

Sean Myles

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

6,868
citations

94269

37
h-index

143772

57
g-index

66
all docs

66
docs citations

66
times ranked

8646
citing authors

#	ARTICLE	IF	CITATIONS
1	Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. <i>Plant Cell</i> , 2009, 21, 2194-2202.	3.1	786
2	Genetic structure and domestication history of the grape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3530-3535.	3.3	684
3	How culture shaped the human genome: bringing genetics and the human sciences together. <i>Nature Reviews Genetics</i> , 2010, 11, 137-148.	7.7	648
4	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	13.7	464
5	LinkImpute: Fast and Accurate Genotype Imputation for Nonmodel Organisms. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2383-2390.	0.8	407
6	Genetic diversity and population structure assessed by SSR and SNP markers in a large germplasm collection of grape. <i>BMC Plant Biology</i> , 2013, 13, 39.	1.6	325
7	A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape. <i>Plant Physiology</i> , 2014, 164, 259-272.	2.3	233
8	The Genetic Structure of Marijuana and Hemp. <i>PLoS ONE</i> , 2015, 10, e0133292.	1.1	232
9	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. <i>PLoS Genetics</i> , 2011, 7, e1002383.	1.5	231
10	Rapid Genomic Characterization of the Genus <i>Vitis</i> . <i>PLoS ONE</i> , 2010, 5, e8219.	1.1	203
11	Targeted high-throughput sequencing of tagged nucleic acid samples. <i>Nucleic Acids Research</i> , 2007, 35, e97.	6.5	171
12	Identifying genes underlying skin pigmentation differences among human populations. <i>Human Genetics</i> , 2006, 120, 613-621.	1.8	128
13	Fast and Cost-Effective Genetic Mapping in Apple Using Next-Generation Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1681-1687.	0.8	123
14	Exploiting Wild Relatives for Genomics-assisted Breeding of Perennial Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 460.	1.7	116
15	Worldwide population differentiation at disease-associated SNPs. <i>BMC Medical Genomics</i> , 2008, 1, 22.	0.7	114
16	Melanesian Blond Hair Is Caused by an Amino Acid Change in <i>TYRP1</i> . <i>Science</i> , 2012, 336, 554-554.	6.0	104
17	Genome to Phenome Mapping in Apple Using Historical Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0113.	1.6	102
18	Genetic evidence in support of a shared Eurasian-North African dairying origin. <i>Human Genetics</i> , 2005, 117, 34-42.	1.8	101

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19	Positive Selection in East Asians for an EDAR Allele that Enhances NF- κ B Activation. PLoS ONE, 2008, 3, e2209.	1.1	91
20	Patterns of genomic and phenomic diversity in wine and table grapes. Horticulture Research, 2017, 4, 17035.	2.9	87
21	Improving fruit and wine: what does genomics have to offer?. Trends in Genetics, 2013, 29, 190-196.	2.9	79
22	The Y-chromosome landscape of the Philippines: extensive heterogeneity and varying genetic affinities of Negrito and non-Negrito groups. European Journal of Human Genetics, 2011, 19, 224-230.	1.4	78
23	Apple whole genome sequences: recent advances and new prospects. Horticulture Research, 2019, 6, 59.	2.9	77
24	Genome-Wide Association Studies in Apple Reveal Loci for Aroma Volatiles, Sugar Composition, and Harvest Date. Plant Genome, 2019, 12, 180104.	1.6	70
25	Identification and Analysis of Genomic Regions with Large Between-Population Differentiation in Humans. Annals of Human Genetics, 2008, 72, 99-110.	0.3	62
26	Topological Data Analysis as a Morphometric Method: Using Persistent Homology to Demarcate a Leaf Morphospace. Frontiers in Plant Science, 2018, 9, 553.	1.7	62
27	A Genome-Wide Association Study of Apple Quality and Scab Resistance. Plant Genome, 2018, 11, 170075.	1.6	61
28	Bridging Near and Remote Oceania: mtDNA and NRY Variation in the Solomon Islands. Molecular Biology and Evolution, 2012, 29, 545-564.	3.5	58
29	Vitis Phylogenomics: Hybridization Intensities from a SNP Array Outperform Genotype Calls. PLoS ONE, 2013, 8, e78680.	1.1	55
30	Genomic consequences of apple improvement. Horticulture Research, 2021, 8, 9.	2.9	53
31	Genetic Support for Phenotype-based Racial Classification in Sorghum. Crop Science, 2011, 51, 224-230.	0.8	52
32	Larger mitochondrial DNA than Y-chromosome differences between matrilineal and patrilineal groups from Sumatra. Nature Communications, 2011, 2, 228.	5.8	51
33	Genome-wide association studies in apple reveal loci of large effect controlling apple polyphenols. Horticulture Research, 2019, 6, 107.	2.9	50
34	Development of marker sets useful in the early selection of Ren4 powdery mildew resistance and seedlessness for table and raisin grape breeding. Theoretical and Applied Genetics, 2012, 124, 23-33.	1.8	49
35	Genomics: A potential panacea for the perennial problem. American Journal of Botany, 2014, 101, 1780-1790.	0.8	49
36	LinkImputeR: user-guided genotype calling and imputation for non-model organisms. BMC Genomics, 2017, 18, 523.	1.2	48

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37	Morphometrics Reveals Complex and Heritable Apple Leaf Shapes. <i>Frontiers in Plant Science</i> , 2017, 8, 2185.	1.7	46
38	Prediction of Cacao (<i>Theobroma cacao</i>) Resistance to <i>Moniliophthora</i> spp. Diseases via Genome-Wide Association Analysis and Genomic Selection. <i>Frontiers in Plant Science</i> , 2018, 9, 343.	1.7	43
39	Genomics Assisted Ancestry Deconvolution in Grape. <i>PLoS ONE</i> , 2013, 8, e80791.	1.1	43
40	Genomic ancestry estimation quantifies use of wild species in grape breeding. <i>BMC Genomics</i> , 2016, 17, 478.	1.2	40
41	Worldwide patterns of haplotype diversity at 9p21.3, a locus associated with type 2 diabetes and coronary heart disease. <i>Genome Medicine</i> , 2009, 1, 51.	3.6	38
42	Testing the thrifty gene hypothesis: the Gly482Ser variant in <i>PPARGC1A</i> is associated with BMI in Tongans. <i>BMC Medical Genetics</i> , 2011, 12, 10.	2.1	38
43	Recent positive selection of a human androgen receptor/ectodysplasin A2 receptor haplotype and its relationship to male pattern baldness. <i>Human Genetics</i> , 2009, 126, 255-264.	1.8	35
44	Population structure, relatedness and ploidy levels in an apple gene bank revealed through genotyping-by-sequencing. <i>PLoS ONE</i> , 2018, 13, e0201889.	1.1	35
45	Identification of a candidate genetic variant for the high prevalence of type II diabetes in Polynesians. <i>European Journal of Human Genetics</i> , 2007, 15, 584-589.	1.4	33
46	Apple Ripening Is Controlled by a NAC Transcription Factor. <i>Frontiers in Genetics</i> , 2021, 12, 671300.	1.1	29
47	Genetic Analysis of East Asian Grape Cultivars Suggests Hybridization with Wild <i>Vitis</i> . <i>PLoS ONE</i> , 2015, 10, e0140841.	1.1	24
48	Cannabis labelling is associated with genetic variation in terpene synthase genes. <i>Nature Plants</i> , 2021, 7, 1330-1334.	4.7	22
49	QTL analysis of soft scald in two apple populations. <i>Horticulture Research</i> , 2016, 3, 16043.	2.9	21
50	Quantifying apple diversity: A phenomic characterization of Canada's Apple Biodiversity Collection. <i>Plants People Planet</i> , 2021, 3, 747-760.	1.6	20
51	Genetic mapping in grapevine using SNP microarray intensity values. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	17
52	Detection of selection signatures for response to Aleutian mink disease virus infection in American mink. <i>Scientific Reports</i> , 2021, 11, 2944.	1.6	16
53	Linkage Disequilibrium, Effective Population Size and Genomic Inbreeding Rates in American Mink Using Genotyping-by-Sequencing Data. <i>Frontiers in Genetics</i> , 2020, 11, 223.	1.1	8
54	Experience levels of individuals in natural bee populations and their ecological implications. <i>Canadian Journal of Zoology</i> , 2005, 83, 492-497.	0.4	7

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55	Phenotypic divergence between the cultivated apple (<i>Malus domestica</i>) and its primary wild progenitor (<i>Malus sieversii</i>). <i>PLoS ONE</i> , 2022, 17, e0250751.	1.1	7
56	An assessment of the portability of ancestry informative markers between human populations. <i>BMC Medical Genomics</i> , 2009, 2, 45.	0.7	4
57	Cider and dessert apples: What is the difference?. <i>Plants People Planet</i> , 0, , .	1.6	4
58	PSVIII-31 Genome-wide estimation of linkage disequilibrium using American mink genotyping-by-sequencing data. <i>Journal of Animal Science</i> , 2019, 97, 267-267.	0.2	0
59	PSXII-24 Identification of selection signatures for response of American mink to Aleutian mink disease virus infection. <i>Journal of Animal Science</i> , 2020, 98, 243-244.	0.2	0