# Mir Asif Iquebal

## List of Publications by Citations

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|---|---|---|---|
| 78<br>papers | 524<br>citations | 13<br>h-index | 18<br>g-index |
| 92<br>ext. papers | 804<br>ext. citations | 3.6<br>avg, IF | 3.74<br>L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 78 | RNAseq analysis reveals drought-responsive molecular pathways with candidate genes and putative molecular markers in root tissue of wheat. *Scientific Reports*, **2019**, 9, 13917 | 4.9 | 38 |
| 77 | Transcriptomic signature of drought response in pearl millet (Pennisetum glaucum (L.) and development of web-genomic resources. *Scientific Reports*, **2018**, 8, 3382 | 4.9 | 31 |
| 76 | Biotic stress resistance in agriculture through antimicrobial peptides. *Peptides*, **2012**, 36, 322-30 | 3.8 | 29 |
| 75 | Uncovering Genomic Regions Associated With 36 Agro-Morphological Traits in Indian Spring Wheat Using GWAS. *Frontiers in Plant Science*, **2019**, 10, 527 | 6.2 | 25 |
| 74 | Genome-Wide Association Studies in Diverse Spring Wheat Panel for Stripe, Stem, and Leaf Rust Resistance. *Frontiers in Plant Science*, **2020**, 11, 748 | 6.2 | 21 |
| 73 | First whole genome based microsatellite DNA marker database of tomato for mapping and variety identification. *BMC Plant Biology*, **2013**, 13, 197 | 5.3 | 20 |
| 72 | Putative Microsatellite DNA Marker-Based Wheat Genomic Resource for Varietal Improvement and Management. *Frontiers in Plant Science*, **2017**, 8, 2009 | 6.2 | 17 |
| 71 | Effects of weed control strategy on weed dynamics, soybean productivity and profitability under conservation agriculture in India. *Field Crops Research*, **2017**, 210, 61-70 | 5.5 | 16 |
| 70 | Origin, Diversity and Genome Sequence of Mango (Mangifera indica L.). *Indian Journal of History of Science*, **2016**, 51, |  | 15 |
| 69 | MiSNPDb: a web-based genomic resources of tropical ecology fruit mango (Mangifera indica L.) for phylogeography and varietal differentiation. *Scientific Reports*, **2017**, 7, 14968 | 4.9 | 14 |
| 68 | Discovery of Putative Herbicide Resistance Genes and Its Regulatory Network in Chickpea Using Transcriptome Sequencing. *Frontiers in Plant Science*, **2017**, 8, 958 | 6.2 | 14 |
| 67 | Harmonizing technological advances in phenomics and genomics for enhanced salt tolerance in rice from a practical perspective. *Rice*, **2019**, 12, 89 | 5.8 | 14 |
| 66 | Characterization of genetic diversity and population structure in wheat using array based SNP markers. *Molecular Biology Reports*, **2020**, 47, 293-306 | 2.8 | 13 |
| 65 | Seasonal parasitism and biological characteristics of Habrobracon hebetor (Hymenoptera: Braconidae) a potential larval ectoparasitoid of Helicoverpa armigera (Lepidoptera: Noctuidae) in a chickpea ecosystem. *Biocontrol Science and Technology*, **2012**, 22, 305-318 | 1.7 | 12 |
| 64 | In silico mining of putative microsatellite markers from whole genome sequence of water buffalo (Bubalus bubalis) and development of first BuffSatDB. *BMC Genomics*, **2013**, 14, 43 | 4.5 | 11 |
| 63 | Evidence of salicylic acid pathway with EDS1 and PAD4 proteins by molecular dynamics simulation for grape improvement. *Journal of Biomolecular Structure and Dynamics*, **2015**, 33, 2180-91 | 3.6 | 10 |
| 62 | Draft whole genome sequence of groundnut stem rot fungus Athelia rolfsii revealing genetic architect of its pathogenicity and virulence. *Scientific Reports*, **2017**, 7, 5299 | 4.9 | 10 |

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| 61 | Recycling of Organic Waste through Four Different Composts for Disease Suppression and Growth Enhancement in Mung Beans. *Clean - Soil, Air, Water*, **2015**, 43, 1066-1071 | 1.6 | 10 |
| 60 | Development of Antimicrobial Peptide Prediction Tool for Aquaculture Industries. *Probiotics and Antimicrobial Proteins*, **2016**, 8, 141-9 | 5.5 | 10 |
| 59 | Assembly and Genome-Wide SNP Discovery in Rohu Carp,. *Frontiers in Genetics*, **2020**, 11, 386 | 4.5 | 9 |
| 58 | Locus minimization in breed prediction using artificial neural network approach. *Animal Genetics*, **2014**, 45, 898-902 | 2.5 | 9 |
| 57 | Selection of pigeonpea genotypes for tolerance to aluminium toxicity. *Plant Breeding*, **2011**, 130, 492-495 | 2.4 | 9 |
| 56 | Draft Genome Sequence of Two Monosporidial Lines of the Karnal Bunt Fungus Tilletia indica Mitra (PSWKBGH-1 and PSWKBGH-2). *Genome Announcements*, **2016**, 4, | | 9 |
| 55 | Muscle transcriptome signature and gene regulatory network analysis in two divergent lines of a hilly bovine species Mithun (Bos frontalis). *Genomics*, **2020**, 112, 252-262 | 4.3 | 9 |
| 54 | The role of conserved residues in the catalytic activity of NDM-1: an approach involving site directed mutagenesis and molecular dynamics. *Physical Chemistry Chemical Physics*, **2019**, 21, 17821-17835 | 3.6 | 8 |
| 53 | Development of model web-server for crop variety identification using throughput SNP genotyping data. *Scientific Reports*, **2019**, 9, 5122 | 4.9 | 7 |
| 52 | Development of transcriptome based web genomic resources of yellow mosaic disease in. *Physiology and Molecular Biology of Plants*, **2017**, 23, 767-777 | 2.8 | 7 |
| 51 | PIPEMicroDB: microsatellite database and primer generation tool for pigeonpea genome. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bas054 | 5 | 7 |
| 50 | Transcriptome analysis of Snow Mountain Garlic for unraveling the organosulfur metabolic pathway. *Genomics*, **2020**, 112, 99-107 | 4.3 | 7 |
| 49 | Deciphering genes associated with root wilt disease of coconut and development of its transcriptomic database (CnTDB). *Physiological and Molecular Plant Pathology*, **2017**, 100, 255-263 | 2.6 | 6 |
| 48 | Assembly and variation analyses of Clarias batrachus mitogenome retrieved from WGS data and its phylogenetic relationship with other catfishes. *Meta Gene*, **2015**, 5, 105-14 | 0.7 | 6 |
| 47 | The Onion Genomic Resource: A genomics and bioinformatics driven resource for onion breeding. *Plant Gene*, **2016**, 8, 9-15 | 3.1 | 6 |
| 46 | Transcriptomic signature reveals mechanism of flower bud distortion in witches'-broom disease of soybean (Glycine max). *BMC Plant Biology*, **2019**, 19, 26 | 5.3 | 6 |
| 45 | Revealing liver specific microRNAs linked with carbohydrate metabolism of farmed carp, Labeo rohita (Hamilton, 1822). *Genomics*, **2020**, 112, 32-44 | 4.3 | 6 |
| 44 | The genome of walking catfish Clarias magur (Hamilton, 1822) unveils the genetic basis that may have facilitated the development of environmental and terrestrial adaptation systems in air-breathing catfishes. *DNA Research*, **2021**, 28, | 4.5 | 6 |

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| 43 | VigSatDB: genome-wide microsatellite DNA marker database of three species of Vigna for germplasm characterization and improvement. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019, | 5 | 5 |
| 42 | Development of a model webserver for breed identification using microsatellite DNA marker. *BMC Genetics*, **2013**, 14, 118 | 2.6 | 5 |
| 41 | A meta-analysis of potential candidate genes associated with salinity stress tolerance in rice. *Agri Gene*, **2016**, 1, 126-134 | 1.9 | 5 |
| 40 | Computational deciphering of biotic stress associated genes in tomato (). *Genomics Data*, **2017**, 14, 82-90 | | 4 |
| 39 | BanSatDB, a whole-genome-based database of putative and experimentally validated microsatellite markers of three Musa species. *Crop Journal*, **2018**, 6, 642-650 | 4.6 | 4 |
| 38 | SBMDb: first whole genome putative microsatellite DNA marker database of sugarbeet for bioenergy and industrial applications. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015, | 5 | 4 |
| 37 | : A Universal Web-Tool for Rapid Polymorphic Microsatellite Marker Discovery From Whole Genome and Transcriptome Data. *Frontiers in Plant Science*, **2018**, 9, 1966 | 6.2 | 4 |
| 36 | Development of species specific putative miRNA and its target prediction tool in wheat (Triticum aestivum L.). *Scientific Reports*, **2019**, 9, 3790 | 4.9 | 3 |
| 35 | Species specific approach to the development of web-based antimicrobial peptides prediction tool for cattle. *Computers and Electronics in Agriculture*, **2015**, 111, 55-61 | 6.5 | 3 |
| 34 | Bootstrap study of parameter estimates for nonlinear Richards growth model through genetic algorithm. *Journal of Applied Statistics*, **2011**, 38, 491-500 | 1 | 3 |
| 33 | An insight into molecular interaction of PGIP with PG for banana cultivar. *Frontiers in Bioscience - Landmark*, **2020**, 25, 335-362 | 2.8 | 3 |
| 32 | Prediction of MHC Binding Peptides and Epitopes from Coat Protein of Mungbean Yellow Mosaic India Virus-Ub05. *Journal of Proteomics and Bioinformatics*, **2010**, 03, 173-178 | 2.1 | 3 |
| 31 | Comparative transcriptome profiling reveals the basis of differential sheath blight disease response in tolerant and susceptible rice genotypes. *Protoplasma*, **2021**, 1 | 3.4 | 3 |
| 30 | De novo transcriptome sequencing assisted identification of terpene synthases from black pepper () berry. *Physiology and Molecular Biology of Plants*, **2021**, 27, 1153-1161 | 2.8 | 3 |
| 29 | Genome Wide Prediction, Mapping and Development of Genomic Resources of Mastitis Associated Genes in Water Buffalo. *Frontiers in Veterinary Science*, **2021**, 8, 593871 | 3.1 | 3 |
| 28 | Low-depth shotgun sequencing resolves complete mitochondrial genome sequence of Labeo rohita. *Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis*, **2016**, 27, 3517-8 | 1.3 | 2 |
| 27 | Transcriptomic signature of Fusarium toxin in chickpea unveiling wilt pathogenicity pathways and marker discovery. *Physiological and Molecular Plant Pathology*, **2017**, 100, 163-177 | 2.6 | 2 |
| 26 | Applications of Bioinformatics in Plant and Agriculture **2015**, 755-789 | | 2 |

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| 25 | Plant virus interaction mechanism and associated pathways in mosaic disease of small cardamom (Elettaria cardamomum Maton) by RNA-Seq approach. *Genomics*, **2020**, 112, 2041-2051 | 4.3 | 2 |
| 24 | Drought responsiveness in black pepper (Piper nigrum L.): Genes associated and development of a web-genomic resource. *Physiologia Plantarum*, **2021**, 172, 669-683 | 4.6 | 2 |
| 23 | Liver-Specific microRNA Identification in Farmed Carp, Labeo bata (Hamilton, 1822), Fed with Starch Diet Using High-Throughput Sequencing. *Marine Biotechnology*, **2019**, 21, 589-595 | 3.4 | 1 |
| 22 | Genetic diversity analysis for quantitative traits in lentil (Lens culinarismedik.) germplasm. *Legume Research*, **2014**, 37, 139 | 1 | 1 |
| 21 | Analysis and functional annotation of expressed sequence tags of water buffalo. *Animal Biotechnology*, **2013**, 24, 25-30 | 1.4 | 1 |
| 20 | A Bootstrap Study of Variance Estimation under Heteroscedasticity Using Genetic Algorithm. *Journal of Statistical Theory and Practice*, **2008**, 2, 55-69 | 0.5 | 1 |
| 19 | Microbiome of Pukzing Cave in India shows high antimicrobial activity against plant and animal pathogens. *Genomics*, **2021**, 113, 4098-4108 | 4.3 | 1 |
| 18 | assisted identification of peppery aroma compound 'rotundone' backbone genes from black pepper. *Journal of Biomolecular Structure and Dynamics*, **2021**, 1-7 | 3.6 | 1 |
| 17 | SNPs in Mammary Gland Epithelial Cells Unraveling Potential Difference in Milk Production Between Jersey and Kashmiri Cattle Using RNA Sequencing. *Frontiers in Genetics*, **2021**, 12, 666015 | 4.5 | 1 |
| 16 | Groundnut Bud Necrosis Virus Modulates the Expression of Innate Immune, Endocytosis, and Cuticle Development-Associated Genes to Circulate and Propagate in Its Vector, .. *Frontiers in Microbiology*, **2022**, 13, 773238 | 5.7 | 1 |
| 15 | Genomic analysis of polycarpellary rice (Oryza sativa L.) through whole genome resequencing. *Journal of Plant Biochemistry and Biotechnology*, **2020**, 30, 364 | 1.6 | 0 |
| 14 | Fruit transcriptional profiling of the contrasting genotypes for shelf life reveals the key candidate genes and molecular pathways regulating post-harvest biology in cucumber.. *Genomics*, **2022**, 114, 110273 | 4.3 | 0 |
| 13 | Establishment of Repertoire of Placentome-Associated MicroRNAs and Their Appearance in Blood Plasma Could Identify Early Establishment of Pregnancy in Buffalo (). *Frontiers in Cell and Developmental Biology*, **2021**, 9, 673765 | 5.7 | 0 |
| 12 | Revelation of candidate genes and molecular mechanism of reproductive seasonality in female rohu (Labeo rohita Ham.) by RNA sequencing. *BMC Genomics*, **2021**, 22, 685 | 4.5 | 0 |
| 11 | GWAS to Identify Novel QTNs for WSCs Accumulation in Wheat Peduncle Under Different Water Regimes.. *Frontiers in Plant Science*, **2022**, 13, 825687 | 6.2 | 0 |
| 10 | Whole-Genome Sequence Resource of Indian Race 4 of pv. , the Causal Agent of Black Rot Disease of var. .. *Plant Disease*, **2022**, PDIS10212217A | 1.5 | 0 |
| 9 | Agro-morphological and molecular diversity in different maturity groups of Indian cauliflower (Brassica oleracea var. botrytis L.). *PLoS ONE*, **2021**, 16, e0260246 | 3.7 | 0 |
| 8 | Transcriptomic Changes of Asia II 1 Induced by Chilli Leaf Curl Virus Trigger Infection and Circulation in Its Vector.. *Frontiers in Microbiology*, **2022**, 13, 890807 | 5.7 | 0 |

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| 7 | Understanding population structure and detection of QTLs for curding-related traits in Indian cauliflower by genotyping by sequencing analysis. *Functional and Integrative Genomics*, **2021**, 21, 679-693 | 3.8 |
| 6 | Intra-varietal stability performance of popular rice landrace C14-8 in the Andaman Islands. *Cereal Research Communications*, **2020**, 48, 103-111 | 1.1 |
| 5 | Genome-Wide Analysis of HSP70 Family Protein in and Coexpression Analysis Under Abiotic and Biotic Stress. *Journal of Computational Biology*, **2020**, 27, 738-754 | 1.7 |
| 4 | Mango Genomic Resources and Databases. *Compendium of Plant Genomes*, **2021**, 219-228 | 0.8 |
| 3 | In Silico Prediction and Functional Characterization of Genes Related to Abiotic and Biotic Stresses in Chickpea (Cicer arietinum). *Current Research in Bioinformatics*, **2018**, 7, 1-35 | 0.2 |
| 2 | Genome-Wide DNA Methylation and Its Effect on Gene Expression During Subclinical Mastitis in Water Buffalo.. *Frontiers in Genetics*, **2022**, 13, 828292 | 4.5 |
| 1 | Whole-Genome-Based Web Genomic Resource for Water Buffalo ().. *Frontiers in Genetics*, **2022**, 13, 809741 | 4.5 |