

# Amanda M Hulse-Kemp

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

2,607  
citations

623734

14  
h-index

552781

26  
g-index

28  
all docs

28  
docs citations

28  
times ranked

2332  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing of allotetraploid cotton ( <i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
2	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
3	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209.	1.8	226
4	Reference quality assembly of the 3.5-Gb genome of <i>Capsicum annuum</i> from a single linked-read library. <i>Horticulture Research</i> , 2018, 5, 4.	6.3	113
5	Sequencing-Based Bin Map Construction of a Tomato Mapping Population, Facilitating High-Resolution Quantitative Trait Loci Detection. <i>Plant Genome</i> , 2019, 12, 180010.	2.8	65
6	Diversity analysis of cotton ( <i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. <i>BMC Plant Biology</i> , 2017, 17, 37.	3.6	56
7	A HapMap leads to a <i>Capsicum annuum</i> SNP infinium array: a new tool for pepper breeding. <i>Horticulture Research</i> , 2016, 3, 16036.	6.3	47
8	<i>Capsicum</i> —An Abbreviated Compendium. <i>Journal of the American Society for Horticultural Science</i> , 2019, 144, 3-22.	1.0	38
9	DNA Sequence Evolution and Rare Homoeologous Conversion in Tetraploid Cotton. <i>PLoS Genetics</i> , 2016, 12, e1006012.	3.5	27
10	Development and bin mapping of gene-associated interspecific SNPs for cotton ( <i>Gossypium hirsutum</i> L.) introgression breeding efforts. <i>BMC Genomics</i> , 2014, 15, 945.	2.8	25
11	Sub genome anchored physical frameworks of the allotetraploid Upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq1 1 0.784314 rgBT /Over 7, 15274.	3.3	23
12	BAC-End Sequence-Based SNP Mining in Allotetraploid Cotton ( <i>Gossypium</i> ) Utilizing Resequencing Data, Phylogenetic Inferences, and Perspectives for Genetic Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1095-1105.	1.8	20
13	Feeding high-oleic peanuts to layer hens enhances egg yolk color and oleic fatty acid content in shell eggs. <i>Poultry Science</i> , 2019, 98, 1732-1748.	3.4	19
14	Enhancing Upland cotton for drought resilience, productivity, and fiber quality: comparative evaluation and genetic dissection. <i>Molecular Genetics and Genomics</i> , 2020, 295, 155-176.	2.1	18
15	High-quality reference genome and annotation aids understanding of berry development for evergreen blueberry ( <i>Vaccinium darrowii</i> ). <i>Horticulture Research</i> , 2021, 8, 228.	6.3	17
16	Comparative transcriptomics and genomic patterns of discordance in Capsiceae (Solanaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 293-302.	2.7	15
17	The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. <i>Genome Biology</i> , 2022, 23, 75.	8.8	15
18	An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. <i>Plant Genome</i> , 2021, 14, e20101.	2.8	13

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19	A Long-Read Transcriptome Assembly of Cotton ( <i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	2.8	12
20	Insights Into Upland Cotton ( <i>Gossypium hirsutum</i> L.) Genetic Recombination Based on 3 High-Density Single-Nucleotide Polymorphism and a Consensus Map Developed Independently With Common Parents. <i>Genomics Insights</i> , 2017, 10, 117863101773510.	3.0	12
21	High-Temperature and Drought-Resilience Traits among Interspecific Chromosome Substitution Lines for Genetic Improvement of Upland Cotton. <i>Plants</i> , 2020, 9, 1747.	3.5	12
22	SNP-Based MAS in Cotton under Depressed Recombination for <i>Ren</i> Flanking Recombinants: Results and Inferences on Wide-Cross Breeding Strategies. <i>Crop Science</i> , 2016, 56, 1526-1539.	1.8	7
23	Genomic Resource Development for <i>Hydrangea</i> ( <i>Hydrangea macrophylla</i> (Thunb.) Ser.)—A Transcriptome Assembly and a High-Density Genetic Linkage Map. <i>Horticulturae</i> , 2021, 7, 25.	2.8	6
24	Population structure and genetic diversity of the Pee Dee cotton breeding program. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
25	Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs. <i>Plants</i> , 2022, 11, 1446.	3.5	4
26	Introduction: Crop Wild Relatives in Plant Breeding. , 2021, , 1-18.		0