

# Meredith D Mcneil

## List of Publications by Year in descending order

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16  
papers

640  
citations

758635

12  
h-index

940134

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

764  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sugarcane Smut, Caused by <i>Sporisorium scitamineum</i> , a Major Disease of Sugarcane: A Contemporary Review. <i>Phytopathology</i> , 2021, 111, 1905-1917.	1.1	27
2	Resistance mechanisms and expression of disease resistance-related genes in sugarcane ( <i>Saccharum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	2
3	Analysis of the resistance mechanisms in sugarcane during <i>Sporisorium scitamineum</i> infection using RNA-seq and microscopy. <i>PLoS ONE</i> , 2018, 13, e0197840.	1.1	37
4	A comprehensive genetic map of sugarcane that provides enhanced map coverage and integrates high-throughput Diversity Array Technology (DART) markers. <i>BMC Genomics</i> , 2014, 15, 152.	1.2	61
5	Comparative mapping in the Poaceae family reveals translocations in the complex polyploid genome of sugarcane. <i>BMC Plant Biology</i> , 2014, 14, 190.	1.6	43
6	Conversion of AFLP markers to high-throughput markers in a complex polyploid, sugarcane. <i>Molecular Breeding</i> , 2011, 27, 395-407.	1.0	10
7	Haplotype analyses in wheat for complex traits: tracking the chromosome 3B and 7B regions associated with late maturity alpha amylase (LMA) in breeding programs. <i>Crop and Pasture Science</i> , 2009, 60, 463.	0.7	13
8	BAC-derived markers for assaying the stem rust resistance gene, Sr2, in wheat breeding programs. <i>Molecular Breeding</i> , 2008, 22, 15-24.	1.0	36
9	The genome structure of the 1-FEH genes in wheat ( <i>Triticum aestivum</i> L.): new markers to track stem carbohydrates and grain filling QTLs in breeding. <i>Molecular Breeding</i> , 2008, 22, 339-351.	1.0	36
10	Wheat genome structure and function: genome sequence data and the International Wheat Genome Sequencing Consortium. <i>Australian Journal of Agricultural Research</i> , 2007, 58, 470.	1.5	12
11	Comparative organization of wheat homoeologous group 3S and 7L using wheat-rice synteny and identification of potential markers for genes controlling xanthophyll content in wheat. <i>Functional and Integrative Genomics</i> , 2004, 4, 118-130.	1.4	30
12	Implementation of markers in Australian wheat breeding. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1349.	1.5	132
13	Validation of molecular markers for wheat breeding. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1357.	1.5	84
14	Implementation of probes for tracing chromosome segments conferring barley yellow dwarf virus resistance. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1389.	1.5	12
15	Development of robust PCR-based DNA markers for each homoeo-allele of granule-bound starch synthase and their application in wheat breeding programs. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1409.	1.5	55
16	Cereal DNA: A rapid high-throughput extraction method for marker assisted selection. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 357-360.	1.0	50