

Kumar Paritosh

List of Publications by Year in descending order

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16
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403
citing authors

| # | 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 chromosome-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 siliqua width in yellow sarson lines of Brassica rapa (subspecies) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 Theoretical and Applied Genetics, 2014, 127, 2359-2369. | 3.6 | 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 rapa and 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 |