Gaurav Sablok

List of Publications by Year
in descending order

85 papers	2,177 citations	236925 25 h-index	265206 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. Molecular Biology Reports, 2013, 40, 2837-2849.	2.3	157
2	Chloroplast Genome Analysis of Resurrection Tertiary Relict Haberlea rhodopensis Highlights Genes Important for Desiccation Stress Response. Frontiers in Plant Science, 2017, 8, 204.	3.6	112
3	High-temperature effect on genes engaged in DNA methylation and affected by DNA methylation in Arabidopsis. Plant Physiology and Biochemistry, 2015, 87, 102-108.	5.8	94
4	The Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*). Plant Physiology, 2016, 172, 272-283.	4.8	88
5	Plastome organization and evolution of chloroplast genes in Cardamine species adapted to contrasting habitats. BMC Genomics, 2015, 16, 306.	2.8	83
6	Integrative analysis of *Arabidopsis thaliana* transcriptomics reveals intuitive splicing mechanism for circular RNA. FEBS Letters, 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. Journal of Experimental Botany, 2016, 67, 1079-1094.	4.8	80
8	Genome-Wide Landscape of Alternative Splicing Events in Brachypodium distachyon. DNA Research, 2013, 20, 163-171.	3.4	69
9	Artificial microRNAs (amiRNAs) engineering â€" On how microRNA-based silencing methods have affected current plant silencing research. Biochemical and Biophysical Research Communications, 2011, 406, 315-319.	2.1	68
10	isomiRex: Webâ€based identification of microRNAs, isomiR variations and differential expression using nextâ€generation sequencing datasets. FEBS Letters, 2013, 587, 2629-2634.	2.8	61
11	Genome-wide cataloging and analysis of alternatively spliced genes in cereal crops. BMC Genomics, 2015, 16, 721.	2.8	53
12	isomiRs: Increasing Evidences of isomiRs Complexity in Plant Stress Functional Biology. Frontiers in Plant Science, 2015, 6, 949.	3.6	51
13	Proteome Analysis Reveals Extensive Light Stress-Response Reprogramming in the Seagrass Zostera muelleri (Alismatales, Zosteraceae) Metabolism. Frontiers in Plant Science, 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. Molecular Biotechnology, 2011, 49, 116-128.	2.4	47
15	Transcriptomics profiling of Indian mustard (Brassica juncea) under arsenate stress identifies key candidate genes and regulatory pathways. Frontiers in Plant Science, 2015, 6, 646.	3.6	46
16	Genome-wide survey of the seagrass Zostera muelleri suggests modification of the ethylene signalling network. Journal of Experimental Botany, 2015, 66, 1489-1498.	4.8	46
17	Plant Circular RNAs (circRNAs): Transcriptional Regulation Beyond miRNAs in Plants. Molecular Plant, 2016, 9, 192-194.	8.3	46
18	The emergence of molecular profiling and omics techniques in seagrass biology; furthering our understanding of seagrasses. Functional and Integrative Genomics, 2016, 16, 465-480.	3.5	41

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19	AtCircDB: a tissue-specific database for *Arabidopsis* circular RNAs. Briefings in Bioinformatics, 2019, 20, 58-65.	6.5	40
20	Thiourea priming enhances salt tolerance through co-ordinated regulation of microRNAs and hormones in Brassica juncea. Scientific Reports, 2017, 7, 45490.	3.3	39
21	Fuelling genetic and metabolic exploration of C$_3$ bioenergy crops through the first reference transcriptome of *Arundo donax L*.. Plant Biotechnology Journal, 2014, 12, 554-567.	8.3	37
22	Phylogenomic discordance suggests polytomies along the backbone of the large genus *Solanum*. American Journal of Botany, 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 Arabidopsis. Plant Physiology and Biochemistry, 2014, 84, 105-114.	5.8	34
24	Bacterial-induced expression of *RAB18* protein in *Orzya sativa* salinity stress and insights into molecular interaction with *GTP* ligand. Journal of Molecular Recognition, 2014, 27, 521-527.	2.1	32
25	Dissection of early transcriptional responses to water stress in Arundo donax L. by unigene-based RNA-seq. Biotechnology for Biofuels, 2016, 9, 54.	6.2	32
26	Evaluation of Codon Biology in Citrus and Poncirus trifoliata Based on Genomic Features and Frame Corrected Expressed Sequence Tags. DNA Research, 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. Nucleic Acids Research, 2017, 45, e42-e42.	14.5	28
28	Transcriptome analysis of Brachypodium during fungal pathogen infection reveals both shared and distinct defense responses with wheat. Scientific Reports, 2017, 7, 17212.	3.3	27
29	ChloroMitoSSRDB: Open Source Repository of Perfect and Imperfect Repeats in Organelle Genomes for Evolutionary Genomics. DNA Research, 2013, 20, 127-133.	3.4	24
30	Clinical Effects of Xinmailong Therapy in Patients with Chronic Heart Failure. International Journal of Medical Sciences, 2013, 10, 624-633.	2.5	24
31	Emerging Roles and Landscape of Translating mRNAs in Plants. Frontiers in Plant Science, 2017, 8, 1443.	3.6	24
32	Genome-wide survey of alternative splicing in the grass Brachypodium distachyon: a emerging model biosystem for plant functional genomics. Biotechnology Letters, 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, Artemisia annua. Biotechnology Letters, 2012, 34, 737-745.	2.2	23
34	Quantitative analysis of the naringenin-inducible proteome in *Rhizobium leguminosarum* by isobaric tagging and mass spectrometry. Proteomics, 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. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav084.	3.0	23
36	Molecular physiology reveals ammonium uptake and related gene expression in the seagrass Zostera muelleri. Marine Environmental Research, 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. DNA Research, 2017, 24, 559-570.	3.4	23
38	Exploring the phylogeny of the marattialean ferns. Cladistics, 2020, 36, 569-593.	3.3	20
39	isomiR2Function: An Integrated Workflow for Identifying MicroRNA Variants in Plants. Frontiers in Plant Science, 2017, 08, 322.	3.6	19
40	Sequencing the Plastid Genome of Giant Ragweed (Ambrosia trifida, Asteraceae) From a Herbarium Specimen. Frontiers in Plant Science, 2019, 10, 218.	3.6	18
41	Comparative landscape of alternative splicing in fruit plants. Current Plant Biology, 2017, 9-10, 29-36.	4.7	16
42	High-Throughput RAD-SNP Genotyping for Characterization of Sugar Beet Genotypes. Plant Molecular Biology Reporter, 2013, 32, 691.	1.8	15
43	Draft Genome Sequence of the Nitrogen-Fixing Rhizobium sullae Type Strain IS123T Focusing on the Key Genes for Symbiosis with its Host Hedysarum coronarium L.. Frontiers in Microbiology, 2017, 8, 1348.	3.5	15
44	Suppression Substractive Hybridization and NGS Reveal Differential Transcriptome Expression Profiles in Wayfaring Tree (Viburnum lantana L.) Treated with Ozone. Frontiers in Plant Science, 2016, 7, 713.	3.6	12
45	SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. Scientific Reports, 2018, 8, 2749.	3.3	12
46	Genome dynamics in three different geographical isolates of white spot syndrome virus (WSSV). Archives of Virology, 2012, 157, 2357-2362.	2.1	10
47	SplicingTypesAnno: Annotating and quantifying alternative splicing events for RNA-Seq data. Computer Methods and Programs in Biomedicine, 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. Crop Journal, 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. BioMed Research International, 2013, 2013, 1-15.	1.9	9
50	nagnag: Identification and quantification of NAGNAG alternative splicing using RNA-Seq data. FEBS Letters, 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 Cynodon dactylon. European Journal of Soil Biology, 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 Scylla serrata: A Molecular Modeling Approach. Interdisciplinary Sciences, Computational Life Sciences, 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, Sesuvium portulacastrum. Plant Gene, 2018, 13, 18-24.	2.3	9
54	In silico identification and characterization of a diverse subset of conserved microRNAs in bioenergy crop Arundo donax L.. Scientific Reports, 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. Scientific Reports, 2019, 9, 1406.	3.3	9
56	Bioinformatic analysis of fruit-specific expressed sequence tag libraries of Diospyros kaki Thunb.: view at the transcriptome at different developmental stages. 3 Biotech, 2011, 1, 35-45.	2.2	8
57	Screening features to improve the class prediction of acute myeloid leukemia and myelodysplastic syndrome. Gene, 2013, 512, 348-354.	2.2	8
58	Chloroplast genomics: Expanding resources for an evolutionary conserved miniature molecule with enigmatic applications. Current Plant Biology, 2016, 7-8, 34-38.	4.7	8
59	Growing Diversity of Plant MicroRNAs and MIR-Derived Small RNAs. RNA Technologies, 2017, , 49-67.	0.3	8
60	tRNA Derived smallRNAs: smallRNAs Repertoire Has Yet to Be Decoded in Plants. Frontiers in Plant Science, 2017, 8, 1167.	3.6	8
61	Combinational effect of mutational bias and translational selection for translation efficiency in tomato (Solanum lycopersicum) cv. Micro-Tom. Genomics, 2013, 101, 290-295.	2.9	7
62	SBMDb: first whole genome putative microsatellite DNA marker database of sugarbeet for bioenergy and industrial applications. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav111.	3.0	7
63	Comparative assessment of chloroplast transcriptional responses highlights conserved and unique patterns across Triticeae members under salt stress. Photosynthesis Research, 2018, 136, 357-369.	2.9	7
64	Plant IsomiR Atlas: Large Scale Detection, Profiling, and Target Repertoire of IsomiRs in Plants. Frontiers in Plant Science, 2018, 9, 1881.	3.6	7
65	Expression patterns of photoperiod and temperature regulated heading date genes in Oryza sativa. Computational Biology and Chemistry, 2013, 45, 36-41.	2.3	5
66	Marine Viruses: the Beneficial Side of a Threat. Applied Biochemistry and Biotechnology, 2014, 174, 2368-2379.	2.9	5
67	Microenvironment and phylogenetic diversity of *P*rochloron inhabiting the surface of crustose didemnid ascidians. Environmental Microbiology, 2015, 17, 4121-4132.	3.8	5
68	Identification of Low Temperature Stress Regulated Transcript Sequences and Gene Families in Italian Cypress. Molecular Biotechnology, 2015, 57, 407-418.	2.4	5
69	PlantFuncSSR: Integrating First and Next Generation Transcriptomics for Mining of SSR-Functional Domains Markers. Frontiers in Plant Science, 2016, 7, 878.	3.6	5
70	Altools: a user friendly NGS data analyser. Biology Direct, 2016, 11, 8.	4.6	5
71	The Evolutionary Basis of Translational Accuracy in Plants. G3: Genes, Genomes, Genetics, 2017, 7, 2363-2373.	1.8	5
72	Method for the Large-Scale Identification of phasiRNAs in Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 187-194.	0.9	5

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73	Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the â€œTriploid Bridgeâ€•in Arundo (Poaceae). International Journal of Molecular Sciences, 2020, 21, 5247.	4.1	5
74	Identification, development, and application of cross-species intron-spanning markers in lentil (Lens) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	5.2	3
75	Response of Bacterial Communities upon Application of Different Innovative Organic Fertilizers in a Greenhouse Experiment Using Low-Nutrient Soil Cultivated with Cynodon dactylon. Soil Systems, 2018, 2, 52.	2.6	3
76	Protocols for miRNA Target Prediction in Plants. Methods in Molecular Biology, 2019, 1970, 65-73.	0.9	3
77	ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. DNA Research, 2017, 24, 327-332.	3.4	2
78	NAMS: Noncoding Assessment of long RNAs in Magnoliophyta Species. Methods in Molecular Biology, 2019, 1933, 257-264.	0.9	2
79	Estimate Codon Usage Bias Using Codon Usage Analyzer (CUA). Methods in Molecular Biology, 2018, 1667, 139-148.	0.9	1
80	Protocol for Coexpression Network Construction and Stress-Responsive Expression Analysis in Brachypodium. Methods in Molecular Biology, 2018, 1667, 203-221.	0.9	1
81	Brachypodium Genomics. Methods in Molecular Biology, 2018, , .	0.9	1
82	Next Generation Sequencing for Better Understanding Alternative Splicing: Way Ahead for Model and Non-Model Plants. Transcriptomics: Open Access, 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 Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 195-201.	0.9	0