

# Joy Roy

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

370  
citations

1040056

9  
h-index

839539

18  
g-index

28  
all docs

28  
docs citations

28  
times ranked

329  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of SSR and SNP markers. , 2022, , 131-144.		3
2	Genetic variation, heritability, genetic advance, micronutrients, and grain morphology trait associations in EMS induced mutant lines of wheat ( <i>Triticum aestivum</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2141-2158.	1.6	3
3	Protein targeting to starch 1, a functional protein of starch biosynthesis in wheat ( <i>Triticum aestivum</i> ) Tj ETQq1 1 0.784314 rgBT /Over	3.9	7
4	High resistant starch mutant wheat â€”TAC 35â€”™ reduced glycemia and ameliorated high fat diet induced metabolic dysregulation in mice. <i>Journal of Cereal Science</i> , 2022, 105, 103459.	3.7	2
5	Whole genome re-sequencing of indian wheat genotypes for identification of genomic variants for grain iron and zinc content. <i>Molecular Biology Reports</i> , 2022, 49, 7123-7133.	2.3	3
6	<i>Trillium govianum</i> . , 2021, , 243-257.		0
7	Understanding the regulatory relationship of abscisic acid and bZIP transcription factors towards amylose biosynthesis in wheat. <i>Molecular Biology Reports</i> , 2021, 48, 2473-2483.	2.3	5
8	Gene Expression and Proteomics Studies Suggest an Involvement of Multiple Pathways Under Day and Night Combined Heat Stresses During Grain Filling in Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 660446.	3.6	10
9	Identification of multiple RNAs using feature fusion. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	1
10	Genome-wide analysis of RING-type E3 ligase family identifies potential candidates regulating high amylose starch biosynthesis in wheat ( <i>Triticum aestivum</i> L.). <i>Scientific Reports</i> , 2021, 11, 11461.	3.3	8
11	Genotyping-by-sequencing based QTL mapping identified a novel waxy allele contributing to high amylose starch in wheat. <i>Euphytica</i> , 2021, 217, 1.	1.2	4
12	Decoding the genome of superior chapatti quality Indian wheat variety â€”C 306â€”™ unravelled novel genomic variants for chapatti and nutrition quality related genes. <i>Genomics</i> , 2021, 113, 1919-1929.	2.9	5
13	Development and evaluation of chapatti quality of high amylose wheat mutants on the basis of physicochemical, textural and sensory characteristics. <i>LWT - Food Science and Technology</i> , 2020, 133, 110051.	5.2	7
14	Large-scale identification and characterization of phenolic compounds and their markerâ€”trait association in wheat. <i>Euphytica</i> , 2020, 216, 1.	1.2	12
15	Genome-wide identification and characterization of novel non-coding RNA-derived SSRs in wheat. <i>Molecular Biology Reports</i> , 2020, 47, 6111-6125.	2.3	12
16	Marker-trait association identified candidate starch biosynthesis pathway genes for starch and amyloseâ€”lipid complex gelatinization in wheat ( <i>Triticum aestivum</i> L.). <i>Euphytica</i> , 2020, 216, 1.	1.2	7
17	Development and characterization of bZIP transcription factor based SSRs in wheat. <i>Gene</i> , 2020, 756, 144912.	2.2	8
18	Sound as a stimulus in associative learning for heat stress in <i>Arabidopsis</i> . <i>Communicative and Integrative Biology</i> , 2020, 13, 1-5.	1.4	11

#	ARTICLE	IF	CITATIONS
19	Novel intron length polymorphic (ILP) markers from starch biosynthesis genes reveal genetic relationships in Indian wheat varieties and related species. <i>Molecular Biology Reports</i> , 2020, 47, 3485-3500.	2.3	12
20	Identification and characterization of long non-coding RNAs regulating resistant starch biosynthesis in bread wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2020, 112, 3065-3074.	2.9	21
21	Development of intron length polymorphic (ILP) markers in onion ( <i>Allium cepa</i> L.), and their cross-species transferability in garlic ( <i>A. sativum</i> L.) and wild relatives. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1379-1388.	1.6	27
22	Pivotal role of bZIPs in amylose biosynthesis by genome survey and transcriptome analysis in wheat ( <i>Triticum aestivum</i> L.) mutants. <i>Scientific Reports</i> , 2018, 8, 17240.	3.3	30
23	Comparative Analysis of Phenolic Compound Characterization and Their Biosynthesis Genes between Two Diverse Bread Wheat ( <i>Triticum aestivum</i> ) Varieties Differing for Chapatti (Unleavened Flat Bread) Quality. <i>Frontiers in Plant Science</i> , 2016, 7, 1870.	3.6	48
24	Development of EMS-induced mutation population for amylose and resistant starch variation in bread wheat ( <i>Triticum aestivum</i> ) and identification of candidate genes responsible for amylose variation. <i>BMC Plant Biology</i> , 2016, 16, 217.	3.6	54
25	Expression patterns of genes involved in starch biosynthesis during seed development in bread wheat ( <i>Triticum aestivum</i> ). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	32
26	Genome-wide transcriptome study in wheat identified candidate genes related to processing quality, majority of them showing interaction (quality x development) and having temporal and spatial distributions. <i>BMC Genomics</i> , 2014, 15, 29.	2.8	36