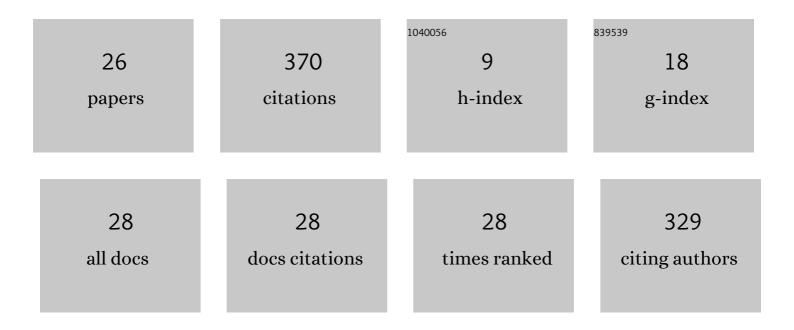


## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/210980/publications.pdf Version: 2024-02-01



#	Article	lF	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 (Triticum aestivum L.). Genetic Resources and Crop Evolution, 2022, 69, 2141-2158.	1.6	3
3	Protein targeting to starch 1, a functional protein of starch biosynthesis in wheat (Triticum aestivum) Tj ETQq1	1 0.784314	4 rgBT /Overle
4	High resistant starch mutant wheat †TAC 35' reduced glycemia and ameliorated high fat diet induced metabolic dysregulation in mice. Journal of Cereal Science, 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. Molecular Biology Reports, 2022, 49, 7123-7133.	2.3	3
6	Trillium govanianum. , 2021, , 243-257.		0
7	Understanding the regulatory relationship of abscisic acid and bZIP transcription factors towards amylose biosynthesis in wheat. Molecular Biology Reports, 2021, 48, 2473-2483.	2.3	5
8	Gene Expression and Proteomics Studies Suggest an Involvement of Multiple Pathways Under Day and Day–Night Combined Heat Stresses During Grain Filling in Wheat. Frontiers in Plant Science, 2021, 12, 660446.	3.6	10
9	Identification of multiple RNAs using feature fusion. Briefings in Bioinformatics, 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 (Triticum aestivum L.). Scientific Reports, 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. Euphytica, 2021, 217, 1.	1.2	4
12	Decoding the genome of superior chapatti quality Indian wheat variety â€~C 306' unravelled novel genomic variants for chapatti and nutrition quality related genes. Genomics, 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. LWT - Food Science and Technology, 2020, 133, 110051.	5.2	7
14	Large-scale identification and characterization of phenolic compounds and their marker–trait association in wheat. Euphytica, 2020, 216, 1.	1.2	12
15	Genome-wide identification and characterization of novel non-coding RNA-derived SSRs in wheat. Molecular Biology Reports, 2020, 47, 6111-6125.	2.3	12
16	Marker-trait association identified candidate starch biosynthesis pathway genes for starch and amylose–lipid complex gelatinization in wheat (Triticum aestivum L.). Euphytica, 2020, 216, 1.	1.2	7
17	Development and characterization of bZIP transcription factor based SSRs in wheat. Gene, 2020, 756, 144912.	2.2	8
18	Sound as a stimulus in associative learning for heat stress in Arabidopsis. Communicative and Integrative Biology, 2020, 13, 1-5.	1.4	11

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