

Justin O Borevitz

List of Publications by Citations

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117
papers

11,731
citations

50
h-index

108
g-index

127
ext. papers

13,737
ext. citations

9.7
avg, IF

5.92
L-index

#	Paper	IF	Citations
117	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. <i>Nature</i> , 2010 , 465, 627-31	50.4	1257
116	Activation tagging identifies a conserved MYB regulator of phenylpropanoid biosynthesis. <i>Plant Cell</i> , 2000 , 12, 2383-2394	11.6	1080
115	Activation tagging in Arabidopsis. <i>Plant Physiology</i> , 2000 , 122, 1003-13	6.6	813
114	The extent of linkage disequilibrium in Arabidopsis thaliana. <i>Nature Genetics</i> , 2002 , 30, 190-3	36.3	393
113	Genome-wide patterns of genetic variation in worldwide Arabidopsis thaliana accessions from the RegMap panel. <i>Nature Genetics</i> , 2012 , 44, 212-6	36.3	356
112	Genome-wide association studies in plants: the missing heritability is in the field. <i>Genome Biology</i> , 2011 , 12, 232	18.3	331
111	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, 10387-92	11.5	316
110	Large-scale identification of single-feature polymorphisms in complex genomes. <i>Genome Research</i> , 2003 , 13, 513-23	9.7	307
109	Agriculture. Increased food and ecosystem security via perennial grains. <i>Science</i> , 2010 , 328, 1638-9	33.3	303
108	Reconsidering plant memory: Intersections between stress recovery, RNA turnover, and epigenetics. <i>Science Advances</i> , 2016 , 2, e1501340	14.3	300
107	Natural allelic variation underlying a major fitness trade-off in Arabidopsis thaliana. <i>Nature</i> , 2010 , 465, 632-6	50.4	273
106	An extracellular aspartic protease functions in Arabidopsis disease resistance signaling. <i>EMBO Journal</i> , 2004 , 23, 980-8	13	269
105	The scale of population structure in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2010 , 6, e1000843	6	251
104	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	6	245
103	Natural variation in light sensitivity of Arabidopsis. <i>Nature Genetics</i> , 2001 , 29, 441-6	36.3	229
102	A methyl transferase links the circadian clock to the regulation of alternative splicing. <i>Nature</i> , 2010 , 468, 112-6	50.4	221
101	Association mapping of local climate-sensitive quantitative trait loci in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 21199-204	11.5	219

100	Natural selection shapes genome-wide patterns of copy-number polymorphism in <i>Drosophila melanogaster</i> . <i>Science</i> , 2008 , 320, 1629-31	33.3	217
99	Root suberin forms an extracellular barrier that affects water relations and mineral nutrition in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000492	6	210
98	Managed Relocation: Integrating the Scientific, Regulatory, and Ethical Challenges. <i>BioScience</i> , 2012 , 62, 732-743	5.7	169
97	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, 2460-5	11.5	167
96	A systematic map of genetic variation in <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2006 , 2, e57	7.6	159
95	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, 12057-62	11.5	147
94	Genome-wide expression profiling of the <i>Arabidopsis</i> female gametophyte identifies families of small, secreted proteins. <i>PLoS Genetics</i> , 2007 , 3, 1848-61	6	146
93	FRIGIDA-independent variation in flowering time of natural <i>Arabidopsis thaliana</i> accessions. <i>Genetics</i> , 2005 , 170, 1197-207	4	128
92	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	6	124
91	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , 2016 , 5,	8.9	121
90	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, 632-40	9.7	120
89	Single-feature polymorphism discovery in the barley transcriptome. <i>Genome Biology</i> , 2005 , 6, R54	18.3	119
88	A framework for incorporating evolutionary genomics into biodiversity conservation and management. <i>Climate Change Responses</i> , 2015 , 2,		110
87	Global analysis of allele-specific expression in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009 , 182, 943-54	4	106
86	Genomics tools for QTL analysis and gene discovery. <i>Current Opinion in Plant Biology</i> , 2004 , 7, 132-6	9.9	103
85	The impact of genomics on the study of natural variation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2003 , 132, 718-25	6.6	103
84	Quantitative trait loci controlling light and hormone response in two accessions of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002 , 160, 683-96	4	101
83	Genomic variation across landscapes: insights and applications. <i>New Phytologist</i> , 2015 , 207, 953-67	9.8	96

82	Cis-regulatory changes at FLOWERING LOCUS T mediate natural variation in flowering responses of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009 , 183, 723-32, 1S1-7S1	4	95
81	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009 , 10, R17	18.3	93
80	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	3.7	87
79	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, 3157-62	11.5	85
78	TraitCapture: genomic and environment modelling of plant phenomic data. <i>Current Opinion in Plant Biology</i> , 2014 , 18, 73-9	9.9	82
77	Rapid array mapping of circadian clock and developmental mutations in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005 , 138, 990-7	6.6	80
76	QTL mapping in new <i>Arabidopsis thaliana</i> advanced intercross-recombinant inbred lines. <i>PLoS ONE</i> , 2009 , 4, e4318	3.7	77
75	Light-response quantitative trait loci identified with composite interval and eXtreme array mapping in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2004 , 167, 907-17	4	74
74	Deep phenotyping: deep learning for temporal phenotype/genotype classification. <i>Plant Methods</i> , 2018 , 14, 66	5.8	72
73	Genetic architecture of regulatory variation in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2011 , 21, 725-33	9.7	68
72	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2017 , 29, 1836-1863	11.6	61
71	Plant genomics: the third wave. <i>Annual Review of Genomics and Human Genetics</i> , 2004 , 5, 443-77	9.7	59
70	Genomic diversity in switchgrass (<i>Panicum virgatum</i>): from the continental scale to a dune landscape. <i>Molecular Ecology</i> , 2011 , 20, 4938-52	5.7	54
69	Source verification of mis-identified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , 2011 , 67, 554-66	6.9	53
68	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	3.2	48
67	Genetic variation for life history sensitivity to seasonal warming in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2014 , 196, 569-77	4	47
66	The next generation of microarray research: applications in evolutionary and ecological genomics. <i>Heredity</i> , 2008 , 100, 141-9	3.6	43
65	Using DNA microarrays to study natural variation. <i>Current Opinion in Genetics and Development</i> , 2006 , 16, 553-8	4.9	40

64	Population genomic variation reveals roles of history, adaptation and ploidy in switchgrass. <i>Molecular Ecology</i> , 2014 , 23, 4059-73	5.7	39
63	Genetics of local adaptation in the laboratory: flowering time quantitative trait loci under geographic and seasonal conditions in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2006 , 1, e105	3.7	38
62	Activation Tagging Identifies a Conserved MYB Regulator of Phenylpropanoid Biosynthesis. <i>Plant Cell</i> , 2000 , 12, 2383	11.6	35
61	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	6.2	33
60	Development of the first consensus genetic map of intermediate wheatgrass (<i>Thinopyrum intermedium</i>) using genotyping-by-sequencing. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 137-150	6	30
59	Landscape genomic prediction for restoration of a foundation species under climate change. <i>ELife</i> , 2018 , 7,	8.9	30
58	Using Phenomic Analysis of Photosynthetic Function for Abiotic Stress Response Gene Discovery. <i>The Arabidopsis Book</i> , 2016 , 14, e0185	3	30
57	kWIP: The k-mer weighted inner product, a de novo estimator of genetic similarity. <i>PLoS Computational Biology</i> , 2017 , 13, e1005727	5	28
56	Association mapping with single-feature polymorphisms. <i>Genetics</i> , 2006 , 173, 1125-33	4	28
55	Natural variation in phytochrome signaling. <i>Seminars in Cell and Developmental Biology</i> , 2000 , 11, 523-307.5		27
54	DNA methylation profiles of diverse <i>Brachypodium distachyon</i> align with underlying genetic diversity. <i>Genome Research</i> , 2016 , 26, 1520-1531	9.7	27
53	Whole genome transcriptome polymorphisms in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008 , 9, R165	18.3	26
52	Genome-wide analysis of cis-regulatory divergence between species in the <i>Arabidopsis</i> genus. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3385-95	8.3	25
51	Widespread interspecific divergence in cis-regulation of transposable elements in the <i>Arabidopsis</i> genus. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1081-91	8.3	25
50	Axe: rapid, competitive sequence read demultiplexing using a trie. <i>Bioinformatics</i> , 2018 , 34, 3924-3925	7.2	24
49	Within and between whorls: comparative transcriptional profiling of <i>Aquilegia</i> and <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2010 , 5, e9735	3.7	24
48	Genotyping and mapping with high-density oligonucleotide arrays. <i>Methods in Molecular Biology</i> , 2006 , 323, 137-45	1.4	23
47	Genetic and epigenetic dissection of cis regulatory variation. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 142-8	9.9	21

46	Population and phylogenomic decomposition via genotyping-by-sequencing in Australian Pelargonium. <i>Molecular Ecology</i> , 2016 , 25, 2000-14	5.7	19
45	Isolation by distance and isolation by environment contribute to population differentiation in (Proteaceae L.), a widespread South African species. <i>American Journal of Botany</i> , 2017 , 104, 674-684	2.7	17
44	Landscape drivers of genomic diversity and divergence in woodland Eucalyptus. <i>Molecular Ecology</i> , 2019 , 28, 5232-5247	5.7	16
43	Genomic breeding for food, environment and livelihoods. <i>Food Security</i> , 2015 , 7, 375-382	6.7	16
42	Genotypic diversity effects on biomass production in native perennial bioenergy cropping systems. <i>GCB Bioenergy</i> , 2016 , 8, 1000-1014	5.6	15
41	New Arabidopsis advanced intercross recombinant inbred lines reveal female control of nonrandom mating. <i>Plant Physiology</i> , 2014 , 165, 175-85	6.6	13
40	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. <i>BMC Bioinformatics</i> , 2019 , 20, 253	3.6	12
39	C(m)CGG methylation-independent parent-of-origin effects on genome-wide transcript levels in isogenic reciprocal F1 triploid plants. <i>DNA Research</i> , 2014 , 21, 141-51	4.5	12
38	Deep Phenotyping: Deep Learning for Temporal Phenotype/Genotype Classification		12
37	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, 5589-98	5.7	10
36	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	5.7	10
35	Genomic diversity guides conservation strategies among rare terrestrial orchid species when taxonomy remains uncertain. <i>Annals of Botany</i> , 2017 , 119, 1267-1277	4.1	9
34	Pervasive admixture between eucalypt species has consequences for conservation and assisted migration. <i>Evolutionary Applications</i> , 2019 , 12, 845-860	4.8	9
33	Selecting informative traits for multivariate quantitative trait locus mapping helps to gain optimal power. <i>Genetics</i> , 2013 , 195, 683-91	4	9
32	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	4	9
31	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, 217-26	2.4	7
30	A Genome-Wide Association Study of Non-Photochemical Quenching in response to local seasonal climates in. <i>Plant Direct</i> , 2019 , 3, e00138	3.3	7
29	Novel Resampling Improves Statistical Power for Multiple-Trait QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 813-822	3.2	7

28	Genomic Diversity and Climate Adaptation in Brachypodium. <i>Plant Genetics and Genomics: Crops and Models</i> , 2015 , 107-127	0.2	7
27	Analysis and visualization of Arabidopsis thaliana GWAS using web 2.0 technologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar014	5	7
26	Inferring population parameters from single-feature polymorphism data. <i>Genetics</i> , 2006 , 173, 2257-67	4	7
25	High-resolution, time-lapse imaging for ecosystem-scale phenotyping in the field. <i>Methods in Molecular Biology</i> , 2012 , 918, 71-96	1.4	6
24	2020 vision for biology: the role of plants in addressing grand challenges in biology. <i>Molecular Plant</i> , 2008 , 1, 561-3	14.4	6
23	Redundancy in genotyping arrays. <i>PLoS ONE</i> , 2007 , 2, e287	3.7	6
22	Mineral-enriched biochar delivers enhanced nutrient recovery and carbon dioxide removal. <i>Communications Earth & Environment</i> , 2022 , 3,	6.1	5
21	libqcpp: A C++14 sequence quality control library. <i>Journal of Open Source Software</i> , 2017 , 2, 232	5.2	4
20	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation		4
19	Axe: rapid, competitive sequence read demultiplexing using a trie		4
18	HOME: A histogram based machine learning approach for effective identification of differentially methylated regions		4
17	Environmental resource deficit may drive the evolution of intraspecific trait variation in invasive plant populations. <i>Oikos</i> , 2019 , 128, 171-184	4	4
16	Genomic evidence of introgression and adaptation in a model subtropical tree species, Eucalyptus grandis. <i>Molecular Ecology</i> , 2021 , 30, 625-638	5.7	4
15	Phenotypic analysis of Arabidopsis mutants: hypocotyl length. <i>Cold Spring Harbor Protocols</i> , 2008 , 2008, pdb.prot4962	1.2	3
14	Cost-conscious generation of multiplexed short-read DNA libraries for whole genome sequencing v1		3
13	Extending the Genotype in by Including DNA Methylation Reveals a Joint Contribution with Genetics on Adaptive Traits. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 1629-1637	3.2	3
12	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, 9316-9342	3.1	2
11	kWIP: The k-mer Weighted Inner Product, a de novo Estimator of Genetic Similarity		2

10	Enhancing natural cycles in agro-ecosystems to boost plant carbon capture and soil storage 2021 , 1,		2
9	Genomic constraints to drought adaptation		2
8	GWAS on multiple traits identifies mitochondrial ACONITASE3 as important for acclimation to submergence stress.. <i>Plant Physiology</i> , 2022 ,	6.6	1
7	Landscape genomic prediction for restoration of a Eucalyptus foundation species under climate change		1
6	Population structure of the Brachypodium species complex and genome wide association of agronomic traits in response to climate		1
5	Plant collections for conservation and restoration: can they be adapted and adaptable?. <i>Molecular Ecology Resources</i> , 2022 ,	8.4	1
4	High-molecular weight DNA extraction, clean-up and size selection for long-read sequencing. <i>PLoS ONE</i> , 2021 , 16, e0253830	3.7	0
3	Chapter Seven Biopanning by activation tagging. <i>Recent Advances in Phytochemistry</i> , 2002 , 36, 111-123		
2	Adaptation genomics: The angel is in the details. <i>Plant, Cell and Environment</i> , 2018 , 41, 2244-2246	8.4	
1	DAESim: A dynamic agro-ecosystem simulation model for natural capital assessment. <i>Ecological Modelling</i> , 2022 , 468, 109930		3