Pallavi Sinha

List of Publications by Year
in descending order

18	973	567281 15	839539 18
papers	citations	h-index	g-index

18	18	18	1258
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	5Gs for crop genetic improvement. Current Opinion in Plant Biology, 2020, 56, 190-196.	7.1	134
2	Nextâ€generation sequencing for identification of candidate genes for Fusarium wilt and sterility mosaic disease in pigeonpea (<scp>C</scp>ajanus cajan). Plant Biotechnology Journal, 2016, 14, 1183-1194.	8.3	108
3	A chickpea genetic variation map based on the sequencing of 3,366 genomes. Nature, 2021, 599, 622-627.	27.8	106
4	Haplotype analysis of key genes governing grain yield and quality traits across 3K <scp>RG</scp> panel reveals scope for the development of tailorâ€made rice with enhanced genetic gains. Plant Biotechnology Journal, 2019, 17, 1612-1622.	8.3	87
5	Indelâ€seq: a fastâ€forward genetics approach for identification of traitâ€associated putative candidate genomic regions and its application in pigeonpea (Cajanus cajan). Plant Biotechnology Journal, 2017, 15, 906-914.	8.3	67
6	Evaluation and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea (Cajanus cajan) Under Drought Stress Conditions. PLoS ONE, 2015, 10, e0122847.	2.5	67
7	Superior haplotypes for haplotypeâ€based breeding for drought tolerance in pigeonpea (Cajanus) Tj ETQq1 1 0.784314 rgBT /Ove	8.3	61
8	Genomics-assisted breeding for boosting crop improvement in pigeonpea (Cajanus cajan). Frontiers in Plant Science, 2015, 6, 50.	3.6	57
9	Selection and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea (Cajanus cajan) under Heat and Salt Stress Conditions. Frontiers in Plant Science, 2015, 6, 1071.	3.6	48
10	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in Pigeonpea (Cajanus cajan L.). Frontiers in Plant Science, 2015, 6, 1065.	3.6	39
11	Genomeâ€wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. Plant Biotechnology Journal, 2020, 18, 1697-1710.	8.3	38
12	Arachis hypogaea gene expression atlas for fastigiata subspecies of cultivated groundnut to accelerate functional and translational genomics applications. Plant Biotechnology Journal, 2020, 18, 2187-2200.	8.3	38
13	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. Functional and Integrative Genomics, 2020, 20, 739-761.	3.5	37
14	Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. Theoretical and Applied Genetics, 2021, 134, 1829-1843.	3.6	32
15	Genetic analysis and molecular mapping of a new fertility restorer gene Rf8 for Triticum timopheevi cytoplasm in wheat (Triticum aestivum L.) using SSR markers. Genetica, 2013, 141, 431-441.	1.1	21
16	Prediction of hybrid performance based on the genetic distance of parental lines in two-line rice (Oryza sativa L.) hybrids. Journal of Crop Science and Biotechnology, 2011, 14, 1-10.	1.5	15
17	Determination of genetic relationships among elite thermosensitive genic male sterile lines (TGMS) of rice (Oryza sativa L.) employing morphological and simple sequence repeat (SSR) markers. Journal of Genetics, 2011, 90, 11-19.	0.7	9
18	QTL-seq for the identification of candidate genes for days to flowering and leaf shape in pigeonpea. Heredity, 2022, 128, 411-419.	2.6	9