Charlene P Wight

List of Publications by Year
in descending order

25 papers	907 citations	516710 16 h-index	580821 25 g-index
25 all docs	25 docs citations	25 times ranked	825 citing authors

#	Article	IF	Citations
1	Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. PLoS ONE, 2014, 9, e102448.	2.5	147
2	A molecular marker map in 'Kanota' Ã— 'Ogle' hexaploid oat (Avenaspp.) enhanced by additional markers and a robust framework. Genome, 2003, 46, 28-47.	2.0	107
3	Haplotypeâ€based genotypingâ€byâ€sequencing in oat genome research. Plant Biotechnology Journal, 2018, 16, 1452-1463.	8.3	86
4	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome, 2016, 9, plantgenome2015.10.0102.	2.8	85
5	High-density marker profiling confirms ancestral genomes of Avena species and identifies D-genome chromosomes of hexaploid oat. Theoretical and Applied Genetics, 2016, 129, 2133-2149.	3.6	56
6	Population Genomics Related to Adaptation in Elite Oat Germplasm. Plant Genome, 2016, 9, plantgenome2015.10.0103.	2.8	55
7	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	50
8	Discovery, localization, and sequence characterization of molecular markers for the crown rust resistance genes Pc38, Pc39, and Pc48 in cultivated oat (Avena sativa L.). Molecular Breeding, 2004, 14, 349-361.	2.1	40
9	Screening Oat Genotypes for Tolerance to Salinity and Alkalinity. Frontiers in Plant Science, 2018, 9, 1302.	3.6	33
10	Comparative linkage mapping of diploid, tetraploid, and hexaploid Avena species suggests extensive chromosome rearrangement in ancestral diploids. Scientific Reports, 2019, 9, 12298.	3.3	26
11	Loci affecting flowering time in oat under short-day conditions. Genome, 2006, 49, 1528-1538.	2.0	25
12	Tagging and mapping candidate loci for vernalization and flower initiation in hexaploid oat. Molecular Breeding, 2012, 30, 1295-1312.	2.1	23
13	Genome analysis in Avena sativa reveals hidden breeding barriers and opportunities for oat improvement. Communications Biology, 2022, 5, 474.	4.4	23
14	GrainGenes: a data-rich repository for small grains genetics and genomics. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	22
15	The identification of random amplified polymorphic DNA markers for daylength insensitivity in oat. Genome, 1994, 37, 910-914.	2.0	21
16	A Set of New Simple Sequence Repeat and Avenin DNA Markers Suitable for Mapping and Fingerprinting Studies in Oat (Avena spp.). Crop Science, 2010, 50, 1207-1218.	1.8	21
17	A genetic linkage map in southernâ€byâ€spring oat identifies multiple quantitative trait loci for adaptation and rust resistance. Plant Breeding, 2019, 138, 82-94.	1.9	17
18	Centromeric position and genomic allocation of a repetitive sequence isolated from chromosome 18D of hexaploid oat, Avena sativa L.. Genetic Resources and Crop Evolution, 2015, 62, 1-4.	1.6	15

#	Article	IF	Citations
19	Genomic relationships among sixteen species of Avena based on (ACT)6 trinucleotide repeat FISH. Genome, 2018, 61, 63-70.	2.0	12
20	Mapping of the stem rust resistance gene Pg13 in cultivated oat. Theoretical and Applied Genetics, 2020, 133, 259-270.	3.6	11
21	New evidence confirming the CD genomic constitutions of the tetraploid Avena species in the section Pachycarpa Baum. PLoS ONE, 2021, 16, e0240703.	2.5	11
22	Discovery, localization, and sequence characterization of molecular markers for the crown rust resistance genes Pc38, Pc39, and Pc48 in cultivated oat (Avena sativa L.). Molecular Breeding, 2005, 14, 349-361.	2.1	8
23	Conferring resistance to pre-harvest sprouting in durum wheat by a QTL identified in Triticum spelta. Euphytica, 2017, 213, 1.	1.2	8
24	Genetic mapping and a new PCR-based marker linked to a dwarfing gene in oat (Avena sativa L.). Genome, 2018, 61, 497-503.	2.0	3
25	GrainGenes: Tools and Content to Assist Breeders Improving Oat Quality. Foods, 2022, 11, 914.	4.3	2