

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	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
2	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
3	The Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005, 3, e196.	2.6	895
4	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
5	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
6	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	6.0	689
7	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
8	An <i>Arabidopsis</i> Example of Association Mapping in Structured Samples. <i>PLoS Genetics</i> , 2007, 3, e4.	1.5	625
9	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	13.5	594
10	A Single IGF1 Allele Is a Major Determinant of Small Size in Dogs. <i>Science</i> , 2007, 316, 112-115.	6.0	587
11	Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. <i>Nature Reviews Genetics</i> , 2002, 3, 380-390.	7.7	582
12	Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2007, 39, 1151-1155.	9.4	497
13	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
14	Linkage disequilibrium: what history has to tell us. <i>Trends in Genetics</i> , 2002, 18, 83-90.	2.9	472
15	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
16	The extent of linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2002, 30, 190-193.	9.4	425
17	Linkage and Association Mapping of <i>Arabidopsis thaliana</i> Flowering Time in Nature. <i>PLoS Genetics</i> , 2010, 6, e1000940.	1.5	415
18	Next-generation genetics in plants. <i>Nature</i> , 2008, 456, 720-723.	13.7	409

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19	Role of FRIGIDA and FLOWERING LOCUS C in Determining Variation in Flowering Time of Arabidopsis. <i>Plant Physiology</i> , 2005, 138, 1163-1173.	2.3	383
20	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
21	Genome-Wide Association Mapping in Arabidopsis Identifies Previously Known Flowering Time and Pathogen Resistance Genes. <i>PLoS Genetics</i> , 2005, 1, e60.	1.5	378
22	Natural allelic variation underlying a major fitness trade-off in Arabidopsis thaliana. <i>Nature</i> , 2010, 465, 632-636.	13.7	378
23	Linkage Disequilibrium, Gene Trees and Selfing: An Ancestral Recombination Graph With Partial Self-Fertilization. <i>Genetics</i> , 2000, 154, 923-929.	1.2	375
24	The Capsella rubella genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	9.4	374
25	Massive genomic variation and strong selection in Arabidopsis thaliana lines from Sweden. <i>Nature Genetics</i> , 2013, 45, 884-890.	9.4	371
26	The Scale of Population Structure in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2010, 6, e1000843.	1.5	338
27	Genome-wide association study of Arabidopsis thaliana leaf microbial community. <i>Nature Communications</i> , 2014, 5, 5320.	5.8	322
28	A Coastal Cline in Sodium Accumulation in Arabidopsis thaliana Is Driven by Natural Variation of the Sodium Transporter AtHKT1;1. <i>PLoS Genetics</i> , 2010, 6, e1001193.	1.5	317
29	The effect of recombination on background selection. <i>Genetical Research</i> , 1996, 67, 159-174.	0.3	311
30	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
31	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
32	High-Resolution Analysis of Parent-of-Origin Allelic Expression in the Arabidopsis Endosperm. <i>PLoS Genetics</i> , 2011, 7, e1002126.	1.5	237
33	Genome-Wide Association Studies Identify Heavy Metal ATPase3 as the Primary Determinant of Natural Variation in Leaf Cadmium in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2012, 8, e1002923.	1.5	224
34	Structured Coalescent Processes on Different Time Scales. <i>Genetics</i> , 1997, 146, 1501-1514.	1.2	222
35	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
36	Sequencing of the genus Arabidopsis identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	9.4	198

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37	50 Years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016, 209, 921-944.	3.5	186
38	Conditions Under Which Genome-Wide Association Studies Will be Positively Misleading. <i>Genetics</i> , 2010, 186, 1045-1052.	1.2	178
39	On the Probability of Neanderthal Ancestry. <i>American Journal of Human Genetics</i> , 1998, 63, 1237-1240.	2.6	177
40	The Coalescent Process With Selfing. <i>Genetics</i> , 1997, 146, 1185-1195.	1.2	175
41	The nature of confounding in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2013, 14, 1-2.	7.7	169
42	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis. <i>Plant Cell</i> , 2013, 24, 4793-4805.	3.1	162
43	The Evolution of Selfing in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 1070-1072.	6.0	160
44	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
45	Genetic Architecture of Skin and Eye Color in an African-European Admixed Population. <i>PLoS Genetics</i> , 2013, 9, e1003372.	1.5	137
46	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
47	The Spontaneous Mutation Rate in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Genetics</i> , 2015, 201, 737-744.	1.2	127
48	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
49	Genome-wide survey of Arabidopsis 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
50	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
51	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
52	A Nonparametric Test Reveals Selection for Rapid Flowering in the Arabidopsis Genome. <i>PLoS Biology</i> , 2006, 4, e137.	2.6	118
53	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
54	The Effect of Gene Conversion on Intralocus Associations. <i>Genetics</i> , 1998, 148, 1397-1399.	1.2	115

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55	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	2.4	114
56	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
57	Evolution and Control of Imprinted FWA Genes in the Genus <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2008, 4, e1000048.	1.5	111
58	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017, 49, 1705-1713.	9.4	107
59	Why structure matters. <i>ELife</i> , 2019, 8, .	2.8	107
60	The Impact of <i>Arabidopsis</i> on Human Health: Diversifying Our Portfolio. <i>Cell</i> , 2008, 133, 939-943.	13.5	101
61	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
62	Population Genomics for Understanding Adaptation in Wild Plant Species. <i>Annual Review of Genetics</i> , 2015, 49, 315-338.	3.2	94
63	Limited Contribution of DNA Methylation Variation to Expression Regulation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2016, 12, e1006141.	1.5	94
64	AraPheno: a public database for <i>Arabidopsis thaliana</i> phenotypes. <i>Nucleic Acids Research</i> , 2017, 45, D1054-D1059.	6.5	91
65	Natural Variation in <i>Arabidopsis</i> . How Do We Find the Causal Genes?. <i>Plant Physiology</i> , 2005, 138, 567-568.	2.3	88
66	"Missing" G x E Variation Controls Flowering Time in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2015, 11, e1005597.	1.5	87
67	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
68	On the post-glacial spread of human commensal <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2017, 8, 14458.	5.8	83
69	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
70	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
71	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
72	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

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73	Genome sequencing reveals the origin of the allotetraploid <i>Arabidopsis suecica</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw299.	3.5	73
74	Selection on Amino Acid Substitutions in <i>Arabidopsis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1375-1383.	3.5	71
75	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
76	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
77	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
78	The Probability and Chromosomal Extent of trans-specific Polymorphism. <i>Genetics</i> , 2004, 168, 2363-2372.	1.2	67
79	Gradual evolution of allopolyploidy in <i>Arabidopsis suecica</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 1367-1381.	3.4	64
80	Source verification of misidentified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , 2011, 67, 554-566.	2.8	63
81	Multiple alleles at a single locus control seed dormancy in Swedish <i>Arabidopsis</i> . <i>ELife</i> , 2016, 5, .	2.8	57
82	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
83	<i>Arabidopsis</i> shoot stem cells display dynamic transcription and DNA methylation patterns. <i>EMBO Journal</i> , 2020, 39, e103667.	3.5	55
84	Recombination or Mutational Hot Spots in Human mtDNA?. <i>Molecular Biology and Evolution</i> , 2002, 19, 1122-1127.	3.5	51
85	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
86	Exploring Population Genetic Models With Recombination Using Efficient Forward-Time Simulations. <i>Genetics</i> , 2008, 178, 2417-2427.	1.2	48
87	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
88	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
89	Unstable Inheritance of 45S rRNA Genes in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1201-1209.	0.8	43
90	Molecular population genetics. <i>Current Opinion in Plant Biology</i> , 2002, 5, 69-73.	3.5	42

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91	Estimating the Rate of Gene Conversion on Human Chromosome 21. <i>American Journal of Human Genetics</i> , 2004, 75, 386-397.	2.6	42
92	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
93	PoolHap: Inferring Haplotype Frequencies from Pooled Samples by Next Generation Sequencing. <i>PLoS ONE</i> , 2011, 6, e15292.	1.1	38
94	The <i>Aquilegia</i> genome reveals a hybrid origin of core eudicots. <i>Genome Biology</i> , 2019, 20, 256.	3.8	38
95	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
96	The Pattern of Polymorphism on Human Chromosome 21. <i>Genome Research</i> , 2003, 13, 1158-1168.	2.4	35
97	Likelihoods and Simulation Methods for a Class of Nonneutral Population Genetics Models. <i>Genetics</i> , 2001, 159, 853-867.	1.2	34
98	Adjust quality scores from alignment and improve sequencing accuracy. <i>Nucleic Acids Research</i> , 2004, 32, 5183-5191.	6.5	33
99	Association Mapping With Single-Feature Polymorphisms. <i>Genetics</i> , 2006, 173, 1125-1133.	1.2	31
100	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
101	Estimating Recombination Rates From Single-Nucleotide Polymorphisms Using Summary Statistics. <i>Genetics</i> , 2006, 174, 1517-1528.	1.2	28
102	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
103	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
104	Adaptive reduction of male gamete number in the selfing plant <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2020, 11, 2885.	5.8	27
105	Global Genetic Heterogeneity in Adaptive Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 4822-4831.	3.5	27
106	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
107	Genetic Architecture of Natural Variation of Telomere Length in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2015, 199, 625-635.	1.2	26
108	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

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109	The maternal environment interacts with genetic variation in regulating seed dormancy in Swedish <i>Arabidopsis thaliana</i> . PLoS ONE, 2017, 12, e0190242.	1.1	24
110	Genetic Variation at Nuclear Loci Fails to Distinguish Two Morphologically Distinct Species of <i>Aquilegia</i> . PLoS ONE, 2010, 5, e8655.	1.1	23
111	The Extent of Linkage Disequilibrium and Haplotype Sharing Around a Polymorphic Site. Genetics, 2003, 165, 437-444.	1.2	22
112	Genomic Rearrangements in <i>Arabidopsis</i> Considered as Quantitative Traits. Genetics, 2017, 205, 1425-1441.	1.2	21
113	A comparison of population types used for QTL mapping in <i>Arabidopsis thaliana</i> . Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 185-188.	0.4	17
114	JAWAMix5: an out-of-core HDF5-based java implementation of whole-genome association studies using mixed models. Bioinformatics, 2013, 29, 1220-1222.	1.8	15
115	Strong Signature of Natural Selection within an FHIT Intron Implicated in Prostate Cancer Risk. PLoS ONE, 2008, 3, e3533.	1.1	13
116	Towards the discovery of novel genetic component involved in stress resistance in <i>Arabidopsis thaliana</i> . New Phytologist, 2014, 201, 810-824.	3.5	12
117	Analysis and visualization of <i>Arabidopsis thaliana</i> GWAS using web 2.0 technologies. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar014-bar014.	1.4	8
118	Revisiting a GWAS peak in <i>Arabidopsis thaliana</i> reveals possible confounding by genetic heterogeneity. Heredity, 2021, 127, 245-252.	1.2	8
119	Female infanticide and human sex ratio evolution. Journal of Theoretical Biology, 1992, 158, 195-198.	0.8	5
120	Transgenerational effects of inter-ploidy cross direction on reproduction and F2 seed development of <i>Arabidopsis thaliana</i> F1 hybrid triploids. Plant Reproduction, 2019, 32, 275-289.	1.3	5
121	Response to a reappraisal of the phylogenetic placement of the <i>Aquilegia</i> whole-genome duplication. Genome Biology, 2020, 21, 297.	3.8	5
122	Genome-wide association mapping using mixed-models: application to GAW15 Problem 3. BMC Proceedings, 2007, 1, S164.	1.8	4
123	Genome-wide association mapping in <i>Arabidopsis thaliana</i> identifies previously known genes responsible for variation in flowering time and pathogen resistance. PLoS Genetics, 2005, preprint, e60.	1.5	3
124	Title is missing!. , 2019, 15, e1008492.		0
125	Title is missing!. , 2019, 15, e1008492.		0
126	Title is missing!. , 2019, 15, e1008492.		0

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127	Title is missing!. , 2019, 15, e1008492.		0