

Atmakuri Ramakrishna Rao

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

1,228
citations

623574

14
h-index

395590

33
g-index

44
all docs

44
docs citations

44
times ranked

1500
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting antimicrobial peptides with improved accuracy by incorporating the compositional, physico-chemical and structural features into Chou's general PseAAC. <i>Scientific Reports</i> , 2017, 7, 42362.	1.6	358
2	Genomic Selection for Drought Tolerance Using Genome-Wide SNPs in Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 550.	1.7	138
3	Identification, Characterization, and Functional Validation of Drought-responsive MicroRNAs in Subtropical Maize Inbreds. <i>Frontiers in Plant Science</i> , 2017, 8, 941.	1.7	74
4	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> , 2020, 16, 40.	1.9	73
5	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> , 2016, 11, e0159343.	1.1	72
6	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> , 2018, 130, 482-492.	2.8	68
7	RNAseq revealed the important gene pathways controlling adaptive mechanisms under waterlogged stress in maize. <i>Scientific Reports</i> , 2017, 7, 10950.	1.6	49
8	Genomewide Expression and Functional Interactions of Genes under Drought Stress in Maize. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	0.8	47
9	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> , 2020, 11, 556136.	1.5	44
10	Prediction of donor splice sites using random forest with a new sequence encoding approach. <i>BioData Mining</i> , 2016, 9, 4.	2.2	33
11	Metagenome analysis from the sediment of river Ganga and Yamuna: In search of beneficial microbiome. <i>PLoS ONE</i> , 2020, 15, e0239594.	1.1	24
12	Variable Level of Dominance of Candidate Genes Controlling Drought Functional Traits in Maize Hybrids. <i>Frontiers in Plant Science</i> , 2017, 8, 940.	1.7	23
13	Comparative transcriptome analysis reveals the genetic basis of coat color variation in Pashmina goat. <i>Scientific Reports</i> , 2019, 9, 6361.	1.6	22
14	ir-HSP: Improved Recognition of Heat Shock Proteins, Their Families and Sub-types Based On g-Spaced Di-peptide Features and Support Vector Machine. <i>Frontiers in Genetics</i> , 2017, 8, 235.	1.1	18
15	Identification of species based on DNA barcode using k-mer feature vector and Random forest classifier. <i>Gene</i> , 2016, 592, 316-324.	1.0	17
16	funbarRF: DNA barcode-based fungal species prediction using multiclass Random Forest supervised learning model. <i>BMC Genetics</i> , 2019, 20, 2.	2.7	17
17	Extrapolation of Inter Domain Communications and Substrate Binding Cavity of Camel HSP70 1A: A Molecular Modeling and Dynamics Simulation Study. <i>PLoS ONE</i> , 2015, 10, e0136630.	1.1	16
18	A statistical approach for 5' splice site prediction using short sequence motifs and without encoding sequence data. <i>BMC Bioinformatics</i> , 2014, 15, 362.	1.2	14

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19	Genome-wide identification and characterization of lncRNAs and miRNAs in cluster bean (<i>Cyamopsis</i>) Tj ETQq1 1 0.784314 rgBT /Ove	1.0	14
20	DIRProt: a computational approach for discriminating insecticide resistant proteins from non-resistant proteins. <i>BMC Bioinformatics</i> , 2017, 18, 190.	1.2	13
21	miRNALoc: predicting miRNA subcellular localizations based on principal component scores of physico-chemical properties and pseudo compositions of di-nucleotides. <i>Scientific Reports</i> , 2020, 10, 14557.	1.6	12
22	Exploring microbiome from sediments of River Ganga using a metagenomic approach. <i>Aquatic Ecosystem Health and Management</i> , 2021, 24, 12-22.	0.3	11
23	ASRmiRNA: Abiotic Stress-Responsive miRNA Prediction in Plants by Using Machine Learning Algorithms with Pseudo K-Tuple Nucleotide Compositional Features. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1612.	1.8	10
24	Metagenomics study in aquatic resource management: Recent trends, applied methodologies and future needs. <i>Gene Reports</i> , 2021, 25, 101372.	0.4	9
25	HRGPred: Prediction of herbicide resistant genes with k-mer nucleotide compositional features and support vector machine. <i>Scientific Reports</i> , 2019, 9, 778.	1.6	8
26	mLoc-mRNA: predicting multiple sub-cellular localization of mRNAs using random forest algorithm coupled with feature selection via elastic net. <i>BMC Bioinformatics</i> , 2021, 22, 342.	1.2	7
27	A computational approach for prediction of donor splice sites with improved accuracy. <i>Journal of Theoretical Biology</i> , 2016, 404, 285-294.	0.8	6
28	Evolutionary and functional characterisation of glutathione peroxidases showed splicing mediated stress responses in Maize. <i>Plant Physiology and Biochemistry</i> , 2022, 178, 40-54.	2.8	6
29	Evaluating the performance of sequence encoding schemes and machine learning methods for splice sites recognition. <i>Gene</i> , 2019, 705, 113-126.	1.0	5
30	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> , 2020, 7, 518.	0.9	5
31	An approach using random forest methodology for disease risk prediction using imbalanced case-control data in GWAS. <i>Current Medicine Research and Practice</i> , 2014, 4, 289-294.	0.1	3
32	MicroRNA-related markers associated with corpus luteum tropism in buffalo (<i>Bubalus bubalis</i>). <i>Genomics</i> , 2020, 112, 108-113.	1.3	3
33	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> , 2015, 3, .	0.8	2
34	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> , 2015, 24, 385-392.	0.9	1
35	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> , 2019, 37, 2641-2651.	2.0	1
36	Computational insights into RNAi-based therapeutics for foot and mouth disease of <i>Bos taurus</i> . <i>Scientific Reports</i> , 2020, 10, 21593.	1.6	1

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37	shRNAPred (version 1.0): An open source and standalone software for short hairpin RNA (shRNA) prediction. <i>Bioinformatics</i> , 2012, 8, 629-633.	0.2	1
38	Molecular modeling and dynamics study of nonsynonymous SNP in bread wheat HSP16.9B gene. , 2016, , .		0
39	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> , 2020, 16, 101.	0.1	0
40	Chemotactic factor inducing Interleukin-8 (IL8) gene is transcriptionally elevated in experimental enterotoxaemia in goats caused by <i>Clostridium perfringens</i> type D. <i>Heliyon</i> , 2021, 7, e07568.	1.4	0
41	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> , 2020, 16, 101.	0.1	0