

# Justin O Borevitz

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	GWAS on multiple traits identifies mitochondrial ACONITASE3 as important for acclimation to submergence stress.. <i>Plant Physiology</i> , <b>2022</b> ,	6.6	1
116	Plant collections for conservation and restoration: can they be adapted and adaptable?. <i>Molecular Ecology Resources</i> , <b>2022</b> ,	8.4	1
115	Mineral-enriched biochar delivers enhanced nutrient recovery and carbon dioxide removal. <i>Communications Earth &amp; Environment</i> , <b>2022</b> , 3,	6.1	5
114	DAESim: A dynamic agro-ecosystem simulation model for natural capital assessment. <i>Ecological Modelling</i> , <b>2022</b> , 468, 109930	3	
113	Multi-platform LiDAR approach for detecting coarse woody debris in a landscape with varied ground cover. <i>International Journal of Remote Sensing</i> , <b>2021</b> , 42, 9316-9342	3.1	2
112	Genomic evidence of introgression and adaptation in a model subtropical tree species, <i>Eucalyptus grandis</i> . <i>Molecular Ecology</i> , <b>2021</b> , 30, 625-638	5.7	4
111	Enhancing natural cycles in agro-ecosystems to boost plant carbon capture and soil storage <b>2021</b> , 1,		2
110	High-molecular weight DNA extraction, clean-up and size selection for long-read sequencing. <i>PLoS ONE</i> , <b>2021</b> , 16, e0253830	3.7	0
109	Spatial, climate and ploidy factors drive genomic diversity and resilience in the widespread grass <i>Themeda triandra</i> . <i>Molecular Ecology</i> , <b>2020</b> , 29, 3872-3888	5.7	10
108	Extending the Genotype in by Including DNA Methylation Reveals a Joint Contribution with Genetics on Adaptive Traits. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 1629-1637	3.2	3
107	Landscape drivers of genomic diversity and divergence in woodland <i>Eucalyptus</i> . <i>Molecular Ecology</i> , <b>2019</b> , 28, 5232-5247	5.7	16
106	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 253	3.6	12
105	Pervasive admixture between eucalypt species has consequences for conservation and assisted migration. <i>Evolutionary Applications</i> , <b>2019</b> , 12, 845-860	4.8	9
104	A Genome-Wide Association Study of Non-Photochemical Quenching in response to local seasonal climates in. <i>Plant Direct</i> , <b>2019</b> , 3, e00138	3.3	7
103	Environmental resource deficit may drive the evolution of intraspecific trait variation in invasive plant populations. <i>Oikos</i> , <b>2019</b> , 128, 171-184	4	4
102	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> , <b>2019</b> , 211, 317-331	4	9
101	Deep phenotyping: deep learning for temporal phenotype/genotype classification. <i>Plant Methods</i> , <b>2018</b> , 14, 66	5.8	72

100	Axe: rapid, competitive sequence read demultiplexing using a trie. <i>Bioinformatics</i> , <b>2018</b> , 34, 3924-3925	7.2	24
99	Landscape genomic prediction for restoration of a foundation species under climate change. <i>ELife</i> , <b>2018</b> , 7,	8.9	30
98	Adaptation genomics: The angel is in the details. <i>Plant, Cell and Environment</i> , <b>2018</b> , 41, 2244-2246	8.4	
97	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> , <b>2017</b> , 104, 674-684	2.7	17
96	Genomic diversity guides conservation strategies among rare terrestrial orchid species when taxonomy remains uncertain. <i>Annals of Botany</i> , <b>2017</b> , 119, 1267-1277	4.1	9
95	kWIP: The k-mer weighted inner product, a de novo estimator of genetic similarity. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005727	5	28
94	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in Arabidopsis. <i>Plant Cell</i> , <b>2017</b> , 29, 1836-1863	11.6	61
93	Development of the first consensus genetic map of intermediate wheatgrass ( <i>Thinopyrum intermedium</i> ) using genotyping-by-sequencing. <i>Theoretical and Applied Genetics</i> , <b>2017</b> , 130, 137-150	6	30
92	Novel Resampling Improves Statistical Power for Multiple-Trait QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 813-822	3.2	7
91	libqcpp: A C++14 sequence quality control library. <i>Journal of Open Source Software</i> , <b>2017</b> , 2, 232	5.2	4
90	Reconsidering plant memory: Intersections between stress recovery, RNA turnover, and epigenetics. <i>Science Advances</i> , <b>2016</b> , 2, e1501340	14.3	300
89	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , <b>2016</b> , 5,	8.9	121
88	Population and phylogenomic decomposition via genotyping-by-sequencing in Australian <i>Pelargonium</i> . <i>Molecular Ecology</i> , <b>2016</b> , 25, 2000-14	5.7	19
87	Genotypic diversity effects on biomass production in native perennial bioenergy cropping systems. <i>GCB Bioenergy</i> , <b>2016</b> , 8, 1000-1014	5.6	15
86	DNA methylation profiles of diverse <i>Brachypodium distachyon</i> align with underlying genetic diversity. <i>Genome Research</i> , <b>2016</b> , 26, 1520-1531	9.7	27
85	Using Phenomic Analysis of Photosynthetic Function for Abiotic Stress Response Gene Discovery. <i>The Arabidopsis Book</i> , <b>2016</b> , 14, e0185	3	30
84	A framework for incorporating evolutionary genomics into biodiversity conservation and management. <i>Climate Change Responses</i> , <b>2015</b> , 2,		110
83	Genomic variation across landscapes: insights and applications. <i>New Phytologist</i> , <b>2015</b> , 207, 953-67	9.8	96

82	Genomic breeding for food, environment and livelihoods. <i>Food Security</i> , <b>2015</b> , 7, 375-382	6.7	16
81	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> , <b>2015</b> , 107, 217-26	2.4	7
80	Genomic Diversity and Climate Adaptation in Brachypodium. <i>Plant Genetics and Genomics: Crops and Models</i> , <b>2015</b> , 107-127	0.2	7
79	Population genomic variation reveals roles of history, adaptation and ploidy in switchgrass. <i>Molecular Ecology</i> , <b>2014</b> , 23, 4059-73	5.7	39
78	C(m)CGG methylation-independent parent-of-origin effects on genome-wide transcript levels in isogenic reciprocal F1 triploid plants. <i>DNA Research</i> , <b>2014</b> , 21, 141-51	4.5	12
77	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> , <b>2014</b> , 23, 5589-98	5.7	10
76	TraitCapture: genomic and environment modelling of plant phenomic data. <i>Current Opinion in Plant Biology</i> , <b>2014</b> , 18, 73-9	9.9	82
75	A chromatin modifying enzyme, SDG8, is involved in morphological, gene expression, and epigenetic responses to mechanical stimulation. <i>Frontiers in Plant Science</i> , <b>2014</b> , 5, 533	6.2	33
74	New Arabidopsis advanced intercross recombinant inbred lines reveal female control of nonrandom mating. <i>Plant Physiology</i> , <b>2014</b> , 165, 175-85	6.6	13
73	Genetic variation for life history sensitivity to seasonal warming in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2014</b> , 196, 569-77	4	47
72	Selecting informative traits for multivariate quantitative trait locus mapping helps to gain optimal power. <i>Genetics</i> , <b>2013</b> , 195, 683-91	4	9
71	High-resolution, time-lapse imaging for ecosystem-scale phenotyping in the field. <i>Methods in Molecular Biology</i> , <b>2012</b> , 918, 71-96	1.4	6
70	Genome-wide patterns of genetic variation in worldwide <i>Arabidopsis thaliana</i> accessions from the RegMap panel. <i>Nature Genetics</i> , <b>2012</b> , 44, 212-6	36.3	356
69	Genome-wide analysis of cis-regulatory divergence between species in the <i>Arabidopsis</i> genus. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3385-95	8.3	25
68	Widespread interspecific divergence in cis-regulation of transposable elements in the <i>Arabidopsis</i> genus. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1081-91	8.3	25
67	Managed Relocation: Integrating the Scientific, Regulatory, and Ethical Challenges. <i>BioScience</i> , <b>2012</b> , 62, 732-743	5.7	169
66	Natural Genetic Variation for Growth and Development Revealed by High-Throughput Phenotyping in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 29-34	3.2	48
65	Analysis and visualization of <i>Arabidopsis thaliana</i> GWAS using web 2.0 technologies. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2011</b> , 2011, bar014	5	7

64	Source verification of mis-identified <i>Arabidopsis thaliana</i> accessions. <i>Plant Journal</i> , <b>2011</b> , 67, 554-66	6.9	53
63	Genomic diversity in switchgrass ( <i>Panicum virgatum</i> ): from the continental scale to a dune landscape. <i>Molecular Ecology</i> , <b>2011</b> , 20, 4938-52	5.7	54
62	Genome-wide association studies in plants: the missing heritability is in the field. <i>Genome Biology</i> , <b>2011</b> , 12, 232	18.3	331
61	Genetic architecture of regulatory variation in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , <b>2011</b> , 21, 725-33	9.7	68
60	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , <b>2010</b> , 465, 627-31	50.4	1257
59	Natural allelic variation underlying a major fitness trade-off in <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2010</b> , 465, 632-6	50.4	273
58	A methyl transferase links the circadian clock to the regulation of alternative splicing. <i>Nature</i> , <b>2010</b> , 468, 112-6	50.4	221
57	Agriculture. Increased food and ecosystem security via perennial grains. <i>Science</i> , <b>2010</b> , 328, 1638-9	33.3	303
56	A coastal cline in sodium accumulation in <i>Arabidopsis thaliana</i> is driven by natural variation of the sodium transporter <i>AtHKT1;1</i> . <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001193	6	245
55	The scale of population structure in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , <b>2010</b> , 6, e1000843	6	251
54	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> , <b>2010</b> , 107, 21199-204	11.5	219
53	Within and between whorls: comparative transcriptional profiling of <i>Aquilegia</i> and <i>Arabidopsis</i> . <i>PLoS ONE</i> , <b>2010</b> , 5, e9735	3.7	24
52	Cis-regulatory changes at FLOWERING LOCUS T mediate natural variation in flowering responses of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2009</b> , 183, 723-32, 1S1-7S1	4	95
51	Global analysis of allele-specific expression in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2009</b> , 182, 943-54	4	106
50	Root suberin forms an extracellular barrier that affects water relations and mineral nutrition in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000492	6	210
49	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , <b>2009</b> , 10, R17	18.3	93
48	QTL mapping in new <i>Arabidopsis thaliana</i> advanced intercross-recombinant inbred lines. <i>PLoS ONE</i> , <b>2009</b> , 4, e4318	3.7	77
47	A common and unstable copy number variant is associated with differences in <i>Glo1</i> expression and anxiety-like behavior. <i>PLoS ONE</i> , <b>2009</b> , 4, e4649	3.7	87

46	The next generation of microarray research: applications in evolutionary and ecological genomics. <i>Heredity</i> , <b>2008</b> , 100, 141-9	3.6	43
45	Phenotypic analysis of Arabidopsis mutants: hypocotyl length. <i>Cold Spring Harbor Protocols</i> , <b>2008</b> , 2008, pdb.prot4962	1.2	3
44	Whole genome transcriptome polymorphisms in Arabidopsis thaliana. <i>Genome Biology</i> , <b>2008</b> , 9, R165	18.3	26
43	2020 vision for biology: the role of plants in addressing grand challenges in biology. <i>Molecular Plant</i> , <b>2008</b> , 1, 561-3	14.4	6
42	Global analysis of genetic, epigenetic and transcriptional polymorphisms in Arabidopsis thaliana using whole genome tiling arrays. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000032	6	124
41	Amino acid polymorphisms in Arabidopsis phytochrome B cause differential responses to light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 3157-62	11.5	85
40	Natural selection shapes genome-wide patterns of copy-number polymorphism in Drosophila melanogaster. <i>Science</i> , <b>2008</b> , 320, 1629-31	33.3	217
39	Genetic and epigenetic dissection of cis regulatory variation. <i>Current Opinion in Plant Biology</i> , <b>2007</b> , 10, 142-8	9.9	21
38	Genome-wide patterns of single-feature polymorphism in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 12057-62	11.5	147
37	Genome-wide expression profiling of the Arabidopsis female gametophyte identifies families of small, secreted proteins. <i>PLoS Genetics</i> , <b>2007</b> , 3, 1848-61	6	146
36	A large number of novel coding small open reading frames in the intergenic regions of the Arabidopsis thaliana genome are transcribed and/or under purifying selection. <i>Genome Research</i> , <b>2007</b> , 17, 632-40	9.7	120
35	Redundancy in genotyping arrays. <i>PLoS ONE</i> , <b>2007</b> , 2, e287	3.7	6
34	Genotyping and mapping with high-density oligonucleotide arrays. <i>Methods in Molecular Biology</i> , <b>2006</b> , 323, 137-45	1.4	23
33	Inferring population parameters from single-feature polymorphism data. <i>Genetics</i> , <b>2006</b> , 173, 2257-67	4	7
32	A systematic map of genetic variation in Plasmodium falciparum. <i>PLoS Pathogens</i> , <b>2006</b> , 2, e57	7.6	159
31	Association mapping with single-feature polymorphisms. <i>Genetics</i> , <b>2006</b> , 173, 1125-33	4	28
30	Using DNA microarrays to study natural variation. <i>Current Opinion in Genetics and Development</i> , <b>2006</b> , 16, 553-8	4.9	40
29	Genetics of local adaptation in the laboratory: flowering time quantitative trait loci under geographic and seasonal conditions in Arabidopsis. <i>PLoS ONE</i> , <b>2006</b> , 1, e105	3.7	38

28	Single-feature polymorphism discovery in the barley transcriptome. <i>Genome Biology</i> , <b>2005</b> , 6, R54	18.3	119
27	FRIGIDA-independent variation in flowering time of natural <i>Arabidopsis thaliana</i> accessions. <i>Genetics</i> , <b>2005</b> , 170, 1197-207	4	128
26	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> , <b>2005</b> , 102, 10387-92	11.5	316
25	Rapid array mapping of circadian clock and developmental mutations in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2005</b> , 138, 990-7	6.6	80
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> , <b>2005</b> , 102, 2460-5	11.5	167
23	Light-response quantitative trait loci identified with composite interval and eXtreme array mapping in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2004</b> , 167, 907-17	4	74
22	An extracellular aspartic protease functions in <i>Arabidopsis</i> disease resistance signaling. <i>EMBO Journal</i> , <b>2004</b> , 23, 980-8	13	269
21	Genomics tools for QTL analysis and gene discovery. <i>Current Opinion in Plant Biology</i> , <b>2004</b> , 7, 132-6	9.9	103
20	Plant genomics: the third wave. <i>Annual Review of Genomics and Human Genetics</i> , <b>2004</b> , 5, 443-77	9.7	59
19	Large-scale identification of single-feature polymorphisms in complex genomes. <i>Genome Research</i> , <b>2003</b> , 13, 513-23	9.7	307
18	The impact of genomics on the study of natural variation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2003</b> , 132, 718-25	6.6	103
17	The extent of linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , <b>2002</b> , 30, 190-3	36.3	393
16	Chapter Seven Biopanning by activation tagging. <i>Recent Advances in Phytochemistry</i> , <b>2002</b> , 36, 111-123		
15	Quantitative trait loci controlling light and hormone response in two accessions of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2002</b> , 160, 683-96	4	101
14	Natural variation in light sensitivity of <i>Arabidopsis</i> . <i>Nature Genetics</i> , <b>2001</b> , 29, 441-6	36.3	229
13	Activation tagging identifies a conserved MYB regulator of phenylpropanoid biosynthesis. <i>Plant Cell</i> , <b>2000</b> , 12, 2383-2394	11.6	1080
12	Activation Tagging Identifies a Conserved MYB Regulator of Phenylpropanoid Biosynthesis. <i>Plant Cell</i> , <b>2000</b> , 12, 2383	11.6	35
11	Activation tagging in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2000</b> , 122, 1003-13	6.6	813

10	Natural variation in phytochrome signaling. <i>Seminars in Cell and Developmental Biology</i> , <b>2000</b> , 11, 523-307.5	27
9	Cost-conscious generation of multiplexed short-read DNA libraries for whole genome sequencing v1	3
8	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation	4
7	kWIP: The k-mer Weighted Inner Product, a de novo Estimator of Genetic Similarity	2
6	Deep Phenotyping: Deep Learning for Temporal Phenotype/Genotype Classification	12
5	Axe: rapid, competitive sequence read demultiplexing using a trie	4
4	Landscape genomic prediction for restoration of a Eucalyptus foundation species under climate change	1
3	HOME: A histogram based machine learning approach for effective identification of differentially methylated regions	4
2	Population structure of the <i>Brachypodium</i> species complex and genome wide association of agronomic traits in response to climate	1
1	Genomic constraints to drought adaptation	2