

# Atmakuri Ramakrishna Rao

## 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.

39  
papers

675  
citations

13  
h-index

25  
g-index

44  
ext. papers

985  
ext. citations

3.7  
avg, IF

4.28  
L-index

#	Paper	IF	Citations
39	ASRmiRNA: Abiotic Stress-Responsive miRNA Prediction in Plants by Using Machine Learning Algorithms with Pseudo -Tuple Nucleotide Compositional Features.. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23,	6.3	2
38	Evolutionary and functional characterisation of glutathione peroxidases showed splicing mediated stress responses in Maize.. <i>Plant Physiology and Biochemistry</i> , <b>2022</b> , 178, 40-54	5.4	0
37	mLoc-mRNA: predicting multiple sub-cellular localization of mRNAs using random forest algorithm coupled with feature selection via elastic net. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 342	3.6	2
36	Chemotactic factor inducing Interleukin-8 (IL8) gene is transcriptionally elevated in experimental enterotoxaemia in goats caused by type D. <i>Heliyon</i> , <b>2021</b> , 7, e07568	3.6	
35	Metagenomics study in aquatic resource management: recent trends, applied methodologies and future needs. <i>Gene Reports</i> , <b>2021</b> , 25, 101372	1.4	0
34	Exploring microbiome from sediments of River Ganga using a metagenomic approach. <i>Aquatic Ecosystem Health and Management</i> , <b>2021</b> , 24, 12-22	1.4	0
33	SpikeSegNet-a deep learning approach utilizing encoder-decoder network with hourglass for spike segmentation and counting in wheat plant from visual imaging. <i>Plant Methods</i> , <b>2020</b> , 16, 40	5.8	25
32	Metagenomic Analysis Reveals Bacterial and Fungal Diversity and Their Bioremediation Potential From Sediments of River Ganga and Yamuna in India. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 556136	5.7	13
31	Metagenome analysis from the sediment of river Ganga and Yamuna: In search of beneficial microbiome. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239594	3.7	6
30	Extrapolating the effect of non-synonymous SNP in bread wheat HSP16.9B gene: a molecular modelling and dynamics study. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2020</b> , 16, 101	0.9	
29	Inferring Relationship of Blood Metabolic Changes and Average Daily Gain With Feed Conversion Efficiency in Murrah Heifers: Machine Learning Approach. <i>Frontiers in Veterinary Science</i> , <b>2020</b> , 7, 518	3.1	1
28	miRNALoc: predicting miRNA subcellular localizations based on principal component scores of physico-chemical properties and pseudo compositions of di-nucleotides. <i>Scientific Reports</i> , <b>2020</b> , 10, 14557	4.9	4
27	Computational insights into RNAi-based therapeutics for foot and mouth disease of Bos taurus. <i>Scientific Reports</i> , <b>2020</b> , 10, 21593	4.9	
26	MicroRNA-related markers associated with corpus luteum tropism in buffalo (Bubalus bubalis). <i>Genomics</i> , <b>2020</b> , 112, 108-113	4.3	2
25	HRGPred: Prediction of herbicide resistant genes with k-mer nucleotide compositional features and support vector machine. <i>Scientific Reports</i> , <b>2019</b> , 9, 778	4.9	5
24	Evaluating the performance of sequence encoding schemes and machine learning methods for splice sites recognition. <i>Gene</i> , <b>2019</b> , 705, 113-126	3.8	2
23	Comparative transcriptome analysis reveals the genetic basis of coat color variation in Pashmina goat. <i>Scientific Reports</i> , <b>2019</b> , 9, 6361	4.9	13

22	In silico site-directed mutagenesis of neutralizing mAb 4C4 and analysis of its interaction with G-H loop of VP1 to explore its therapeutic applications against FMD. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2019</b> , 37, 2641-2651	3.6	
21	funbarRF: DNA barcode-based fungal species prediction using multiclass Random Forest supervised learning model. <i>BMC Genetics</i> , <b>2019</b> , 20, 2	2.6	8
20	Transcriptome analysis reveals interplay between hormones, ROS metabolism and cell wall biosynthesis for drought-induced root growth in wheat. <i>Plant Physiology and Biochemistry</i> , <b>2018</b> , 130, 482-492	5.4	27
19	Genome-wide identification and characterization of lncRNAs and miRNAs in cluster bean ( <i>Cyamopsis tetragonoloba</i> ). <i>Gene</i> , <b>2018</b> , 667, 112-121	3.8	7
18	Predicting antimicrobial peptides with improved accuracy by incorporating the compositional, physico-chemical and structural features into Chou's general PseAAC. <i>Scientific Reports</i> , <b>2017</b> , 7, 42362	4.9	233
17	Genomewide Expression and Functional Interactions of Genes under Drought Stress in Maize. <i>International Journal of Genomics</i> , <b>2017</b> , 2017, 2568706	2.5	25
16	ir-HSP: Improved Recognition of Heat Shock Proteins, Their Families and Sub-types Based On -Spaced Di-peptide Features and Support Vector Machine. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 235	4.5	13
15	RNAseq revealed the important gene pathways controlling adaptive mechanisms under waterlogged stress in maize. <i>Scientific Reports</i> , <b>2017</b> , 7, 10950	4.9	31
14	DIRProt: a computational approach for discriminating insecticide resistant proteins from non-resistant proteins. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 190	3.6	11
13	Genomic Selection for Drought Tolerance Using Genome-Wide SNPs in Maize. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 550	6.2	83
12	Variable Level of Dominance of Candidate Genes Controlling Drought Functional Traits in Maize Hybrids. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 940	6.2	8
11	Identification, Characterization, and Functional Validation of Drought-responsive MicroRNAs in Subtropical Maize Inbreds. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 941	6.2	43
10	Prediction of donor splice sites using random forest with a new sequence encoding approach. <i>BioData Mining</i> , <b>2016</b> , 9, 4	4.3	25
9	A computational approach for prediction of donor splice sites with improved accuracy. <i>Journal of Theoretical Biology</i> , <b>2016</b> , 404, 285-294	2.3	5
8	Genome Wide Single Locus Single Trait, Multi-Locus and Multi-Trait Association Mapping for Some Important Agronomic Traits in Common Wheat ( <i>T. aestivum</i> L.). <i>PLoS ONE</i> , <b>2016</b> , 11, e0159343	3.7	41
7	Identification of species based on DNA barcode using k-mer feature vector and Random forest classifier. <i>Gene</i> , <b>2016</b> , 592, 316-24	3.8	9
6	Draft Genome Sequence of the Extremely Halophilic Bacterium <i>Halomonas salina</i> Strain CIFR11, Isolated from the East Coast of India. <i>Genome Announcements</i> , <b>2015</b> , 3,		2
5	Extrapolation of Inter Domain Communications and Substrate Binding Cavity of Camel HSP70 1A: A Molecular Modeling and Dynamics Simulation Study. <i>PLoS ONE</i> , <b>2015</b> , 10, e0136630	3.7	12

4	Determination of window size and identification of suitable method for prediction of donor splice sites in rice ( <i>Oryza sativa</i> ) genome. <i>Journal of Plant Biochemistry and Biotechnology</i> , <b>2015</b> , 24, 385-392	1.6	1
3	A statistical approach for 5Ysplice site prediction using short sequence motifs and without encoding sequence data. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 362	3.6	13
2	An approach using random forest methodology for disease risk prediction using imbalanced case-control data in GWAS. <i>Current Medicine Research and Practice</i> , <b>2014</b> , 4, 289-294	2.7	2
1	shRNAPred (version 1.0): An open source and standalone software for short hairpin RNA (shRNA) prediction. <i>Bioinformatics</i> , <b>2012</b> , 8, 629-33	1.1	1