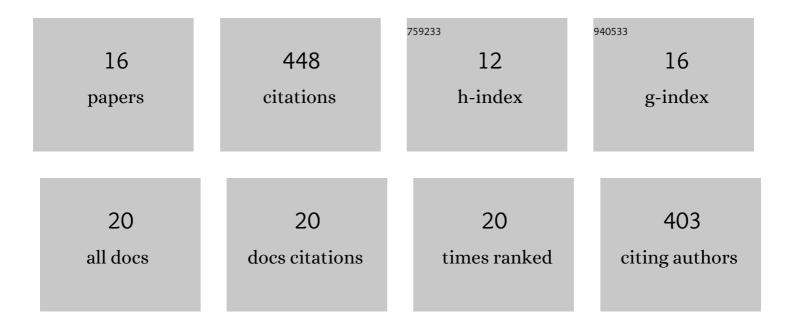
Kumar Paritosh

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Brassica juncea Genome Assemblies—Characteristics and Utilization. Compendium of Plant Genomes, 2022, , 241-255.	0.5	0
2	Comparative Analysis of Seed Transcriptome and Coexpression Analysis Reveal Candidate Genes for Enhancing Seed Size/Weight in Brassica juncea. Frontiers in Genetics, 2022, 13, 814486.	2.3	6
3	A chromosomeâ€scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. Plant Biotechnology Journal, 2021, 19, 602-614.	8.3	62
4	A highly contiguous genome assembly of Brassica nigra (BB) and revised nomenclature for the pseudochromosomes. BMC Genomics, 2020, 21, 887.	2.8	26
5	BjuWRR1, a CC-NB-LRR gene identified in Brassica juncea, confers resistance to white rust caused by Albugo candida. Theoretical and Applied Genetics, 2019, 132, 2223-2236.	3.6	50
6	Comparative genomics of Alternaria species provides insights into the pathogenic lifestyle of Alternaria brassicae – a pathogen of the Brassicaceae family. BMC Genomics, 2019, 20, 1036.	2.8	28
7	A Mapped Locus on LG A6 of Brassica juncea Line Tumida Conferring Resistance to White Rust Contains a CNL Type R Gene. Frontiers in Plant Science, 2019, 10, 1690.	3.6	24
8	Identification and characterization of the promoter of a gene expressing mainly in the tapetum tissue of cotton (Gossypium hirsutum L.). Plant Biotechnology Reports, 2018, 12, 377-388.	1.5	4
9	Identification of genic SSRs and construction of a SSR-based linkage map in Brassica juncea. Euphytica, 2017, 213, 1.	1.2	32
10	High Expression of Cry1Ac Protein in Cotton (Gossypium hirsutum) by Combining Independent Transgenic Events that Target the Protein to Cytoplasm and Plastids. PLoS ONE, 2016, 11, e0158603.	2.5	17
11	Tetralocular ovary and high silique width in yellow sarson lines of Brassica rapa (subspecies) Tj ETQq1 1 0.7843 Theoretical and Applied Genetics, 2014, 127, 2359-2369.	14 rgBT /O 3.6	verlock 10 Tf 17
12	RNA-seq based SNPs for mapping in Brassica juncea (AABB): synteny analysis between the two constituent genomes A (from B. rapa) and B (from B. nigra) shows highly divergent gene block arrangement and unique block fragmentation patterns. BMC Genomics, 2014, 15, 396.	2.8	61
13	Two Plastid DNA Lineages—Rapa/Oleracea and Nigra—within the Tribe Brassiceae Can Be Best Explained by Reciprocal Crosses at Hexaploidy: Evidence from Divergence Times of the Plastid Genomes and R-Block Genes of the A and B Genomes of Brassica juncea. PLoS ONE, 2014, 9, e93260.	2.5	22
14	Structural and Transcriptional Characterization of rbcS Genes of Cotton (Gossypium hirsutum). Plant Molecular Biology Reporter, 2013, 31, 1176-1183.	1.8	4
15	RNA-seq based SNPs in some agronomically important oleiferous lines of Brassica rapaand their use for genome-wide linkage mapping and specific-region fine mapping. BMC Genomics, 2013, 14, 463.	2.8	32
16	Detrimental effect of expression of Bt endotoxin Cry1Ac on in vitro regeneration, in vivo growth and development of tobacco and cotton transgenics. Journal of Biosciences, 2011, 36, 363-376.	1.1	42