Jeffrey B Endelman

List of Publications by Year
in descending order

39	4,166	304368	301761
papers	citations	22	39
		h-index	g-index

47	47	47	4247
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. Molecular Plant, 2022, 15, 520-536.	3.9	72
2	The genetic architectures of vine and skin maturity in tetraploid potato. Theoretical and Applied Genetics, 2022, 135, 2943-2951.	1.8	2
3	Characterization of a Late Blight Resistance Gene Homologous to R2 in Potato Variety Payette Russet. American Journal of Potato Research, 2021, 98, 78-84.	0.5	5
4	Haplotype reconstruction in connected tetraploid F1 populations. Genetics, 2021, 219, .	1.2	26
5	QTL mapping in outbred tetraploid (and diploid) diallel populations. Genetics, 2021, 219, .	1.2	15
6	FIELDimageR: An R package to analyze orthomosaic images from agricultural fieldÂtrials. The Plant Phenome Journal, 2020, 3, e20005.	1.0	58
7	Imageâ€based phenotyping and genetic analysis of potato skin set and color. Crop Science, 2020, 60, 202-210.	0.8	13
8	Impact of dominance effects on autotetraploid genomic prediction. Crop Science, 2020, 60, 656-665.	0.8	28
9	On the accuracy of genomic prediction models considering multi-trait and allele dosage in Urochloa spp. interspecific tetraploid hybrids. Molecular Breeding, 2019, 39, 1.	1.0	37
10	Genomic Prediction of Autotetraploids; Influence of Relationship Matrices, Allele Dosage, and Continuous Genotyping Calls in Phenotype Prediction. G3: Genes, Genomes, Genetics, 2019, 9, 1189-1198.	0.8	60
11	Impact of Dominance Effects on Autotetraploid Genomic Prediction. Crop Science, 2019, .	0.8	25
12	Expected Genotype Quality and Diploidized Marker Data from Genotypingâ€byâ€Sequencing of <i>Urochloa</i> spp. Tetraploids. Plant Genome, 2019, 12, 1-9.	1.6	13
13	Genetic Covariance of Environments in the Potato National Chip Processing Trial. Crop Science, 2019, 59, 107-114.	0.8	6
14	Genetic Variance Partitioning and Genome-Wide Prediction with Allele Dosage Information in Autotetraploid Potato. Genetics, 2018, 209, 77-87.	1.2	117
15	Evaluation of genetic diversity among Russet potato clones and varieties from breeding programs across the United States. PLoS ONE, 2018, 13, e0201415.	1.1	10
16	Automated tetraploid genotype calling by hierarchical clustering. Theoretical and Applied Genetics, 2017, 130, 717-726.	1.8	61
17	Pedigree Reconstruction with Genome-Wide Markers in Potato. American Journal of Potato Research, 2017, 94, 184-190.	0.5	19
18	Reliability of Measurement and Genotype Ã— Environment Interaction for Potato Specific Gravity. Crop Science, 2017, 57, 1966-1972.	0.8	11

#	ARTICLE	IF	CITATIONS
19	Acrylamide‐Forming Potential and Agronomic Properties of Elite US Potato Germplasm from the National Fry Processing Trial. Crop Science, 2016, 56, 30-39.	0.8	9
20	Software for Genome‐Wide Association Studies in Autopolyploids and Its Application to Potato. Plant Genome, 2016, 9, plantgenome2015.08.0073.	1.6	191
21	Genetic mapping with an inbred line-derived F2 population in potato. Theoretical and Applied Genetics, 2016, 129, 935-943.	1.8	74
22	Compost carryover: nitrogen, phosphorus and FT-IR analysis of soil organic matter. Nutrient Cycling in Agroecosystems, 2015, 101, 317-331.	1.1	9
23	Optimal Design of Preliminary Yield Trials with Genome‐Wide Markers. Crop Science, 2014, 54, 48-59.	0.8	100
24	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. PLoS ONE, 2014, 9, e94688.	1.1	188
25	LPmerge: an R package for merging genetic maps by linear programming. Bioinformatics, 2014, 30, 1623-1624.	1.8	140
26	Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and β-glucan in US barley breeding germplasm. Molecular Breeding, 2014, 34, 1229-1243.	1.0	35
27	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. BMC Genomics, 2014, 15, 171.	1.2	41
28	Genomic Predictability of Interconnected Biparental Maize Populations. Genetics, 2013, 194, 493-503.	1.2	180
29	The use of unbalanced historical data for genomic selection in an international wheat breeding program. Field Crops Research, 2013, 154, 12-22.	2.3	100
30	Shrinkage Estimation of the Realized Relationship Matrix. G3: Genes, Genomes, Genetics, 2012, 2, 1405-1413.	0.8	420
31	Ridge Regression and Other Kernels for Genomic Selection with R Package rrBLUP. Plant Genome, 2011, 4, 250-255.	1.6	1,588
32	New algorithm improves fine structure of the barley consensus SNP map. BMC Genomics, 2011, 12, 407.	1.2	13
33	A New Decay Series for Organic Crop Production. Agronomy Journal, 2010, 102, 457-463.	0.9	11
34	Economically Optimal Compost Rates for Organic Crop Production. Agronomy Journal, 2010, 102, 1283-1289.	0.9	5
35	Structure-Guided Recombination Creates an Artificial Family of Cytochromes P450. PLoS Biology, 2006, 4, e112.	2.6	133
36	SCHEMA-Guided Protein Recombination. Methods in Enzymology, 2004, 388, 35-42.	0.4	31

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37	Functional Evolution and Structural Conservation in Chimeric Cytochromes P450. Chemistry and Biology, 2004, 11, 309-318.	6.2	97
38	Site-directed protein recombination as a shortest-path problem. Protein Engineering, Design and Selection, 2004, 17, 589-594.	1.0	70
39	Library analysis of SCHEMA-guided protein recombination. Protein Science, 2003, 12, 1686-1693.	3.1	138