

# Mir Asif Iquebal

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

78  
papers

524  
citations

13  
h-index

18  
g-index

92  
ext. papers

804  
ext. citations

3.6  
avg, IF

3.74  
L-index

#	Paper	IF	Citations
78	Fruit transcriptional profiling of the contrasting genotypes for shelf life reveals the key candidate genes and molecular pathways regulating post-harvest biology in cucumber.. <i>Genomics</i> , <b>2022</b> , 114, 110273	4.3	0
77	GWAS to Identify Novel QTNs for WSCs Accumulation in Wheat Peduncle Under Different Water Regimes.. <i>Frontiers in Plant Science</i> , <b>2022</b> , 13, 825687	6.2	0
76	Genome-Wide DNA Methylation and Its Effect on Gene Expression During Subclinical Mastitis in Water Buffalo.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 828292	4.5	
75	Groundnut Bud Necrosis Virus Modulates the Expression of Innate Immune, Endocytosis, and Cuticle Development-Associated Genes to Circulate and Propagate in Its Vector, .. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 773238	5.7	1
74	Whole-Genome Sequence Resource of Indian Race 4 of pv. , the Causal Agent of Black Rot Disease of var. .. <i>Plant Disease</i> , <b>2022</b> , PDIS10212217A	1.5	0
73	Whole-Genome-Based Web Genomic Resource for Water Buffalo (). <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 809745	4.5	
72	Transcriptomic Changes of Asia II 1 Induced by Chilli Leaf Curl Virus Trigger Infection and Circulation in Its Vector.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 890807	5.7	0
71	Microbiome of Pukzing Cave in India shows high antimicrobial activity against plant and animal pathogens. <i>Genomics</i> , <b>2021</b> , 113, 4098-4108	4.3	1
70	Understanding population structure and detection of QTLs for curding-related traits in Indian cauliflower by genotyping by sequencing analysis. <i>Functional and Integrative Genomics</i> , <b>2021</b> , 21, 679-693	3.8	
69	Comparative transcriptome profiling reveals the basis of differential sheath blight disease response in tolerant and susceptible rice genotypes. <i>Protoplasma</i> , <b>2021</b> , 1	3.4	3
68	De novo transcriptome sequencing assisted identification of terpene synthases from black pepper () berry. <i>Physiology and Molecular Biology of Plants</i> , <b>2021</b> , 27, 1153-1161	2.8	3
67	Genome Wide Prediction, Mapping and Development of Genomic Resources of Mastitis Associated Genes in Water Buffalo. <i>Frontiers in Veterinary Science</i> , <b>2021</b> , 8, 593871	3.1	3
66	Drought responsiveness in black pepper ( <i>Piper nigrum</i> L.): Genes associated and development of a web-genomic resource. <i>Physiologia Plantarum</i> , <b>2021</b> , 172, 669-683	4.6	2
65	Mango Genomic Resources and Databases. <i>Compendium of Plant Genomes</i> , <b>2021</b> , 219-228	0.8	
64	assisted identification of peppery aroma compound 'rotundone' backbone genes from black pepper. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2021</b> , 1-7	3.6	1
63	Establishment of Repertoire of Placentome-Associated MicroRNAs and Their Appearance in Blood Plasma Could Identify Early Establishment of Pregnancy in Buffalo (). <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 673765	5.7	0
62	SNPs in Mammary Gland Epithelial Cells Unraveling Potential Difference in Milk Production Between Jersey and Kashmiri Cattle Using RNA Sequencing. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 666015	4.5	1

61	Revelation of candidate genes and molecular mechanism of reproductive seasonality in female rohu ( <i>Labeo rohita</i> Ham.) by RNA sequencing. <i>BMC Genomics</i> , <b>2021</b> , 22, 685	4.5	0
60	The genome of walking catfish <i>Clarias magur</i> (Hamilton, 1822) unveils the genetic basis that may have facilitated the development of environmental and terrestrial adaptation systems in air-breathing catfishes. <i>DNA Research</i> , <b>2021</b> , 28,	4.5	6
59	Agro-morphological and molecular diversity in different maturity groups of Indian cauliflower ( <i>Brassica oleracea</i> var. <i>botrytis</i> L.). <i>PLoS ONE</i> , <b>2021</b> , 16, e0260246	3.7	0
58	Genomic analysis of polycarpellary rice ( <i>Oryza sativa</i> L.) through whole genome resequencing. <i>Journal of Plant Biochemistry and Biotechnology</i> , <b>2020</b> , 30, 364	1.6	0
57	Assembly and Genome-Wide SNP Discovery in Rohu Carp,. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 386	4.5	9
56	Genome-Wide Association Studies in Diverse Spring Wheat Panel for Stripe, Stem, and Leaf Rust Resistance. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 748	6.2	21
55	An insight into molecular interaction of PGIP with PG for banana cultivar. <i>Frontiers in Bioscience - Landmark</i> , <b>2020</b> , 25, 335-362	2.8	3
54	Plant virus interaction mechanism and associated pathways in mosaic disease of small cardamom ( <i>Elettaria cardamomum</i> Maton) by RNA-Seq approach. <i>Genomics</i> , <b>2020</b> , 112, 2041-2051	4.3	2
53	Intra-varietal stability performance of popular rice landrace [14-8] in the Andaman Islands. <i>Cereal Research Communications</i> , <b>2020</b> , 48, 103-111	1.1	
52	Muscle transcriptome signature and gene regulatory network analysis in two divergent lines of a hilly bovine species Mithun ( <i>Bos frontalis</i> ). <i>Genomics</i> , <b>2020</b> , 112, 252-262	4.3	9
51	Characterization of genetic diversity and population structure in wheat using array based SNP markers. <i>Molecular Biology Reports</i> , <b>2020</b> , 47, 293-306	2.8	13
50	Transcriptome analysis of Snow Mountain Garlic for unraveling the organosulfur metabolic pathway. <i>Genomics</i> , <b>2020</b> , 112, 99-107	4.3	7
49	Revealing liver specific microRNAs linked with carbohydrate metabolism of farmed carp, <i>Labeo rohita</i> (Hamilton, 1822). <i>Genomics</i> , <b>2020</b> , 112, 32-44	4.3	6
48	Genome-Wide Analysis of HSP70 Family Protein in and Coexpression Analysis Under Abiotic and Biotic Stress. <i>Journal of Computational Biology</i> , <b>2020</b> , 27, 738-754	1.7	
47	RNAseq analysis reveals drought-responsive molecular pathways with candidate genes and putative molecular markers in root tissue of wheat. <i>Scientific Reports</i> , <b>2019</b> , 9, 13917	4.9	38
46	Development of species specific putative miRNA and its target prediction tool in wheat ( <i>Triticum aestivum</i> L.). <i>Scientific Reports</i> , <b>2019</b> , 9, 3790	4.9	3
45	Uncovering Genomic Regions Associated With 36 Agro-Morphological Traits in Indian Spring Wheat Using GWAS. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 527	6.2	25
44	Development of model web-server for crop variety identification using throughput SNP genotyping data. <i>Scientific Reports</i> , <b>2019</b> , 9, 5122	4.9	7

43	VigSatDB: genome-wide microsatellite DNA marker database of three species of Vigna for germplasm characterization and improvement. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2019</b> , 2019,	5	5
42	The role of conserved residues in the catalytic activity of NDM-1: an approach involving site directed mutagenesis and molecular dynamics. <i>Physical Chemistry Chemical Physics</i> , <b>2019</b> , 21, 17821-17835	3.6	8
41	Liver-Specific microRNA Identification in Farmed Carp, <i>Labeo bata</i> (Hamilton, 1822), Fed with Starch Diet Using High-Throughput Sequencing. <i>Marine Biotechnology</i> , <b>2019</b> , 21, 589-595	3.4	1
40	Harmonizing technological advances in phenomics and genomics for enhanced salt tolerance in rice from a practical perspective. <i>Rice</i> , <b>2019</b> , 12, 89	5.8	14
39	Transcriptomic signature reveals mechanism of flower bud distortion in witches'-broom disease of soybean ( <i>Glycine max</i> ). <i>BMC Plant Biology</i> , <b>2019</b> , 19, 26	5.3	6
38	Transcriptomic signature of drought response in pearl millet ( <i>Pennisetum glaucum</i> (L.) and development of web-genomic resources. <i>Scientific Reports</i> , <b>2018</b> , 8, 3382	4.9	31
37	BanSatDB, a whole-genome-based database of putative and experimentally validated microsatellite markers of three <i>Musa</i> species. <i>Crop Journal</i> , <b>2018</b> , 6, 642-650	4.6	4
36	: A Universal Web-Tool for Rapid Polymorphic Microsatellite Marker Discovery From Whole Genome and Transcriptome Data. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1966	6.2	4
35	In Silico Prediction and Functional Characterization of Genes Related to Abiotic and Biotic Stresses in Chickpea ( <i>Cicer arietinum</i> ). <i>Current Research in Bioinformatics</i> , <b>2018</b> , 7, 1-35	0.2	
34	Effects of weed control strategy on weed dynamics, soybean productivity and profitability under conservation agriculture in India. <i>Field Crops Research</i> , <b>2017</b> , 210, 61-70	5.5	16
33	Deciphering genes associated with root wilt disease of coconut and development of its transcriptomic database (CnTDB). <i>Physiological and Molecular Plant Pathology</i> , <b>2017</b> , 100, 255-263	2.6	6
32	Transcriptomic signature of <i>Fusarium</i> toxin in chickpea unveiling wilt pathogenicity pathways and marker discovery. <i>Physiological and Molecular Plant Pathology</i> , <b>2017</b> , 100, 163-177	2.6	2
31	Computational deciphering of biotic stress associated genes in tomato ( <i>S. lycopersicon</i> ). <i>Genomics Data</i> , <b>2017</b> , 14, 82-90		4
30	Development of transcriptome based web genomic resources of yellow mosaic disease in. <i>Physiology and Molecular Biology of Plants</i> , <b>2017</b> , 23, 767-777	2.8	7
29	Draft whole genome sequence of groundnut stem rot fungus <i>Athelia rolfsii</i> revealing genetic architect of its pathogenicity and virulence. <i>Scientific Reports</i> , <b>2017</b> , 7, 5299	4.9	10
28	MiSNPDb: a web-based genomic resources of tropical ecology fruit mango ( <i>Mangifera indica</i> L.) for phylogeography and varietal differentiation. <i>Scientific Reports</i> , <b>2017</b> , 7, 14968	4.9	14
27	Discovery of Putative Herbicide Resistance Genes and Its Regulatory Network in Chickpea Using Transcriptome Sequencing. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 958	6.2	14
26	Putative Microsatellite DNA Marker-Based Wheat Genomic Resource for Varietal Improvement and Management. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 2009	6.2	17

25	Low-depth shotgun sequencing resolves complete mitochondrial genome sequence of <i>Labeo rohita</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , <b>2016</b> , 27, 3517-8	1.3	2
24	Origin, Diversity and Genome Sequence of Mango ( <i>Mangifera indica</i> L.). <i>Indian Journal of History of Science</i> , <b>2016</b> , 51,		15
23	Draft Genome Sequence of Two Monosporidial Lines of the Karnal Bunt Fungus <i>Tilletia indica</i> Mitra (PSWKBGH-1 and PSWKBGH-2). <i>Genome Announcements</i> , <b>2016</b> , 4,		9
22	Development of Antimicrobial Peptide Prediction Tool for Aquaculture Industries. <i>Probiotics and Antimicrobial Proteins</i> , <b>2016</b> , 8, 141-9	5.5	10
21	A meta-analysis of potential candidate genes associated with salinity stress tolerance in rice. <i>Agri Gene</i> , <b>2016</b> , 1, 126-134	1.9	5
20	The Onion Genomic Resource: A genomics and bioinformatics driven resource for onion breeding. <i>Plant Gene</i> , <b>2016</b> , 8, 9-15	3.1	6
19	Assembly and variation analyses of <i>Clarias batrachus</i> mitogenome retrieved from WGS data and its phylogenetic relationship with other catfishes. <i>Meta Gene</i> , <b>2015</b> , 5, 105-14	0.7	6
18	Applications of Bioinformatics in Plant and Agriculture <b>2015</b> , 755-789		2
17	Evidence of salicylic acid pathway with EDS1 and PAD4 proteins by molecular dynamics simulation for grape improvement. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2015</b> , 33, 2180-91	3.6	10
16	Recycling of Organic Waste through Four Different Composts for Disease Suppression and Growth Enhancement in Mung Beans. <i>Clean - Soil, Air, Water</i> , <b>2015</b> , 43, 1066-1071	1.6	10
15	SBMDb: first whole genome putative microsatellite DNA marker database of sugarbeet for bioenergy and industrial applications. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2015</b> , 2015,	5	4
14	Species specific approach to the development of web-based antimicrobial peptides prediction tool for cattle. <i>Computers and Electronics in Agriculture</i> , <b>2015</b> , 111, 55-61	6.5	3
13	Locus minimization in breed prediction using artificial neural network approach. <i>Animal Genetics</i> , <b>2014</b> , 45, 898-902	2.5	9
12	Genetic diversity analysis for quantitative traits in lentil ( <i>Lens culinaris</i> Medik.) germplasm. <i>Legume Research</i> , <b>2014</b> , 37, 139	1	1
11	In silico mining of putative microsatellite markers from whole genome sequence of water buffalo ( <i>Bubalus bubalis</i> ) and development of first BuffSatDB. <i>BMC Genomics</i> , <b>2013</b> , 14, 43	4.5	11
10	Development of a model webserver for breed identification using microsatellite DNA marker. <i>BMC Genetics</i> , <b>2013</b> , 14, 118	2.6	5
9	First whole genome based microsatellite DNA marker database of tomato for mapping and variety identification. <i>BMC Plant Biology</i> , <b>2013</b> , 13, 197	5.3	20
8	PIPEMicroDB: microsatellite database and primer generation tool for pigeonpea genome. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bas054	5	7

7	Analysis and functional annotation of expressed sequence tags of water buffalo. <i>Animal Biotechnology</i> , <b>2013</b> , 24, 25-30	1.4	1
6	Seasonal parasitism and biological characteristics of <i>Habrobracon hebetor</i> (Hymenoptera: Braconidae) as potential larval ectoparasitoid of <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae) in a chickpea ecosystem. <i>Biocontrol Science and Technology</i> , <b>2012</b> , 22, 305-318	1.7	12
5	Biotic stress resistance in agriculture through antimicrobial peptides. <i>Peptides</i> , <b>2012</b> , 36, 322-30	3.8	29
4	Selection of pigeonpea genotypes for tolerance to aluminium toxicity. <i>Plant Breeding</i> , <b>2011</b> , 130, 492-495.	5.4	9
3	Bootstrap study of parameter estimates for nonlinear Richards growth model through genetic algorithm. <i>Journal of Applied Statistics</i> , <b>2011</b> , 38, 491-500	1	3
2	Prediction of MHC Binding Peptides and Epitopes from Coat Protein of Mungbean Yellow Mosaic India Virus-Ub05. <i>Journal of Proteomics and Bioinformatics</i> , <b>2010</b> , 03, 173-178	2.1	3
1	A Bootstrap Study of Variance Estimation under Heteroscedasticity Using Genetic Algorithm. <i>Journal of Statistical Theory and Practice</i> , <b>2008</b> , 2, 55-69	0.5	1