

# 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	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
2	Genetic Dissection of Phosphorous Uptake and Utilization Efficiency Traits Using GWAS in Mungbean. <i>Agronomy</i> , 2021, 11, 1401.	3.0	11
3	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
4	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
5	Revisiting the Decoded Genomes to Promptly Reveal their Genomic Perspectives. <i>Current Science</i> , 2017, 112, 279.	0.8	0
6	mQTL-seq delineates functionally relevant candidate gene harbouring a major QTL regulating pod number in chickpea. <i>DNA Research</i> , 2016, 23, dsv036.	3.4	33
7	Genome-Wide Scans for Delineation of Candidate Genes Regulating Seed-Protein Content in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 302.	3.6	60
8	Genetic dissection of seed-iron and zinc concentrations in chickpea. <i>Scientific Reports</i> , 2016, 6, 24050.	3.3	132
9	Identification of candidate genes for dissecting complex branch number trait in chickpea. <i>Plant Science</i> , 2016, 245, 61-70.	3.6	21
10	Genome-wide high-throughput SNP discovery and genotyping for understanding natural (functional) allelic diversity and domestication patterns in wild chickpea. <i>Scientific Reports</i> , 2015, 5, 12468.	3.3	80
11	Development of genome-wide informative simple sequence repeat markers for large-scale genotyping applications in chickpea and development of web resource. <i>Frontiers in Plant Science</i> , 2015, 6, 645.	3.6	30
12	A Genome-wide Combinatorial Strategy Dissects Complex Genetic Architecture of Seed Coat Color in Chickpea. <i>Frontiers in Plant Science</i> , 2015, 6, 979.	3.6	25
13	A genome-scale integrated approach aids in genetic dissection of complex flowering time trait in chickpea. <i>Plant Molecular Biology</i> , 2015, 89, 403-420.	3.9	53
14	A combinatorial approach of comprehensive QTL-based comparative genome mapping and transcript profiling identified a seed weight-regulating candidate gene in chickpea. <i>Scientific Reports</i> , 2015, 5, 9264.	3.3	61
15	Ultra-high density intra-specific genetic linkage maps accelerate identification of functionally relevant molecular tags governing important agronomic traits in chickpea. <i>Scientific Reports</i> , 2015, 5, 9468.	3.3	74
16	Deploying QTL-seq for rapid delineation of a potential candidate gene underlying major trait-associated QTL in chickpea. <i>DNA Research</i> , 2015, 22, 193-203.	3.4	140
17	Employing genome-wide SNP discovery and genotyping strategy to extrapolate the natural allelic diversity and domestication patterns in chickpea. <i>Frontiers in Plant Science</i> , 2015, 6, 162.	3.6	104
18	A genome-wide SNP scan accelerates trait-regulatory genomic loci identification in chickpea. <i>Scientific Reports</i> , 2015, 5, 11166.	3.3	76

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19	Genome-wide conserved non-coding microsatellite (CNMS) marker-based integrative genetical genomics for quantitative dissection of seed weight in chickpea. <i>Journal of Experimental Botany</i> , 2015, 66, 1271-1290.	4.8	46
20	Genome-wide insertion-deletion (InDel) marker discovery and genotyping for genomics-assisted breeding applications in chickpea. <i>DNA Research</i> , 2015, 22, 377-386.	3.4	53
21	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
22	Natural Allelic Diversity, Genetic Structure and Linkage Disequilibrium Pattern in Wild Chickpea. <i>PLoS ONE</i> , 2014, 9, e107484.	2.5	59
23	An Integrated Genomic Approach for Rapid Delineation of Candidate Genes Regulating Agro-Morphological Traits in Chickpea. <i>DNA Research</i> , 2014, 21, 695-710.	3.4	70