

Justin O Borevitz

List of Publications by Year in descending order

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Version: 2024-02-01

113
papers

14,827
citations

34076

52
h-index

23514

111
g-index

127
all docs

127
docs citations

127
times ranked

16762
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	Activation Tagging Identifies a Conserved MYB Regulator of Phenylpropanoid Biosynthesis. <i>Plant Cell</i> , 2000, 12, 2383-2393.	3.1	1,310
3	Activation Tagging in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2000, 122, 1003-1014.	2.3	896
4	Genome-wide association studies in plants: the missing heritability is in the field. <i>Genome Biology</i> , 2011, 12, 232.	13.9	502
5	Reconsidering plant memory: Intersections between stress recovery, RNA turnover, and epigenetics. <i>Science Advances</i> , 2016, 2, e1501340.	4.7	477
6	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
7	The extent of linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2002, 30, 190-193.	9.4	425
8	Increased Food and Ecosystem Security via Perennial Grains. <i>Science</i> , 2010, 328, 1638-1639.	6.0	397
9	LUX ARRHYTHMO encodes a Myb domain protein essential for circadian rhythms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10387-10392.	3.3	381
10	Natural allelic variation underlying a major fitness trade-off in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2010, 465, 632-636.	13.7	378
11	Large-Scale Identification of Single-Feature Polymorphisms in Complex Genomes. <i>Genome Research</i> , 2003, 13, 513-523.	2.4	345
12	The Scale of Population Structure in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2010, 6, e1000843.	1.5	338
13	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
14	An extracellular aspartic protease functions in <i>Arabidopsis</i> disease resistance signaling. <i>EMBO Journal</i> , 2004, 23, 980-988.	3.5	311
15	A methyl transferase links the circadian clock to the regulation of alternative splicing. <i>Nature</i> , 2010, 468, 112-116.	13.7	286
16	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
17	Root Suberin Forms an Extracellular Barrier That Affects Water Relations and Mineral Nutrition in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2009, 5, e1000492.	1.5	277
18	Natural variation in light sensitivity of <i>Arabidopsis</i> . <i>Nature Genetics</i> , 2001, 29, 441-446.	9.4	261

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19	Natural Selection Shapes Genome-Wide Patterns of Copy-Number Polymorphism in <i>Drosophila melanogaster</i> . <i>Science</i> , 2008, 320, 1629-1631.	6.0	241
20	Managed Relocation: Integrating the Scientific, Regulatory, and Ethical Challenges. <i>BioScience</i> , 2012, 62, 732-743.	2.2	212
21	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , 2016, 5, .	2.8	181
22	A Systematic Map of Genetic Variation in <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2006, 2, e57.	2.1	176
23	A framework for incorporating evolutionary genomics into biodiversity conservation and management. <i>Climate Change Responses</i> , 2015, 2, .	2.6	175
24	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.	3.3	174
25	Genome-Wide Expression Profiling of the Arabidopsis Female Gametophyte Identifies Families of Small, Secreted Proteins. <i>PLoS Genetics</i> , 2007, 3, e171.	1.5	165
26	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
27	A large number of novel coding small open reading frames in the intergenic regions of the <i>Arabidopsis thaliana</i> genome are transcribed and/or under purifying selection. <i>Genome Research</i> , 2007, 17, 632-640.	2.4	157
28	Global Analysis of Genetic, Epigenetic and Transcriptional Polymorphisms in <i>Arabidopsis thaliana</i> Using Whole Genome Tiling Arrays. <i>PLoS Genetics</i> , 2008, 4, e1000032.	1.5	150
29	Activation Tagging Identifies a Conserved MYB Regulator of Phenylpropanoid Biosynthesis. <i>Plant Cell</i> , 2000, 12, 2383.	3.1	145
30	Global Analysis of Allele-Specific Expression in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009, 182, 943-954.	1.2	139
31	FRIGIDA-Independent Variation in Flowering Time of Natural <i>Arabidopsis thaliana</i> Accessions. <i>Genetics</i> , 2005, 170, 1197-1207.	1.2	138
32	Single-feature polymorphism discovery in the barley transcriptome. <i>Genome Biology</i> , 2005, 6, R54.	13.9	130
33	Quantitative Trait Loci Controlling Light and Hormone Response in Two Accessions of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002, 160, 683-696.	1.2	127
34	Deep phenotyping: deep learning for temporal phenotype/genotype classification. <i>Plant Methods</i> , 2018, 14, 66.	1.9	116
35	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
36	Genomic variation across landscapes: insights and applications. <i>New Phytologist</i> , 2015, 207, 953-967.	3.5	113

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37	Genomics tools for QTL analysis and gene discovery. <i>Current Opinion in Plant Biology</i> , 2004, 7, 132-136.	3.5	109
38	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.	1.2	109
39	A Common and Unstable Copy Number Variant Is Associated with Differences in Glo1 Expression and Anxiety-Like Behavior. <i>PLoS ONE</i> , 2009, 4, e4649.	1.1	108
40	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009, 10, R17.	13.9	103
41	TraitCapture: genomic and environment modelling of plant phenomic data. <i>Current Opinion in Plant Biology</i> , 2014, 18, 73-79.	3.5	101
42	Amino acid polymorphisms in <i>Arabidopsis</i> phytochrome B cause differential responses to light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3157-3162.	3.3	97
43	QTL Mapping in New <i>Arabidopsis thaliana</i> Advanced Intercross-Recombinant Inbred Lines. <i>PLoS ONE</i> , 2009, 4, e4318.	1.1	92
44	Genetic architecture of regulatory variation in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2011, 21, 725-733.	2.4	91
45	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2017, 29, 1836-1863.	3.1	90
46	Rapid Array Mapping of Circadian Clock and Developmental Mutations in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 138, 990-997.	2.3	85
47	Light-Response Quantitative Trait Loci Identified with Composite Interval and eXtreme Array Mapping in <i>Arabidopsis thaliana</i> Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY394847 and AY466496. <i>Genetics</i> , 2004, 167, 907-917.	1.2	83
48	Genomic diversity in switchgrass (<i>Panicum virgatum</i>): from the continental scale to a dune landscape. <i>Molecular Ecology</i> , 2011, 20, 4938-4952.	2.0	69
49	Genetic Variation for Life History Sensitivity to Seasonal Warming in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2014, 196, 569-577.	1.2	69
50	PLANT GENOMICS: The Third Wave. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 443-477.	2.5	68
51	Source verification of misidentified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , 2011, 67, 554-566.	2.8	63
52	Natural Genetic Variation for Growth and Development Revealed by High-Throughput Phenotyping in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 29-34.	0.8	56
53	Landscape genomic prediction for restoration of a <i>Eucalyptus</i> foundation species under climate change. <i>ELife</i> , 2018, 7, .	2.8	54
54	The next generation of microarray research: applications in evolutionary and ecological genomics. <i>Heredity</i> , 2008, 100, 141-149.	1.2	50

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55	Population genomic variation reveals roles of history, adaptation and ploidy in switchgrass. <i>Molecular Ecology</i> , 2014, 23, 4059-4073.	2.0	49
56	Using Phenomic Analysis of Photosynthetic Function for Abiotic Stress Response Gene Discovery. <i>The Arabidopsis Book</i> , 2016, 14, e0185.	0.5	48
57	Axe: rapid, competitive sequence read demultiplexing using a trie. <i>Bioinformatics</i> , 2018, 34, 3924-3925.	1.8	48
58	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. <i>BMC Bioinformatics</i> , 2019, 20, 253.	1.2	45
59	Genetics of Local Adaptation in the Laboratory: Flowering Time Quantitative Trait Loci under Geographic and Seasonal Conditions in Arabidopsis. <i>PLoS ONE</i> , 2006, 1, e105.	1.1	44
60	A chromatin modifying enzyme, SDG8, is involved in morphological, gene expression, and epigenetic responses to mechanical stimulation. <i>Frontiers in Plant Science</i> , 2014, 5, 533.	1.7	44
61	Using DNA microarrays to study natural variation. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 553-558.	1.5	43
62	Development of the first consensus genetic map of intermediate wheatgrass (<i>Thinopyrum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td	1.8	43
63	kWIP: The k-mer weighted inner product, a de novo estimator of genetic similarity. <i>PLoS Computational Biology</i> , 2017, 13, e1005727.	1.5	39
64	Mineral-enriched biochar delivers enhanced nutrient recovery and carbon dioxide removal. <i>Communications Earth & Environment</i> , 2022, 3, .	2.6	39
65	Genome-wide Analysis of Cis-regulatory Divergence between Species in the Arabidopsis Genus. <i>Molecular Biology and Evolution</i> , 2012, 29, 3385-3395.	3.5	34
66	DNA methylation profiles of diverse <i>Brachypodium distachyon</i> align with underlying genetic diversity. <i>Genome Research</i> , 2016, 26, 1520-1531.	2.4	34
67	Landscape drivers of genomic diversity and divergence in woodland Eucalyptus. <i>Molecular Ecology</i> , 2019, 28, 5232-5247.	2.0	34
68	Natural variation in phytochrome signaling. <i>Seminars in Cell and Developmental Biology</i> , 2000, 11, 523-530.	2.3	32
69	Association Mapping With Single-Feature Polymorphisms. <i>Genetics</i> , 2006, 173, 1125-1133.	1.2	31
70	Widespread Interspecific Divergence in Cis-Regulation of Transposable Elements in the Arabidopsis Genus. <i>Molecular Biology and Evolution</i> , 2012, 29, 1081-1091.	3.5	29
71	Genotypic diversity effects on biomass production in native perennial bioenergy cropping systems. <i>GCB Bioenergy</i> , 2016, 8, 1000-1014.	2.5	29
72	Whole genome transcriptome polymorphisms in Arabidopsis thaliana. <i>Genome Biology</i> , 2008, 9, R165.	13.9	26

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73	Within and between Whorls: Comparative Transcriptional Profiling of <i>Aquilegia</i> and <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2010, 5, e9735.	1.1	26
74	Genotyping and Mapping With High-Density Oligonucleotide Arrays. , 2006, 323, 137-146.		25
75	Genetic and epigenetic dissection of cis regulatory variation. <i>Current Opinion in Plant Biology</i> , 2007, 10, 142-148.	3.5	25
76	Population and phylogenomic decomposition via genotyping-by-sequencing in Australian <i>Pelargonium</i> . <i>Molecular Ecology</i> , 2016, 25, 2000-2014.	2.0	25
77	A Genome-Wide Association Study of Non-Photochemical Quenching in response to local seasonal climates in <i>Arabidopsis thaliana</i> . <i>Plant Direct</i> , 2019, 3, e00138.	0.8	25
78	Genomic breeding for food, environment and livelihoods. <i>Food Security</i> , 2015, 7, 375-382.	2.4	23
79	High-molecular weight DNA extraction, clean-up and size selection for long-read sequencing. <i>PLoS ONE</i> , 2021, 16, e0253830.	1.1	23
80	Spatial, climate and ploidy factors drive genomic diversity and resilience in the widespread grass <i>Themeda triandra</i> . <i>Molecular Ecology</i> , 2020, 29, 3872-3888.	2.0	22
81	New <i>Arabidopsis</i> Advanced Intercross Recombinant Inbred Lines Reveal Female Control of Nonrandom Mating. <i>Plant Physiology</i> , 2014, 165, 175-185.	2.3	21
82	Isolation by distance and isolation by environment contribute to population differentiation in <i>Protea repens</i> (Proteaceae L.), a widespread South African species. <i>American Journal of Botany</i> , 2017, 104, 674-684.	0.8	21
83	Genomic diversity guides conservation strategies among rare terrestrial orchid species when taxonomy remains uncertain. <i>Annals of Botany</i> , 2017, 119, 1267-1277.	1.4	18
84	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. <i>Genetics</i> , 2019, 211, 317-331.	1.2	17
85	Pervasive admixture between eucalypt species has consequences for conservation and assisted migration. <i>Evolutionary Applications</i> , 2019, 12, 845-860.	1.5	15
86	CmCGG Methylation-Independent Parent-of-Origin Effects on Genome-Wide Transcript Levels in Isogenic Reciprocal F1 Triploid Plants. <i>DNA Research</i> , 2014, 21, 141-151.	1.5	14
87	Genomic Diversity and Climate Adaptation in <i>Brachypodium</i> . <i>Plant Genetics and Genomics: Crops and Models</i> , 2015, , 107-127.	0.3	13
88	GWAS on multiple traits identifies mitochondrial ACONITASE3 as important for acclimation to submergence stress. <i>Plant Physiology</i> , 2022, 188, 2039-2058.	2.3	13
89	Gene flow between nascent species: geographic, genotypic and phenotypic differentiation within and between <i>Aquilegia formosa</i> and <i>A. pubescens</i> . <i>Molecular Ecology</i> , 2014, 23, 5589-5598.	2.0	12
90	Genomic evidence of introgression and adaptation in a model subtropical tree species, <i>Eucalyptus grandis</i> . <i>Molecular Ecology</i> , 2021, 30, 625-638.	2.0	12

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91	Methylation's mark on inheritance. <i>Nature</i> , 2013, 495, 181-182.	13.7	10
92	Selecting Informative Traits for Multivariate Quantitative Trait Locus Mapping Helps to Gain Optimal Power. <i>Genetics</i> , 2013, 195, 683-691.	1.2	9
93	Examining the efficacy of a genotyping-by-sequencing technique for population genetic analysis of the mushroom <i>Laccaria bicolor</i> and evaluating whether a reference genome is necessary to assess homology. <i>Mycologia</i> , 2015, 107, 217-226.	0.8	9
94	Novel Resampling Improves Statistical Power for Multiple-Trait QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 813-822.	0.8	9
95	2020 Vision for Biology: The Role of Plants in Addressing Grand Challenges in Biology. <i>Molecular Plant</i> , 2008, 1, 561-563.	3.9	8
96	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
97	High-Resolution, Time-Lapse Imaging for Ecosystem-Scale Phenotyping in the Field. <i>Methods in Molecular Biology</i> , 2012, 918, 71-96.	0.4	8
98	Inferring Population Parameters From Single-Feature Polymorphism Data. <i>Genetics</i> , 2006, 173, 2257-2267.	1.2	7
99	Environmental resource deficit may drive the evolution of intraspecific trait variation in invasive plant populations. <i>Oikos</i> , 2019, 128, 171-184.	1.2	7
100	Redundancy in Genotyping Arrays. <i>PLoS ONE</i> , 2007, 2, e287.	1.1	7
101	Mapping a plant's chemical vocabulary. <i>Nature Genetics</i> , 2006, 38, 737-738.	9.4	6
102	Enhancing natural cycles in agro-ecosystems to boost plant carbon capture and soil storage. <i>Oxford Open Climate Change</i> , 2021, 1, .	0.6	5
103	Utilizing genomics to understand and respond to global climate change. <i>Genome Biology</i> , 2021, 22, 91.	3.8	5
104	Plant collections for conservation and restoration: Can they be adapted and adaptable?. <i>Molecular Ecology Resources</i> , 2022, 22, 2171-2182.	2.2	5
105	libqcpp: A C++14 sequence quality control library. <i>Journal of Open Source Software</i> , 2017, 2, 232.	2.0	4
106	Multi-platform LiDAR approach for detecting coarse woody debris in a landscape with varied ground cover. <i>International Journal of Remote Sensing</i> , 2021, 42, 9324-9350.	1.3	4
107	Phenotypic Analysis of <i>Arabidopsis</i> Mutants: Hypocotyl Length. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot4962.	0.2	3
108	Extending the Genotype in <i>Brachypodium</i> by Including DNA Methylation Reveals a Joint Contribution with Genetics on Adaptive Traits. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1629-1637.	0.8	3

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109	The first long-read nuclear genome assembly of <i>Oryza australiensis</i> , a wild rice from northern Australia. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
110	DAESim: A dynamic agro-ecosystem simulation model for natural capital assessment. <i>Ecological Modelling</i> , 2022, 468, 109930.	1.2	2
111	Genomic consequences of artificial selection during early domestication of a wood fibre crop. <i>New Phytologist</i> , 2022, 235, 1944-1956.	3.5	1
112	Chapter Seven Biopanning by activation tagging. <i>Recent Advances in Phytochemistry</i> , 2002, 36, 111-123.	0.5	0
113	Adaptation genomics: The angel is in the details. <i>Plant, Cell and Environment</i> , 2018, 41, 2244-2246.	2.8	0