1386-1394.	2.6	243
113	Linkage disequilibrium: what history has to tell us. <i>Trends in Genetics</i> , 2002, 18, 83-90.	2.9	472
114	Molecular population genetics. <i>Current Opinion in Plant Biology</i> , 2002, 5, 69-73.	3.5	42
115	The extent of linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2002, 30, 190-193.	9.4	425
116	Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. <i>Nature Reviews Genetics</i> , 2002, 3, 380-390.	7.7	582
117	Sequence Variation and Haplotype Structure Surrounding the Flowering Time Locus <i>FRI</i> in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002, 161, 289-298.	1.2	76
118	Likelihoods and Simulation Methods for a Class of Nonneutral Population Genetics Models. <i>Genetics</i> , 2001, 159, 853-867.	1.2	34
119	Linkage Disequilibrium, Gene Trees and Selfing: An Ancestral Recombination Graph With Partial Self-Fertilization. <i>Genetics</i> , 2000, 154, 923-929.	1.2	375
120	The effect of seed and rosette cold treatment on germination and flowering time in some <i>Arabidopsis thaliana</i> (Brassicaceae) ecotypes. <i>American Journal of Botany</i> , 1999, 86, 470-475.	0.8	117
121	On the Probability of Neanderthal Ancestry. <i>American Journal of Human Genetics</i> , 1998, 63, 1237-1240.	2.6	177
122	The Effect of Gene Conversion on Intralocus Associations. <i>Genetics</i> , 1998, 148, 1397-1399.	1.2	115
123	The effects of local selection, balanced polymorphism and background selection on equilibrium patterns of genetic diversity in subdivided populations. <i>Genetical Research</i> , 1997, 70, 155-174.	0.3	668
124	The Coalescent Process With Selfing. <i>Genetics</i> , 1997, 146, 1185-1195.	1.2	175
125	Structured Coalescent Processes on Different Time Scales. <i>Genetics</i> , 1997, 146, 1501-1514.	1.2	222
126	The effect of recombination on background selection. <i>Genetical Research</i> , 1996, 67, 159-174.	0.3	311

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127	Female infanticide and human sex ratio evolution. <i>Journal of Theoretical Biology</i> , 1992, 158, 195-198.	0.8	5