

Gaurav Sablok

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

2,177
citations

236912

25
h-index

265191

42
g-index

91
all docs

91
docs citations

91
times ranked

3260
citing authors

#	ARTICLE	IF	CITATIONS
1	Review: role of carbon sources for in vitro plant growth and development. <i>Molecular Biology Reports</i> , 2013, 40, 2837-2849.	2.3	157
2	Chloroplast Genome Analysis of Resurrection Tertiary Relict <i>Haberlea rhodopensis</i> Highlights Genes Important for Desiccation Stress Response. <i>Frontiers in Plant Science</i> , 2017, 8, 204.	3.6	112
3	High-temperature effect on genes engaged in DNA methylation and affected by DNA methylation in <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2015, 87, 102-108.	5.8	94
4	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). <i>Plant Physiology</i> , 2016, 172, 272-283.	4.8	88
5	Plastome organization and evolution of chloroplast genes in <i>Cardamine</i> species adapted to contrasting habitats. <i>BMC Genomics</i> , 2015, 16, 306.	2.8	83
6	Integrative analysis of <i>Arabidopsis thaliana</i> transcriptomics reveals intuitive splicing mechanism for circular RNA. <i>FEBS Letters</i> , 2016, 590, 3510-3516.	2.8	80
7	Transcriptome analysis reveals the role of the root hairs as environmental sensors to maintain plant functions under water-deficiency conditions. <i>Journal of Experimental Botany</i> , 2016, 67, 1079-1094.	4.8	80
8	Genome-Wide Landscape of Alternative Splicing Events in <i>Brachypodium distachyon</i> . <i>DNA Research</i> , 2013, 20, 163-171.	3.4	69
9	Artificial microRNAs (amiRNAs) engineering – On how microRNA-based silencing methods have affected current plant silencing research. <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 315-319.	2.1	68
10	isomiRex: Web-based identification of microRNAs, isomiR variations and differential expression using next-generation sequencing datasets. <i>FEBS Letters</i> , 2013, 587, 2629-2634.	2.8	61
11	Genome-wide cataloging and analysis of alternatively spliced genes in cereal crops. <i>BMC Genomics</i> , 2015, 16, 721.	2.8	53
12	isomiRs: Increasing Evidences of isomiRs Complexity in Plant Stress Functional Biology. <i>Frontiers in Plant Science</i> , 2015, 6, 949.	3.6	51
13	Proteome Analysis Reveals Extensive Light Stress-Response Reprogramming in the Seagrass <i>Zostera muelleri</i> (Alismatales, Zosteraceae) Metabolism. <i>Frontiers in Plant Science</i> , 2016, 7, 2023.	3.6	48
14	Synonymous Codon Usage, GC3, and Evolutionary Patterns Across Plastomes of Three Pooid Model Species: Emerging Grass Genome Models for Monocots. <i>Molecular Biotechnology</i> , 2011, 49, 116-128.	2.4	47
15	Transcriptomics profiling of Indian mustard (<i>Brassica juncea</i>) under arsenate stress identifies key candidate genes and regulatory pathways. <i>Frontiers in Plant Science</i> , 2015, 6, 646.	3.6	46
16	Genome-wide survey of the seagrass <i>Zostera muelleri</i> suggests modification of the ethylene signalling network. <i>Journal of Experimental Botany</i> , 2015, 66, 1489-1498.	4.8	46
17	Plant Circular RNAs (circRNAs): Transcriptional Regulation Beyond miRNAs in Plants. <i>Molecular Plant</i> , 2016, 9, 192-194.	8.3	46
18	The emergence of molecular profiling and omics techniques in seagrass biology; furthering our understanding of seagrasses. <i>Functional and Integrative Genomics</i> , 2016, 16, 465-480.	3.5	41

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19	AtCircDB: a tissue-specific database for <i>Arabidopsis</i> circular RNAs. <i>Briefings in Bioinformatics</i> , 2019, 20, 58-65.	6.5	40
20	Thiourea priming enhances salt tolerance through co-ordinated regulation of microRNAs and hormones in <i>Brassica juncea</i> . <i>Scientific Reports</i> , 2017, 7, 45490.	3.3	39
21	Fuelling genetic and metabolic exploration of <i>C₃</i> bioenergy crops through the first reference transcriptome of <i>Azadirachta indica</i> . <i>Plant Biotechnology Journal</i> , 2014, 12, 554-567.	8.3	37
22	Phylogenomic discordance suggests polytomies along the backbone of the large genus <i>Solanum</i> . <i>American Journal of Botany</i> , 2022, 109, 580-601.	1.7	36
23	Insight into small RNA abundance and expression in high- and low-temperature stress response using deep sequencing in <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2014, 84, 105-114.	5.8	34
24	Bacterial-induced expression of <i>RAB18</i> protein in <i>Orzya sativa</i> salinity stress and insights into molecular interaction with <i>GTP</i> ligand. <i>Journal of Molecular Recognition</i> , 2014, 27, 521-527.	2.1	32
25	Dissection of early transcriptional responses to water stress in <i>Arundo donax</i> L. by unigene-based RNA-seq. <i>Biotechnology for Biofuels</i> , 2016, 9, 54.	6.2	32
26	Evaluation of Codon Biology in <i>Citrus</i> and <i>Poncirus trifoliata</i> Based on Genomic Features and Frame Corrected Expressed Sequence Tags. <i>DNA Research</i> , 2013, 20, 135-150.	3.4	28
27	miRTar2GO: a novel rule-based model learning method for cell line specific microRNA target prediction that integrates Ago2 CLIP-Seq and validated microRNA target interaction data. <i>Nucleic Acids Research</i> , 2017, 45, e42-e42.	14.5	28
28	Transcriptome analysis of <i>Brachypodium</i> during fungal pathogen infection reveals both shared and distinct defense responses with wheat. <i>Scientific Reports</i> , 2017, 7, 17212.	3.3	27
29	ChloroMitoSSRDB: Open Source Repository of Perfect and Imperfect Repeats in Organelle Genomes for Evolutionary Genomics. <i>DNA Research</i> , 2013, 20, 127-133.	3.4	24
30	Clinical Effects of Xinmailong Therapy in Patients with Chronic Heart Failure. <i>International Journal of Medical Sciences</i> , 2013, 10, 624-633.	2.5	24
31	Emerging Roles and Landscape of Translating mRNAs in Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1443.	3.6	24
32	Genome-wide survey of alternative splicing in the grass <i>Brachypodium distachyon</i> : a emerging model biosystem for plant functional genomics. <i>Biotechnology Letters</i> , 2011, 33, 629-636.	2.2	23
33	Mining of miRNAs and potential targets from gene oriented clusters of transcripts sequences of the anti-malarial plant, <i>Artemisia annua</i> . <i>Biotechnology Letters</i> , 2012, 34, 737-745.	2.2	23
34	Quantitative analysis of the naringenin-inducible proteome in <i>Rhizobium leguminosarum</i> by isobaric tagging and mass spectrometry. <i>Proteomics</i> , 2013, 13, 1961-1972.	2.2	23
35	ChloroMitoSSRDB 2.00: more genomes, more repeats, unifying SSRs search patterns and on-the-fly repeat detection. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav084.	3.0	23
36	Molecular physiology reveals ammonium uptake and related gene expression in the seagrass <i>Zostera muelleri</i> . <i>Marine Environmental Research</i> , 2016, 122, 126-134.	2.5	23

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37	Expression properties exhibit correlated patterns with the fate of duplicated genes, their divergence, and transcriptional plasticity in Saccharomycotina. <i>DNA Research</i> , 2017, 24, 559-570.	3.4	23
38	Exploring the phylogeny of the marattialean ferns. <i>Cladistics</i> , 2020, 36, 569-593.	3.3	20
39	isomiR2Function: An Integrated Workflow for Identifying MicroRNA Variants in Plants. <i>Frontiers in Plant Science</i> , 2017, 08, 322.	3.6	19
40	Sequencing the Plastid Genome of Giant Ragweed (<i>Ambrosia trifida</i> , Asteraceae) From a Herbarium Specimen. <i>Frontiers in Plant Science</i> , 2019, 10, 218.	3.6	18
41	Comparative landscape of alternative splicing in fruit plants. <i>Current Plant Biology</i> , 2017, 9-10, 29-36.	4.7	16
42	High-Throughput RAD-SNP Genotyping for Characterization of Sugar Beet Genotypes. <i>Plant Molecular Biology Reporter</i> , 2013, 32, 691.	1.8	15
43	Draft Genome Sequence of the Nitrogen-Fixing <i>Rhizobium sulae</i> Type Strain IS123T Focusing on the Key Genes for Symbiosis with its Host <i>Hedysarum coronarium</i> L. <i>Frontiers in Microbiology</i> , 2017, 8, 1348.	3.5	15
44	Suppression Subtractive Hybridization and NGS Reveal Differential Transcriptome Expression Profiles in Wayfaring Tree (<i>Viburnum lantana</i> L.) Treated with Ozone. <i>Frontiers in Plant Science</i> , 2016, 7, 713.	3.6	12
45	SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. <i>Scientific Reports</i> , 2018, 8, 2749.	3.3	12
46	Genome dynamics in three different geographical isolates of white spot syndrome virus (WSSV). <i>Archives of Virology</i> , 2012, 157, 2357-2362.	2.1	10
47	SplicingTypesAnno: Annotating and quantifying alternative splicing events for RNA-Seq data. <i>Computer Methods and Programs in Biomedicine</i> , 2015, 119, 53-62.	4.7	10
48	Development of a panel of unigene-derived polymorphic EST-SSR markers in lentil using public database information. <i>Crop Journal</i> , 2016, 4, 425-433.	5.2	10
49	Molecular Dynamic Simulation and Inhibitor Prediction of Cysteine Synthase Structured Model as a Potential Drug Target for Trichomoniasis. <i>BioMed Research International</i> , 2013, 2013, 1-15.	1.9	9
50	nagnag: Identification and quantification of NAGNAG alternative splicing using RNA-Seq data. <i>FEBS Letters</i> , 2015, 589, 1766-1770.	2.8	9
51	Dynamics of soil prokaryotes catalyzing nitrification and denitrification in response to different fertilizers in a greenhouse experiment with <i>Cynodon dactylon</i> . <i>European Journal of Soil Biology</i> , 2016, 76, 83-91.	3.2	9
52	Investigating the Conformational Structure and Potential Site Interactions of SOD Inhibitors on Ec-SOD in Marine Mud Crab <i>Scylla serrata</i> : A Molecular Modeling Approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 312-318.	3.6	9
53	Identification and validation of reference genes for quantitative real-time PCR under salt stress in a halophyte, <i>Sesuvium portulacastrum</i> . <i>Plant Gene</i> , 2018, 13, 18-24.	2.3	9
54	In silico identification and characterization of a diverse subset of conserved microRNAs in bioenergy crop <i>Arundo donax</i> L.. <i>Scientific Reports</i> , 2018, 8, 16667.	3.3	9

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55	Diff isomiRs: Large-scale detection of differential isomiRs for understanding non-coding regulated stress omics in plants. <i>Scientific Reports</i> , 2019, 9, 1406.	3.3	9
56	Bioinformatic analysis of fruit-specific expressed sequence tag libraries of <i>Diospyros kaki</i> Thunb.: view at the transcriptome at different developmental stages. <i>3 Biotech</i> , 2011, 1, 35-45.	2.2	8
57	Screening features to improve the class prediction of acute myeloid leukemia and myelodysplastic syndrome. <i>Gene</i> , 2013, 512, 348-354.	2.2	8
58	Chloroplast genomics: Expanding resources for an evolutionary conserved miniature molecule with enigmatic applications. <i>Current Plant Biology</i> , 2016, 7-8, 34-38.	4.7	8
59	Growing Diversity of Plant MicroRNAs and MIR-Derived Small RNAs. <i>RNA Technologies</i> , 2017, , 49-67.	0.3	8
60	tRNA Derived smallRNAs: smallRNAs Repertoire Has Yet to Be Decoded in Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1167.	3.6	8
61	Combinational effect of mutational bias and translational selection for translation efficiency in tomato (<i>Solanum lycopersicum</i>) cv. Micro-Tom. <i>Genomics</i> , 2013, 101, 290-295.	2.9	7
62	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.	3.0	7
63	Comparative assessment of chloroplast transcriptional responses highlights conserved and unique patterns across Triticeae members under salt stress. <i>Photosynthesis Research</i> , 2018, 136, 357-369.	2.9	7
64	Plant IsomiR Atlas: Large Scale Detection, Profiling, and Target Repertoire of IsomiRs in Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 1881.	3.6	7
65	Expression patterns of photoperiod and temperature regulated heading date genes in <i>Oryza sativa</i> . <i>Computational Biology and Chemistry</i> , 2013, 45, 36-41.	2.3	5
66	Marine Viruses: the Beneficial Side of a Threat. <i>Applied Biochemistry and Biotechnology</i> , 2014, 174, 2368-2379.	2.9	5
67	Microenvironment and phylogenetic diversity of <i>rochloron</i> inhabiting the surface of crustose didemnid ascidians. <i>Environmental Microbiology</i> , 2015, 17, 4121-4132.	3.8	5
68	Identification of Low Temperature Stress Regulated Transcript Sequences and Gene Families in Italian Cypress. <i>Molecular Biotechnology</i> , 2015, 57, 407-418.	2.4	5
69	PlantFuncSSR: Integrating First and Next Generation Transcriptomics for Mining of SSR-Functional Domains Markers. <i>Frontiers in Plant Science</i> , 2016, 7, 878.	3.6	5
70	Altools: a user friendly NGS data analyser. <i>Biology Direct</i> , 2016, 11, 8.	4.6	5
71	The Evolutionary Basis of Translational Accuracy in Plants. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2363-2373.	1.8	5
72	Method for the Large-Scale Identification of phasiRNAs in <i>Brachypodium distachyon</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 187-194.	0.9	5

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73	Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the "Triplod Bridge" in <i>Arundo</i> (Poaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5247.	4.1	5
74	Identification, development, and application of cross-species intron-spanning markers in lentil (<i>Lens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	9.2	3
75	Response of Bacterial Communities upon Application of Different Innovative Organic Fertilizers in a Greenhouse Experiment Using Low-Nutrient Soil Cultivated with <i>Cynodon dactylon</i> . <i>Soil Systems</i> , 2018, 2, 52.	2.6	3
76	Protocols for miRNA Target Prediction in Plants. <i>Methods in Molecular Biology</i> , 2019, 1970, 65-73.	0.9	3
77	ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. <i>DNA Research</i> , 2017, 24, 327-332.	3.4	2
78	NAMS: Noncoding Assessment of long RNAs in Magnoliophyta Species. <i>Methods in Molecular Biology</i> , 2019, 1933, 257-264.	0.9	2
79	Estimate Codon Usage Bias Using Codon Usage Analyzer (CUA). <i>Methods in Molecular Biology</i> , 2018, 1667, 139-148.	0.9	1
80	Protocol for Coexpression Network Construction and Stress-Responsive Expression Analysis in <i>Brachypodium</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 203-221.	0.9	1
81	<i>Brachypodium</i> Genomics. <i>Methods in Molecular Biology</i> , 2018, , .	0.9	1
82	Next Generation Sequencing for Better Understanding Alternative Splicing: Way Ahead for Model and Non-Model Plants. <i>Transcriptomics: Open Access</i> , 2013, 01, .	0.2	1
83	AtNAGNAG. , 2018, , .		1
84	Pretty cloud: Visualizing weighted and grouped genomic context with mathematical curves. , 2017, , .		0
85	Evaluation of Genome-Wide Markers and Orthologous Markers in <i>Brachypodium distachyon</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 195-201.	0.9	0