Reyaz Mir

List of Publications by Year
in descending order

88 papers	3,373 citations	218677 26 h-index	168389 53 g-index
101 all docs	101 docs citations	101 times ranked	3525 citing authors

#	Article	IF	Citations
1	Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. Theoretical and Applied Genetics, 2012, 125, 625-645.	3.6	397
2	Array-based high-throughput DNA markers for crop improvement. Heredity, 2008, 101, 5-18.	2.6	285
3	Marker-assisted wheat breeding: present status and future possibilities. Molecular Breeding, 2010, 26, 145-161.	2.1	245
4	Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (Arachis hypogaea L.). Theoretical and Applied Genetics, 2011, 122, 1119-1132.	3.6	188
5	Wheat Genomics: Present Status and Future Prospects. International Journal of Plant Genomics, 2008, 2008, 1-36.	2.2	178
6	High-throughput phenotyping for crop improvement in the genomics era. Plant Science, 2019, 282, 60-72.	3.6	176
7	Prehospital transdermal glyceryl trinitrate in patients with ultra-acute presumed stroke (RIGHT-2): an ambulance-based, randomised, sham-controlled, blinded, phase 3 trial. Lancet, The, 2019, 393, 1009-1020.	13.7	119
8	Genetic dissection of grain weight in bread wheat through quantitative trait locus interval and association mapping. Molecular Breeding, 2012, 29, 963-972.	2.1	92
9	Genome-wide QTL analysis for pre-harvest sprouting tolerance in bread wheat. Euphytica, 2009, 168, 319-329.	1.2	86
10	Introgression of a major gene for high grain protein content in some Indian bread wheat cultivars. Field Crops Research, 2011, 123, 226-233.	5.1	83
11	Genomics-assisted breeding for drought tolerance in chickpea. Functional Plant Biology, 2014, 41, 1178.	2.1	75
12	Genome Wide Single Locus Single Trait, Multi-Locus and Multi-Trait Association Mapping for Some Important Agronomic Traits in Common Wheat (T. aestivum L.). PLoS ONE, 2016, 11, e0159343.	2.5	72
13	Association mapping for pre-harvest sprouting tolerance in common wheat (Triticum aestivum L.). Euphytica, 2012, 188, 89-102.	1.2	69
14	A preliminary genetic analysis of fibre traits and the use of new genomic SSRs for genetic diversity in jute. Euphytica, 2008, 161, 413-427.	1.2	62
15	Candidate gene analysis for determinacy in pigeonpea (Cajanus spp.). Theoretical and Applied Genetics, 2014, 127, 2663-2678.	3.6	59
16	Marker-assisted pyramiding of eight QTLs/genes for seven different traits in common wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.1	57
17	Interval mapping and meta-QTL analysis of grain traits in common wheat (Triticum aestivum L.). Euphytica, 2015, 201, 367-380.	1.2	55
18	Markerâ€assisted selection for preâ€harvest sprouting tolerance and leaf rust resistance in bread wheat. Plant Breeding, 2010, 129, 617-621.	1.9	51

#	Article	IF	Citations
19	Integrated physical, genetic and genome map of chickpea (Cicer arietinum L.). Functional and Integrative Genomics, 2014, 14, 59-73.	3.5	49
20	Development and Characterization of Largeâ€Scale Simple Sequence Repeats in Jute. Crop Science, 2009, 49, 1687-1694.	1.8	47
21	Development of SSR markers and construction of a linkage map in jute. Journal of Genetics, 2012, 91, 21-31.	0.7	44
22	SSR and RAPD analysis of genetic diversity in walnut (Juglans regia L.) genotypes from Jammu and Kashmir, India. Physiology and Molecular Biology of Plants, 2012, 18, 149-160.	3.1	38
23	Altered Expression of an FT Cluster Underlies a Major Locus Controlling Domestication-Related Changes to Chickpea Phenology and Growth Habit. Frontiers in Plant Science, 2019, 10, 824.	3.6	38
24	Improving protein content and nutrition quality.. , 2011, , 314-328.		38
25	A study of genetic diversity among Indian bread wheat (Triticum aestivum L.) cultivars released during last 100Âyears. Genetic Resources and Crop Evolution, 2012, 59, 717-726.	1.6	37
26	Comprehensive Mechanism of Gene Silencing and Its Role in Plant Growth and Development. Frontiers in Plant Science, 2021, 12, 705249.	3.6	36
27	Evolving Molecular Marker Technologies in Plants: From RFLPs to GBS. , 2013, , 229-247.		35
28	Gene/QTL discovery for Anthracnose in common bean (Phaseolus vulgaris L.) from North-western Himalayas. PLoS ONE, 2018, 13, e0191700.	2.5	34
29	QTL analysis for some quantitative traits in bread wheat. Journal of Zhejiang University: Science B, 2007, 8, 807-814.	2.8	33
30	Heat Stress-Mediated Constraints in Maize (Zea mays) Production: Challenges and Solutions. Frontiers in Plant Science, 2022, 13, .	3.6	31
31	Plant microRNAs: biogenesis, gene silencing, web-based analysis tools and their use as molecular markers. 3 Biotech, 2019, 9, 413.	2.2	29
32	Proteomics for abiotic stresses in legumes: present status and future directions. Critical Reviews in Biotechnology, 2023, 43, 171-190.	9.0	26
33	Allelic Diversity, Structural Analysis, and Genome-Wide Association Study (GWAS) for Yield and Related Traits Using Unexplored Common Bean (Phaseolus vulgaris L.) Germplasm From Western Himalayas. Frontiers in Genetics, 2020, 11, 609603.	2.3	25
34	Development and use of miRNA-derived SSR markers for the study of genetic diversity, population structure, and characterization of genotypes for breeding heat tolerant wheat varieties. PLoS ONE, 2021, 16, e0231063.	2.5	25
35	An Update on Resistance Genes and Their Use in the Development of Leaf Rust Resistant Cultivars in Wheat. Frontiers in Genetics, 2022, 13, 816057.	2.3	25
36	Discovery of miRNAs and Development of Heat-Responsive miRNA-SSR Markers for Characterization of Wheat Germplasm for Terminal Heat Tolerance Breeding. Frontiers in Genetics, 2021, 12, 699420.	2.3	22

#	Article	IF	Citations
37	QTL identification for molecular breeding of fibre yield and fibre quality traits in jute. Euphytica, 2012, 187, 175-189.	1.2	21
38	Array-Based High-Throughput DNA Markers and Genotyping Platforms for Cereal Genetics and Genomics. , 2013, , 11-55.		20
39	Insight into the origin of common bean (Phaseolus vulgaris L.) grown in the state of Jammu and Kashmir of north-western Himalayas. Genetic Resources and Crop Evolution, 2018, 65, 963-977.	1.6	20
40	Advances in Molecular Markers and Their Use in Genetic Improvement of Wheat. , 2021, , 139-174.		19
41	QTL Mapping: Methodology and Applications in Cereal Breeding. , 2013, , 275-318.		18
42	Genotyping-by-sequencing and multilocation evaluation of two interspecific backcross populations identify QTLs for yield-related traits in pigeonpea. Theoretical and Applied Genetics, 2020, 133, 737-749.	3.6	18
43	Approaches for gene targeting and targeted gene expression in plants. GM Crops, 2011, 2, 150-162.	1.9	16
44	Wholeâ€genome scanning for mapping determinacy in Pigeonpea (Cajanus spp.). Plant Breeding, 2013, 132, 472-478.	1.9	15
45	Multi-locus genome-wide association studies (ML-GWAS) reveal novel genomic regions associated with seedling and adult plant stage leaf rust resistance in bread wheat (Triticum aestivum L.). Heredity, 2022, 128, 434-449.	2.6	15
46	Assessment of cold tolerance in chickpea (Cicer spp.) grown under cold/freezing weather conditions of North-Western Himalayas of Jammu and Kashmir, India. Physiology and Molecular Biology of Plants, 2021, 27, 1105-1118.	3.1	14
47	Functional Dissection of the Chickpea (Cicer arietinum L.) Stay-Green Phenotype Associated with Molecular Variation at an Ortholog of Mendelâ€™s I Gene for Cotyledon Color: Implications for Crop Production and Carotenoid Biofortification. International Journal of Molecular Sciences, 2019, 20, 5562.	4.1	13
48	Assessment of molecular genetic diversity of 384 chickpea genotypes and development of core set of 192 genotypes for chickpea improvement programs. Genetic Resources and Crop Evolution, 2022, 69, 1193-1205.	1.6	13
49	Characterization of common bean (<scp>Phaseolus vulgaris</scp> L.) germplasm for morphological and seed nutrient traits from Western Himalayas. , 2021, 3, e86.		11
50	Development and characterization of nitrogen and phosphorus use efficiency responsive genic and miRNA derived SSR markers in wheat. Heredity, 2022, 128, 391-401.	2.6	11
51	Validation of QTL for grain weight using MAS-derived pairs of NILs in bread wheat (Triticum aestivum) Tj ETQq1 1 0.784314 rgBT /Ove	1.7	9
52			

#	Article	IF	Citations
55			

#	Article	IF	Citations
73	Molecular and phenotypic characterization of variation related to pea enation mosaic virus resistance in lentil (Lens culinaris Medik.). Canadian Journal of Plant Science, 2014, 94, 1333-1344.	0.9	2
74	Genetic and Genomic Resources in Rice Bean (Vigna umbellata Thunb.): Availability, Advancements, and Applications. , 2021, , 191-202.		2
75	Editorial: Genetics and Genomics to Enhance Crop Production, Towards Food Security. Frontiers in Genetics, 2021, 12, 798308.	2.3	2
76	Exploration, collection and characterization of Kala zeera (Bunium persicum Boiss. Fedtsch.) germplasm from northwestern Himalayas. Plant Genetic Resources: Characterisation and Utilisation, 2022, 20, 62-65.	0.8	2
77	Identification of Sources of Resistance in Chickpea (Cicer arietinum) against Wilt (Fusarium) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf of Current Microbiology and Applied Sciences, 2018, 7, 190-194.	0.1	1
78	Physical localization of 45S rDNA in Cymbopogon and the analysis of differential distribution of rDNA in homologous chromosomes of Cymbopogon winterianus. PLoS ONE, 2021, 16, e0257115.	2.5	1
79	Cytogenetics to functional genomics: six decades journey of Professor P.K. Gupta. Plant Biotechnology Journal, 2022, , .	8.3	1
80	Validation of Early Dynamic Model (EDM) in Predicting the Outcome of Acute Liver Failure (ALF): A Prospective Study. Journal of Clinical and Experimental Hepatology, 2015, 5, S8-S9.	0.9	0
81	Genomic-assisted breeding for abiotic stress tolerance in horticultural crops. , 2021, , 91-118.		0
82	Cronkhite-Canada syndrome: A rare form of gastrointestinal polyposis causing malabsorption. International Journal of Health & Allied Sciences, 2014, 3, 70.	0.1	0
83	Morphological Diversity and Yellow Rust Resistance in Bread Wheat Germplasm Lines. Journal of Cereal Research, 2018, 9, .	0.2	0
84	Identification of Sources of Resistance against Wilt (Fusarium oxysporum f. sp. ciceri) in Chickpea Genotypes under Temperate Agro-Climatic Conditions of Kashmir. International Journal of Current Microbiology and Applied Sciences, 2018, 7, 195-199.	0.1	0
85	Productivity and resilience based indices for identification of water stress resilient genotypes in cowpea (Vigna unguiculata L.). Agricultural Reviews, 2019, , .	0.1	0
86	Characterising response of root and shoot traits in cowpea (Vigna unguiculata L.) under water stress in laboratory and greenhouse. Agricultural Research Journal, 2020, 57, 315.	0.2	0
87	Assessment of variability in phenological, morphological and yield traits in a biparental RIL population in wheat (Triticum aestivum L). Electronic Journal of Plant Breeding, 2020, 11, .	0.1	0
88	Evaluation of stress tolerance indices in huw-234 x huw-468 derived wheat (Triticum aestivum L.) ril mapping population for identification of heat tolerant genotypes. Applied Biological Research, 2020, 22, 184.	0.2	0