

Mir Asif Iquebal

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

1,013
citations

623188

14
h-index

580395

25
g-index

92
all docs

92
docs citations

92
times ranked

1215
citing authors

#	ARTICLE	IF	CITATIONS
1	Uncovering Genomic Regions Associated With 36 Agro-Morphological Traits in Indian Spring Wheat Using GWAS. <i>Frontiers in Plant Science</i> , 2019, 10, 527.	1.7	70
2	RNAseq analysis reveals drought-responsive molecular pathways with candidate genes and putative molecular markers in root tissue of wheat. <i>Scientific Reports</i> , 2019, 9, 13917.	1.6	60
3	Characterization of genetic diversity and population structure in wheat using array based SNP markers. <i>Molecular Biology Reports</i> , 2020, 47, 293-306.	1.0	60

4

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19	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> , 2021, 28, .	1.5	16
20	Transcriptomic signature reveals mechanism of flower bud distortion in witches' broom disease of soybean (<i>Glycine max</i>). <i>BMC Plant Biology</i> , 2019, 19, 26.	1.6	15
21	PolyMorphPredict: A Universal Web-Tool for Rapid Polymorphic Microsatellite Marker Discovery From Whole Genome and Transcriptome Data. <i>Frontiers in Plant Science</i> , 2018, 9, 1966.	1.7	15
22	Transcriptome analysis of Snow Mountain Garlic for unraveling the organosulfur metabolic pathway. <i>Genomics</i> , 2020, 112, 99-107.	1.3	15
23	PIPEMicroDB: microsatellite database and primer generation tool for pigeonpea genome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas054.	1.4	14
24	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> , 2019, 21, 17821-17835.	1.3	14
25	Seasonal parasitism and biological characteristics of <i>Habrobracon hebetor</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overloc	0.5	13
26	Locus minimization in breed prediction using artificial neural network approach. <i>Animal Genetics</i> , 2014, 45, 898-902.	0.6	13
27	Recycling of Organic Waste through Four Different Composts for Disease Suppression and Growth Enhancement in Mung Beans. <i>Clean - Soil, Air, Water</i> , 2015, 43, 1066-1071.	0.7	13
28	Selection of pigeonpea genotypes for tolerance to aluminium toxicity. <i>Plant Breeding</i> , 2011, 130, 492-495.	1.0	12
29	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> , 2015, 33, 2180-2191.	2.0	12
30	Deciphering genes associated with root wilt disease of coconut and development of its transcriptomic database (CnTDB). <i>Physiological and Molecular Plant Pathology</i> , 2017, 100, 255-263.	1.3	12
31	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> , 2020, 112, 252-262.	1.3	12
32	Groundnut Bud Necrosis Virus Modulates the Expression of Innate Immune, Endocytosis, and Cuticle Development-Associated Genes to Circulate and Propagate in Its Vector, Thrips palmi. <i>Frontiers in Microbiology</i> , 2022, 13, 773238.	1.5	12
33	Draft Genome Sequence of Two Monosporial Lines of the Karnal Bunt Fungus <i>Tilletia indica</i> Mitra (PSWKBGH-1 and PSWKBGH-2). <i>Genome Announcements</i> , 2016, 4, .	0.8	11
34	Development of transcriptome based web genomic resources of yellow mosaic disease in <i>Vigna mungo</i> . <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 767-777.	1.4	11
35	Revealing liver specific microRNAs linked with carbohydrate metabolism of farmed carp, <i>Labeo rohita</i> (Hamilton, 1822). <i>Genomics</i> , 2020, 112, 32-44.	1.3	11
36	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> , 2015, 5, 105-114.	0.3	9

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37	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	9
38	Comparative transcriptome profiling reveals the basis of differential sheath blight disease response in tolerant and susceptible rice genotypes. <i>Protoplasma</i> , 2022, 259, 61-73.	1.0	9
39	Genome Wide Prediction, Mapping and Development of Genomic Resources of Mastitis Associated Genes in Water Buffalo. <i>Frontiers in Veterinary Science</i> , 2021, 8, 593871.	0.9	8
40	Bootstrap study of parameter estimates for nonlinear Richards growth model through genetic algorithm. <i>Journal of Applied Statistics</i> , 2011, 38, 491-500.	0.6	7
41	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> , 2015, 2015, bav111.	1.4	7
42	The Onion Genomic Resource: A genomics and bioinformatics driven resource for onion breeding. <i>Plant Gene</i> , 2016, 8, 9-15.	1.4	7
43	Development of species specific putative miRNA and its target prediction tool in wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	1.6	7
44	Drought responsiveness in black pepper (<i>Piper nigrum</i> L.): Genes associated and development of a web-based genomic resource. <i>Physiologia Plantarum</i> , 2021, 172, 669-683.	2.6	7
45	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> , 2022, 114, 110273.	1.3	7
46	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> , 2021, 16, e0260246.	1.1	7
47	RNA-Seq Analysis of Developing Grains of Wheat to Intrigue Into the Complex Molecular Mechanism of the Heat Stress Response. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7
48	Development of a model webserver for breed identification using microsatellite DNA marker. <i>BMC Genetics</i> , 2013, 14, 118.	2.7	6
49	Applications of Bioinformatics in Plant and Agriculture. , 2015, , 755-789.		6
50	A meta-analysis of potential candidate genes associated with salinity stress tolerance in rice. <i>Agri Gene</i> , 2016, 1, 126-134.	1.9	6
51	Revealing Alteration in the Hepatic Glucose Metabolism of Genetically Improved Carp, <i>Jayanti Rohu Labeo rohita</i> Fed a High Carbohydrate Diet Using Transcriptome Sequencing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8180.	1.8	6
52	De novo transcriptome sequencing assisted identification of terpene synthases from black pepper (<i>Piper nigrum</i>) berry. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1153-1161.	1.4	6
53	Computational deciphering of biotic stress associated genes in tomato (<i>Solanum lycopersicum</i>). <i>Genomics Data</i> , 2017, 14, 82-90.	1.3	5
54	BanSatDB, a whole-genome-based database of putative and experimentally validated microsatellite markers of three <i>Musa</i> species. <i>Crop Journal</i> , 2018, 6, 642-650.	2.3	5

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55	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> , 2020, 112, 2041-2051.	1.3	5
56	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> , 2021, 12, 666015.	1.1	5
57	An insight into molecular interaction of PGIP with PG for banana cultivar. <i>Frontiers in Bioscience - Landmark</i> , 2020, 25, 335-362.	3.0	5
58	Microbiome of Pukzing Cave in India shows high antimicrobial activity against plant and animal pathogens. <i>Genomics</i> , 2021, 113, 4098-4108.	1.3	5
59	Centenary of Soil and Air Borne Wheat Karnal Bunt Disease Research: A Review. <i>Biology</i> , 2021, 10, 1152.	1.3	5
60	GWAS to Identify Novel QTNs for WSCs Accumulation in Wheat Peduncle Under Different Water Regimes. <i>Frontiers in Plant Science</i> , 2022, 13, 825687.	1.7	5
61	Genome-Wide DNA Methylation and Its Effect on Gene Expression During Subclinical Mastitis in Water Buffalo. <i>Frontiers in Genetics</i> , 2022, 13, 828292.	1.1	5
62	Whole-Genome Sequence Resource of Indian Race 4 of <i>Xanthomonas campestris</i> pv. <i>campestris</i> , the Causal Agent of Black Rot Disease of <i>Brassica oleracea</i> var. <i>capitata</i> . <i>Plant Disease</i> , 2022, 106, 1502-1505.	0.7	5
63	Transcriptomic Changes of Bemisia tabaci Asia II 1 Induced by Chilli Leaf Curl Virus Trigger Infection and Circulation in Its Vector. <i>Frontiers in Microbiology</i> , 2022, 13, 890807.	1.5	5
64	Genetic diversity analysis for quantitative traits in lentil (<i>Lens culinaris</i> Medik.) germplasm. <i>Legume Research</i> , 2014, 37, 139.	0.0	4
65	Species specific approach to the development of web-based antimicrobial peptides prediction tool for cattle. <i>Computers and Electronics in Agriculture</i> , 2015, 111, 55-61.	3.7	4
66	Transcriptomic signature of Fusarium toxin in chickpea unveiling wilt pathogenicity pathways and marker discovery. <i>Physiological and Molecular Plant Pathology</i> , 2017, 100, 163-177.	1.3	4
67	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> , 2019, 21, 589-595.	1.1	4
68	Fungal Genomic Resources for Strain Identification and Diversity Analysis of 1900 Fungal Species. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 288.	1.5	4
69	Whole-Genome-Based Web Genomic Resource for Water Buffalo (<i>Bubalus bubalis</i>). <i>Frontiers in Genetics</i> , 2022, 13, 809741.	1.1	4
70	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> , 2021, 22, 685.	1.2	3
71	Prediction of MHC Binding Peptides and Epitopes from Coat Protein of Mungbean Yellow Mosaic India Virus-Ub05. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 173-178.	0.4	3
72	Assessment of Groundwater Recharge in a Small Ravine Watershed in Semi-arid Region of India. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2018, 7, 2552-2565.	0.0	3

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73	Low-depth shotgun sequencing resolves complete mitochondrial genome sequence of <i>Labeo rohita</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3517-3518.	0.7	2
74	Genomic analysis of polycarpellary rice (<i>Oryza sativa</i> L.) through whole genome resequencing. Journal of Plant Biochemistry and Biotechnology, 2020, 30, 364.	0.9	2
75	In silico assisted identification of peppery aroma compound α -rotundone backbone genes from black pepper. Journal of Biomolecular Structure and Dynamics, 2021, , 1-7.	2.0	2
76	Establishment of Repertoire of Placentome-Associated MicroRNAs and Their Appearance in Blood Plasma Could Identify Early Establishment of Pregnancy in Buffalo (<i>Bubalus bubalis</i>). Frontiers in Cell and Developmental Biology, 2021, 9, 673765.	1.8	2
77	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.	1.4	2
78	Rapid Genome-Wide Location-Specific Polymorphic SSR Marker Discovery in Black Pepper by GBS Approach. Frontiers in Plant Science, 2022, 13, .	1.7	2
79	A Bootstrap Study of Variance Estimation under Heteroscedasticity Using Genetic Algorithm. Journal of Statistical Theory and Practice, 2008, 2, 55-69.	0.3	1
80	Analysis and Functional Annotation of Expressed Sequence Tags of Water Buffalo. Animal Biotechnology, 2013, 24, 25-30.	0.7	1
81	Designing and validating e-learning module on Good Agricultural Practices for grapes. Indian Journal of Horticulture, 2015, 72, 489.	0.1	1
82	Development of Smart Weighing Lysimeter for Measuring Evapotranspiration and Developing Crop Coefficient for Greenhouse Chrysanthemum. SSRN Electronic Journal, 0, , .	0.4	1
83	In Silico Prediction and Functional Characterization of Genes Related to Abiotic and Biotic Stresses in Chickpea (<i>Cicer arietinum</i>). Current Research in Bioinformatics, 2018, 7, 1-35.	0.0	0
84	Genome-Wide Analysis of HSP70 Family Protein in <i>Vigna radiata</i> and Coexpression Analysis Under Abiotic and Biotic Stress. Journal of Computational Biology, 2020, 27, 738-754.	0.8	0
85	Intra-varietal stability performance of popular rice landrace α -C14-8 in the Andaman Islands. Cereal Research Communications, 2020, 48, 103-111.	0.8	0
86	Mango Genomic Resources and Databases. Compendium of Plant Genomes, 2021, , 219-228.	0.3	0
87	Determination of MHC Binding Peptides and Epitopes from Non- Structural Movement (NSm) Protein of Groundnut Bud Necrosis Virus. Current Drug Discovery Technologies, 2010, 7, 117-122.	0.6	0
88	Introduction to Technology Forecasting and Assessment methods. Bhartiya Krishi Anusandhan Patrika, 2019, 34, .	0.0	0