Amanda M Hulse-Kemp

List of Publications by Year
in descending order

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	The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. Genome Biology, 2022, 23, 75.	8.8	15
2	Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs. Plants, 2022, 11, 1446.	3.5	4
3	Introduction: Crop Wild Relatives in Plant Breeding. , 2021, , 1-18.		0
4	Genomic Resource Development for Hydrangea (Hydrangea macrophylla (Thunb.) Ser.)â€"A Transcriptome Assembly and a High-Density Genetic Linkage Map. Horticulturae, 2021, 7, 25.	2.8	6
5	Population structure and genetic diversity of the Pee Dee cotton breeding program. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	4
6	An anchored chromosomeâ€scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. Plant Genome, 2021, 14, e20101.	2.8	13
7	High-quality reference genome and annotation aids understanding of berry development for evergreen blueberry (Vaccinium darrowii). Horticulture Research, 2021, 8, 228.	6.3	17
8	Enhancing Upland cotton for drought resilience, productivity, and fiber quality: comparative evaluation and genetic dissection. Molecular Genetics and Genomics, 2020, 295, 155-176.	2.1	18
9	High-Temperature and Drought-Resilience Traits among Interspecific Chromosome Substitution Lines for Genetic Improvement of Upland Cotton. Plants, 2020, 9, 1747.	3.5	12
10	Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature Genetics, 2020, 52, 525-533.	21.4	249
11	Feeding high-oleic peanuts to layer hens enhances egg yolk color and oleic fatty acid content in shell eggs. Poultry Science, 2019, 98, 1732-1748.	3.4	19
12	Sequencingâ€Based Bin Map Construction of a Tomato Mapping Population, Facilitating Highâ€Resolution Quantitative Trait Loci Detection. Plant Genome, 2019, 12, 180010.	2.8	65
13	Capsicumâ€"An Abbreviated Compendium. Journal of the American Society for Horticultural Science, 2019, 144, 3-22.	1.0	38
14	Reference quality assembly of the 3.5-Gb genome of Capsicum annuum from a single linked-read library. Horticulture Research, 2018, 5, 4.	6.3	113
15	Comparative transcriptomics and genomic patterns of discordance in Capsiceae (Solanaceae). Molecular Phylogenetics and Evolution, 2018, 126, 293-302.	2.7	15
16	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (Gossypium hirsutum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 7, 15274.	3.3	23
17	Diversity analysis of cotton (Gossypium hirsutum L.) germplasm using the CottonSNP63K Array. BMC Plant Biology, 2017, 17, 37.	3.6	56
18	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. Genomics Insights, 2017, 10, 117863101773510.	3.0	12

#	Article	IF	Citations
19	SNP‐Based MAS in Cotton under Depressed‐Recombination for *Ren*^{*lon*}‐Flanking Recombinants: Results and Inferences on Wide‐Cross Breeding Strategies. Crop Science, 2016, 56, 1526-1539.	1.8	7
20	DNA Sequence Evolution and Rare Homoeologous Conversion in Tetraploid Cotton. PLoS Genetics, 2016, 12, e1006012.	3.5	27
21	A HapMap leads to a Capsicum annuum SNP infinium array: a new tool for pepper breeding. Horticulture Research, 2016, 3, 16036.	6.3	47
22	A Long‐Read Transcriptome Assembly of Cotton (Gossypium hirsutum L.) and Intraspecific Single Nucleotide Polymorphism Discovery. Plant Genome, 2015, 8, eplantgenome2014.10.0068.	2.8	12
23	BAC-End Sequence-Based SNP Mining in Allotetraploid Cotton (*Gossypium*) Utilizing Resequencing Data, Phylogenetic Inferences, and Perspectives for Genetic Mapping. G3: Genes, Genomes, Genetics, 2015, 5, 1095-1105.	1.8	20
24	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of *Gossypium* spp.. G3: Genes, Genomes, Genetics, 2015, 5, 1187-1209.	1.8	226
25	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
26	Development and bin mapping of gene-associated interspecific SNPs for cotton (Gossypium hirsutum L.) introgression breeding efforts. BMC Genomics, 2014, 15, 945.	2.8	25