

# Melanie L Hand

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

914  
citations

471061

17  
h-index

610482

24  
g-index

24  
all docs

24  
docs citations

24  
times ranked

961  
citing authors

#	ARTICLE	IF	CITATIONS
1	Seeds of doubt: Mendel's choice of <i>Hieracium</i> to study inheritance, a case of right plant, wrong trait. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2253-2266.	1.8	13
2	Generation of an integrated <i>Hieracium</i> genomic and transcriptomic resource enables exploration of small RNA pathways during apomixis initiation. <i>BMC Biology</i> , 2016, 14, 86.	1.7	19
3	A Comparison of In Vitro and In Vivo Asexual Embryogenesis. <i>Methods in Molecular Biology</i> , 2016, 1359, 3-23.	0.4	14
4	A reference genetic linkage map of apomictic <i>Hieracium</i> species based on expressed markers derived from developing ovule transcripts. <i>Annals of Botany</i> , 2015, 115, 567-580.	1.4	10
5	Evolution of apomixis loci in <i>Pilosella</i> and <i>Hieracium</i> (Asteraceae) inferred from the conservation of apomixis-linked markers in natural and experimental populations. <i>Heredity</i> , 2015, 114, 17-26.	1.2	40
6	Development and implementation of a multiplexed single nucleotide polymorphism genotyping tool for differentiation of ryegrass species and cultivars. <i>Molecular Breeding</i> , 2014, 33, 435-451.	1.0	19
7	The Genetic Control of Apomixis: Asexual Seed Formation. <i>Genetics</i> , 2014, 197, 441-450.	1.2	260
8	Resources and strategies for implementation of genomic selection in breeding of forage species. <i>Crop and Pasture Science</i> , 2014, 65, 1238.	0.7	17
9	Nucleotide diversity of vernalization and flowering-related genes in a germplasm collection of meadow fescue ( <i>Festuca pratensis</i> syn. <i>Lolium</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50	0.7	17
10	Plastome Sequence Determination and Comparative Analysis for Members of the <i>Lolium-Festuca</i> Grass Species Complex. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 607-616.	0.8	36
11	Candidate gene-based association genetics analysis of herbage quality traits in perennial ryegrass ( <i>Lolium perenne</i> L.). <i>Crop and Pasture Science</i> , 2013, 64, 244.	0.7	9
12	Genetic Diversity and Host Specificity of Fungal Endophyte Taxa in Fescue Pasture Grasses. <i>Crop Science</i> , 2012, 52, 2243-2252.	0.8	34
13	Genome-wide SNP identification in multiple morphotypes of allohexaploid tall fescue ( <i>Festuca</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50	1.2	14
14	Molecular characterisation and interpretation of genetic diversity within globally distributed germplasm collections of tall fescue ( <i>Festuca arundinacea</i> Schreb.) and meadow fescue ( <i>F. pratensis</i> ) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50	0.8	10
15	Identification of QTLs for morphological traits influencing waterlogging tolerance in perennial ryegrass ( <i>Lolium perenne</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 609-622.	1.8	27
16	Identification of genetic factors influencing salt stress tolerance in white clover ( <i>Trifolium repens</i> ) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50	1.8	36
17	Evolutionary history of tall fescue morphotypes inferred from molecular phylogenetics of the <i>Lolium-Festuca</i> species complex. <i>BMC Evolutionary Biology</i> , 2010, 10, 303.	3.2	70
18	Comparison of homoeolocus organisation in paired BAC clones from white clover ( <i>Trifolium repens</i> ) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50	1.6	12

#	ARTICLE	IF	CITATIONS
19	Genetic map construction and QTL mapping of resistance to blackleg ( <i>Leptosphaeria maculans</i> ) disease in Australian canola ( <i>Brassica napus</i> L.) cultivars. <i>Theoretical and Applied Genetics</i> , 2009, 120, 71-83.	1.8	85
20	Assessment of genetic diversity in Australian canola ( <i>Brassica napus</i> L.) cultivars using SSR markers. <i>Crop and Pasture Science</i> , 2009, 60, 1193.	0.7	34
21	Identification of homologous, homoeologous and paralogous sequence variants in an outbreeding allopolyploid species based on comparison with progenitor taxa. <i>Molecular Genetics and Genomics</i> , 2008, 280, 293-304.	1.0	35
22	Characterization of simple sequence repeat markers derived in silico from <i>Brassica rapa</i> bacterial artificial chromosome sequences and their application in <i>Brassica napus</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 273-277.	1.7	27
23	Sixteen new simple sequence repeat markers from <i>Brassica juncea</i> expressed sequences and their cross-species amplification. <i>Molecular Ecology Notes</i> , 2007, 7, 697-700.	1.7	36
24	Identification and characterization of simple sequence repeat markers from <i>Brassica napus</i> expressed sequences. <i>Molecular Ecology Notes</i> , 2007, 7, 886-889.	1.7	29