

Shouvik Das

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2610425/publications.pdf>

Version: 2024-02-01

23
papers

1,178
citations

471509

17
h-index

713466

21
g-index

23
all docs

23
docs citations

23
times ranked

1018
citing authors

#	ARTICLE	IF	CITATIONS
1	Deploying QTL-seq for rapid delineation of a potential candidate gene underlying major trait-associated QTL in chickpea. DNA Research, 2015, 22, 193-203.	3.4	140
2	Genetic dissection of seed-iron and zinc concentrations in chickpea. Scientific Reports, 2016, 6, 24050.	3.3	132
3	Employing genome-wide SNP discovery and genotyping strategy to extrapolate the natural allelic diversity and domestication patterns in chickpea. Frontiers in Plant Science, 2015, 6, 162.	3.6	104
4	Genome-wide high-throughput SNP discovery and genotyping for understanding natural (functional) allelic diversity and domestication patterns in wild chickpea. Scientific Reports, 2015, 5, 12468.	3.3	80
5	A genome-wide SNP scan accelerates trait-regulatory genomic loci identification in chickpea. Scientific Reports, 2015, 5, 11166.	3.3	76
6	Ultra-high density intra-specific genetic linkage maps accelerate identification of functionally relevant molecular tags governing important agronomic traits in chickpea. Scientific Reports, 2015, 5, 9468.	3.3	74
7	An Integrated Genomic Approach for Rapid Delineation of Candidate Genes Regulating Agro-Morphological Traits in Chickpea. DNA Research, 2014, 21, 695-710.	3.4	70
8	A combinatorial approach of comprehensive QTL-based comparative genome mapping and transcript profiling identified a seed weight-regulating candidate gene in chickpea. Scientific Reports, 2015, 5, 9264.	3.3	61
9	Genome-Wide Scans for Delineation of Candidate Genes Regulating Seed-Protein Content in Chickpea. Frontiers in Plant Science, 2016, 7, 302.	3.6	60
10	Natural Allelic Diversity, Genetic Structure and Linkage Disequilibrium Pattern in Wild Chickpea. PLoS ONE, 2014, 9, e107484.	2.5	59
11	A genome-scale integrated approach aids in genetic dissection of complex flowering time trait in chickpea. Plant Molecular Biology, 2015, 89, 403-420.	3.9	53
12	Genome-wide insertion-deletion (InDel) marker discovery and genotyping for genomics-assisted breeding applications in chickpea. DNA Research, 2015, 22, 377-386.	3.4	53
13	Genome-wide conserved non-coding microsatellite (CNMS) marker-based integrative genetical genomics for quantitative dissection of seed weight in chickpea. Journal of Experimental Botany, 2015, 66, 1271-1290.	4.8	46
14	mQTL-seq delineates functionally relevant candidate gene harbouring a major QTL regulating pod number in chickpea. DNA Research, 2016, 23, dsv036.	3.4	33
15	Development of genome-wide informative simple sequence repeat markers for large-scale genotyping applications in chickpea and development of web resource. Frontiers in Plant Science, 2015, 6, 645.	3.6	30
16	Genome-Wide Association Analysis for Phosphorus Use Efficiency Traits in Mungbean (<i>Vigna radiata</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10	3.6	28
17	A Genome-wide Combinatorial Strategy Dissects Complex Genetic Architecture of Seed Coat Color in Chickpea. Frontiers in Plant Science, 2015, 6, 979.	3.6	25
18	Identification of candidate genes for dissecting complex branch number trait in chickpea. Plant Science, 2016, 245, 61-70.	3.6	21

#	ARTICLE	IF	CITATIONS
19	Yield optimization, microbial load analysis, and sensory evaluation of mungbean (<i>Vigna radiata</i> L.), lentil (<i>Lens culinaris</i> subsp. <i>culinaris</i>), and Indian mustard (<i>Brassica juncea</i> L.) microgreens grown under greenhouse conditions. <i>PLoS ONE</i> , 2022, 17, e0268085.	2.5	13
20	Genetic Dissection of Phosphorous Uptake and Utilization Efficiency Traits Using GWAS in Mungbean. <i>Agronomy</i> , 2021, 11, 1401.	3.0	11
21	Genotype by Environment Interaction Effect on Grain Iron and Zinc Concentration of Indian and Mediterranean Lentil Genotypes. <i>Agronomy</i> , 2021, 11, 1761.	3.0	9
22	CNMS: The preferred genic markers for comparative genomic, molecular phylogenetic, functional genetic diversity and differential gene regulatory expression analyses in chickpea. <i>Journal of Biosciences</i> , 2015, 40, 579-592.	1.1	0
23	Revisiting the Decoded Genomes to Promptly Reveal their Genomic Perspectives. <i>Current Science</i> , 2017, 112, 279.	0.8	0