

Anil Kumar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3915706/publications.pdf>

Version: 2024-02-01

50
papers

1,549
citations

236925

25
h-index

330143

37
g-index

52
all docs

52
docs citations

52
times ranked

1073
citing authors

#	ARTICLE	IF	CITATIONS
1	Seed Priming with Iron Oxide Nanoparticles Triggers Iron Acquisition and Biofortification in Wheat (<i>Triticum aestivum</i> L.) Grains. <i>Journal of Plant Growth Regulation</i> , 2019, 38, 122-131.	5.1	103
2	Comparative Genomics and Association Mapping Approaches for Blast Resistant Genes in Finger Millet Using SSRs. <i>PLoS ONE</i> , 2014, 9, e99182.	2.5	72
3	Plant ionomics: a newer approach to study mineral transport and its regulation. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 2641-2653.	2.1	65
4	Development and molecular characterization of genic molecular markers for grain protein and calcium content in finger millet (<i>Eleusine coracana</i> (L.) Gaertn.). <i>Molecular Biology Reports</i> , 2014, 41, 1189-1200.	2.3	65
5	Gene Discovery and Advances in Finger Millet [<i>Eleusine coracana</i> (L.) Gaertn.] Genomics—An Important Nutri-Cereal of Future. <i>Frontiers in Plant Science</i> , 2016, 7, 1634.	3.6	63
6	Comparative genomics and association mapping approaches for opaque2 modifier genes in finger millet accessions using genic, genomic and candidate gene-based simple sequence repeat markers. <i>Molecular Breeding</i> , 2014, 34, 1261-1279.	2.1	61
7	Transcriptome Wide Identification and Validation of Calcium Sensor Gene Family in the Developing Spikes of Finger Millet Genotypes for Elucidating Its Role in Grain Calcium Accumulation. <i>PLoS ONE</i> , 2014, 9, e103963.	2.5	55
8	Genotyping-by-Sequencing Analysis for Determining Population Structure of Finger Millet Germplasm of Diverse Origins. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0058.	2.8	55
9	Transcriptional expression analysis of genes involved in regulation of calcium translocation and storage in finger millet (<i>Eleusine coracana</i> L. Gaertn.). <i>Gene</i> , 2014, 550, 171-179.	2.2	51
10	Association mapping of agro-morphological characters among the global collection of finger millet genotypes using genomic SSR markers. <i>Molecular Biology Reports</i> , 2014, 41, 5287-5297.	2.3	51
11	Phenomics and genomics of finger millet: current status and future prospects. <i>Planta</i> , 2019, 250, 731-751.	3.2	51
12	Genome wide association mapping of agro-morphological traits among a diverse collection of finger millet (<i>Eleusine coracana</i> L.) genotypes using SNP markers. <i>PLoS ONE</i> , 2018, 13, e0199444.	2.5	46
13	Efficiency of RAPD, SSR and Cytochrome P450 gene based markers in accessing genetic variability amongst finger millet (<i>Eleusine coracana</i>) accessions. <i>Molecular Biology Reports</i> , 2010, 37, 4075-4082.	2.3	39
14	Nitrate signals determine the sensing of nitrogen through differential expression of genes involved in nitrogen uptake and assimilation in finger millet. <i>Functional and Integrative Genomics</i> , 2013, 13, 179-190.	3.5	39
15	Functional markers based molecular characterization and cloning of resistance gene analogs encoding NBS-LRR disease resistance proteins in finger millet (<i>Eleusine coracana</i>). <i>Molecular Biology Reports</i> , 2011, 38, 3427-3436.	2.3	37
16	Use of SSR, RAPD markers and protein profiles based analysis to differentiate <i>Eleusine coracana</i> genotypes differing in their protein content. <i>Molecular Biology Reports</i> , 2012, 39, 4949-4960.	2.3	36
17	Isolation, Characterization and Immunolocalization of a Seed Dominant CaM from Finger Millet (<i>Eleusine coracana</i> L. Gaertn.) for Studying Its Functional Role in Differential Accumulation of Calcium in Developing Grains. <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 2955-2973.	2.9	36
18	Fluctuation of Dof1/Dof2 expression ratio under the influence of varying nitrogen and light conditions: involvement in differential regulation of nitrogen metabolism in two genotypes of finger millet (<i>Eleusine coracana</i> L.). <i>Gene</i> , 2014, 546, 327-335.	2.2	36

#	ARTICLE	IF	CITATIONS
19	Calcium transport from source to sink: understanding the mechanism(s) of acquisition, translocation, and accumulation for crop biofortification. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	2.1	36
20	In-silico mining, type and frequency analysis of genic microsatellites of finger millet (<i>Eleusine</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 <i>Molecular Biology Reports</i> , 2014, 41, 3081-3090.	2.3	34
21	Identification and characterization of calcium transporter gene family in finger millet in relation to grain calcium content. <i>Gene</i> , 2015, 566, 37-46.	2.2	32
22	Genome-Wide Comparative in silico Analysis of Calcium Transporters of Rice and Sorghum. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 138-150.	6.9	31
23	Influence of different nitrogen inputs on the members of ammonium transporter and glutamine synthetase genes in two rice genotypes having differential responsiveness to nitrogen. <i>Molecular Biology Reports</i> , 2012, 39, 8035-8044.	2.3	29
24	Modeling of the jasmonate signaling pathway in <i>Arabidopsis thaliana</i> with respect to pathophysiology of <i>Alternaria</i> blight in Brassica. <i>Scientific Reports</i> , 2017, 7, 16790.	3.3	28
25	Understanding the differential nitrogen sensing mechanism in rice genotypes through expression analysis of high and low affinity ammonium transporter genes. <i>Molecular Biology Reports</i> , 2012, 39, 2233-2241.	2.3	27
26	Simple sequence repeat (SSR) analysis in relation to calcium transport and signaling genes reveals transferability among grasses and a conserved behavior within finger millet genotypes. <i>Plant Systematics and Evolution</i> , 2014, 300, 1561-1568.	0.9	26
27	Molecular characterization of EcCIPK24 gene of finger millet (<i>Eleusine coracana</i>) for investigating its regulatory role in calcium transport. <i>3 Biotech</i> , 2017, 7, 267.	2.2	26
28	Genome-wide association mapping for seed protein content in finger millet (<i>Eleusine coracana</i>) global collection through genotyping by sequencing. <i>Journal of Cereal Science</i> , 2020, 91, 102888.	3.7	25
29	Identification of genes involved in carbon metabolism from <i>Eleusine coracana</i> (L.) for understanding their light-mediated entrainment and regulation. <i>Plant Cell Reports</i> , 2014, 33, 1403-1411.	5.6	23
30	Draft genome sequence of Karnal bunt pathogen (<i>Tilletia indica</i>) of wheat provides insights into the pathogenic mechanisms of quarantined fungus. <i>PLoS ONE</i> , 2017, 12, e0171323.	2.5	22
31	Augmentation of crop productivity through interventions of omics technologies in India: challenges and opportunities. <i>3 Biotech</i> , 2018, 8, 454.	2.2	21
32	Integrated proteomics, genomics, metabolomics approaches reveal oxalic acid as pathogenicity factor in <i>Tilletia indica</i> inciting Karnal bunt disease of wheat. <i>Scientific Reports</i> , 2018, 8, 7826.	3.3	21
33	Jasmonate signal induced expression of cystatin genes for providing resistance against Karnal bunt in wheat. <i>Plant Signaling and Behavior</i> , 2011, 6, 821-830.	2.4	18
34	Transcriptome-wide identification of genes involved in Ascorbateâ€“Glutathione cycle (Halliwellâ€“Asada pathway) and related pathway for elucidating its role in antioxidative potential in finger millet (<i>Eleusine coracana</i> (L.)). <i>3 Biotech</i> , 2018, 8, 499.	2.2	17
35	Complementary Proteomics, Genomics approaches identifies potential pathogenicity/virulence factors in <i>Tilletia indica</i> induced under the influence of host factor. <i>Scientific Reports</i> , 2019, 9, 553.	3.3	16
36	Comparative genomic analysis of monosporidial and monoteliosporic cultures for unraveling the complexity of molecular pathogenesis of <i>Tilletia indica</i> pathogen of wheat. <i>Scientific Reports</i> , 2019, 9, 8185.	3.3	16

#	ARTICLE	IF	CITATIONS
37	Spatial distribution pattern analysis of Dof1 transcription factor in different tissues of three Eleusine coracana genotypes differing in their grain colour, yield and photosynthetic efficiency. Molecular Biology Reports, 2012, 39, 2089-2095.	2.3	15
38	Secretome Analysis Identifies Potential Pathogenicity/Virulence Factors of <i>Tilletia indica</i> , a Quarantined Fungal Pathogen Inciting Karnal Bunt Disease in Wheat. Proteomics, 2018, 18, e1700473.	2.2	15
39	Identification and molecular characterization of Dof transcription factor gene family preferentially expressed in developing spikes of Eleusine coracana L.. 3 Biotech, 2018, 8, 82.	2.2	15
40	Molecular and Phenotypic Characterization of 149 Finger Millet Accessions Using Microsatellite and Agro-Morphological Markers. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2017, 87, 1217-1228.	1.0	13
41	Cloning, in silico characterization and induction of TiKpp2 MAP kinase in <i>Tilletia indica</i> under the influence of host factor(s) from wheat spikes. Molecular Biology Reports, 2013, 40, 4967-4978.	2.3	12
42	Determination of calcium responsiveness towards exogenous application in two genotypes of Eleusine coracana L. differing in their grain calcium content. Acta Physiologiae Plantarum, 2014, 36, 2521-2529.	2.1	11
43	Identification and characterization of finger millet OPAQUE2 transcription factor gene under different nitrogen inputs for understanding their role during accumulation of prolamin seed storage protein. 3 Biotech, 2018, 8, 163.	2.2	11
44	Identification and validation of candidate genes for high calcium content in finger millet [<i>Eleusine coracana</i> (L.) Gaertn.] through genome-wide association study. Journal of Cereal Science, 2022, 107, 103517.	3.7	11
45	Improved Draft Genome Sequence of a Monoteliosporic Culture of the Karnal Bunt (<i>Tilletia indica</i>) Pathogen of Wheat. Genome Announcements, 2018, 6, .	0.8	8
46	Systems biology of seeds: decoding the secret of biochemical seed factories for nutritional security. 3 Biotech, 2018, 8, 460.	2.2	8
47	Computational analysis of microarray data of <i>Arabidopsis thaliana</i> challenged with <i>Alternaria brassicicola</i> for identification of key genes in Brassica. Journal of Genetic Engineering and Biotechnology, 2020, 18, 17.	3.3	7
48	Transcriptome wide identification and characterization of regulatory genes involved in EAA metabolism and validation through expression analysis in different developmental stages of finger millet spikes. 3 Biotech, 2020, 10, 347.	2.2	6
49	Comparative analysis of ROS-scavenging gene families in finger millet, rice, sorghum, and foxtail millet revealed potential targets for antioxidant activity and drought tolerance improvement. Network Modeling Analysis in Health Informatics and Bioinformatics, 2020, 9, 1.	2.1	6
50	Isolation and Characterization of Oviduct-specific Glycoproteins from Ampulla and Isthmus Parts of Cyclic and Acyclic Buffalo for Studying Differential Microenvironment. Applied Biochemistry and Biotechnology, 2012, 166, 1814-1830.	2.9	2