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	Phylogenomic discordance suggests polytomies along the backbone of the large genus <i>Solanum</i>. American Journal of Botany, 2022, 109, 580-601.	1.7	36
2	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
3	Exploring the phylogeny of the marattialean ferns. Cladistics, 2020, 36, 569-593.	3.3	20
4	NAMS: Noncoding Assessment of long RNAs in Magnoliophyta Species. Methods in Molecular Biology, 2019, 1933, 257-264.	0.9	2
5	Sequencing the Plastid Genome of Giant Ragweed (Ambrosia trifida, Asteraceae) From a Herbarium Specimen. Frontiers in Plant Science, 2019, 10, 218.	3.6	18
6	Protocols for miRNA Target Prediction in Plants. Methods in Molecular Biology, 2019, 1970, 65-73.	0.9	3
7	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
8	AtCircDB: a tissue-specific database for<i>Arabidopsis</i>circular RNAs. Briefings in Bioinformatics, 2019, 20, 58-65.	6.5	40
9	SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. Scientific Reports, 2018, 8, 2749.	3.3	12
10	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
11	Estimate Codon Usage Bias Using Codon Usage Analyzer (CUA). Methods in Molecular Biology, 2018, 1667, 139-148.	0.9	1
12	Evaluation of Genome-Wide Markers and Orthologous Markers in Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 195-201.	0.9	0
13	Method for the Large-Scale Identification of phasiRNAs in Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 187-194.	0.9	5
14	Protocol for Coexpression Network Construction and Stress-Responsive Expression Analysis in Brachypodium. Methods in Molecular Biology, 2018, 1667, 203-221.	0.9	1
15	Brachypodium Genomics. Methods in Molecular Biology, 2018, , .	0.9	1
16	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
17	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
18	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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19	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
20	Plant IsomiR Atlas: Large Scale Detection, Profiling, and Target Repertoire of IsomiRs in Plants. Frontiers in Plant Science, 2018, 9, 1881.	3.6	7
21	AtNAGNAG. , 2018, , .		1
22	ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. DNA Research, 2017, 24, 327-332.	3.4	2
23	Growing Diversity of Plant MicroRNAs and MIR-Derived Small RNAs. RNA Technologies, 2017, , 49-67.	0.3	8
24	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
25	The Evolutionary Basis of Translational Accuracy in Plants. G3: Genes, Genomes, Genetics, 2017, 7, 2363-2373.	1.8	5
26	Thiourea priming enhances salt tolerance through co-ordinated regulation of microRNAs and hormones in Brassica juncea. Scientific Reports, 2017, 7, 45490.	3.3	39
27	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
28	Comparative landscape of alternative splicing in fruit plants. Current Plant Biology, 2017, 9-10, 29-36.	4.7	16
29	Pretty cloud: Visualizing weighted and grouped genomic context with mathematical curves. , 2017, , .		0
30	miRTar2GO: a novel rule-based model learning method for cell line specific microRNA target prediction that integrates Ago2 CLIP-Seq and validated microRNAâ€"target interaction data. Nucleic Acids Research, 2017, 45, e42-e42.	14.5	28
31	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
32	isomiR2Function: An Integrated Workflow for Identifying MicroRNA Variants in Plants. Frontiers in Plant Science, 2017, 08, 322.	3.6	19
33	tRNA Derived smallRNAs: smallRNAs Repertoire Has Yet to Be Decoded in Plants. Frontiers in Plant Science, 2017, 8, 1167.	3.6	8
34	Emerging Roles and Landscape of Translating mRNAs in Plants. Frontiers in Plant Science, 2017, 8, 1443.	3.6	24
35	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
36	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

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37	PlantFuncSSR: Integrating First and Next Generation Transcriptomics for Mining of SSR-Functional Domains Markers. Frontiers in Plant Science, 2016, 7, 878.	3.6	5
38	Chloroplast genomics: Expanding resources for an evolutionary conserved miniature molecule with enigmatic applications. Current Plant Biology, 2016, 7-8, 34-38.	4.7	8
39	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
40	Integrative analysis of *Arabidopsis thaliana* transcriptomics reveals intuitive splicing mechanism for circular RNA. FEBS Letters, 2016, 590, 3510-3516.	2.8	80
41	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
42	The Genome of a Southern Hemisphere Seagrass Species (*Zostera muelleri*). Plant Physiology, 2016, 172, 272-283.	4.8	88
43	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
44	Molecular physiology reveals ammonium uptake and related gene expression in the seagrass Zostera muelleri. Marine Environmental Research, 2016, 122, 126-134.	2.5	23
45	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
46	Altools: a user friendly NGS data analyser. Biology Direct, 2016, 11, 8.	4.6	5
47	Plant Circular RNAs (circRNAs): Transcriptional Regulation Beyond miRNAs in Plants. Molecular Plant, 2016, 9, 192-194.	8.3	46
48	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
49	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
50	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
51	Microenvironment and phylogenetic diversity of *P*rochloron inhabiting the surface of crustose didemnid ascidians. Environmental Microbiology, 2015, 17, 4121-4132.	3.8	5
52	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
53	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
54	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

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55	isomiRs: Increasing Evidences of isomiRs Complexity in Plant Stress Functional Biology. Frontiers in Plant Science, 2015, 6, 949.	3.6	51
56	nagnag: Identification and quantification of NAGNAG alternative splicing using RNA‑Seq data. FEBS Letters, 2015, 589, 1766-1770.	2.8	9
57	Genome-wide cataloging and analysis of alternatively spliced genes in cereal crops. BMC Genomics, 2015, 16, 721.	2.8	53
58	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
59	Identification of Low Temperature Stress Regulated Transcript Sequences and Gene Families in Italian Cypress. Molecular Biotechnology, 2015, 57, 407-418.	2.4	5
60	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
61	SplicingTypesAnno: Annotating and quantifying alternative splicing events for RNA-Seq data. Computer Methods and Programs in Biomedicine, 2015, 119, 53-62.	4.7	10
62	Plastome organization and evolution of chloroplast genes in Cardamine species adapted to contrasting habitats. BMC Genomics, 2015, 16, 306.	2.8	83
63	Fuelling genetic and metabolic exploration of C_3 bioenergy crops through the first reference transcriptome of *A*rundo donax *L*.. Plant Biotechnology Journal, 2014, 12, 554-567.	8.3	37
64	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
65	Marine Viruses: the Beneficial Side of a Threat. Applied Biochemistry and Biotechnology, 2014, 174, 2368-2379.	2.9	5
66	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
67	isomiRex: Web‑based identification of microRNAs, isomiR variations and differential expression using next‑generation sequencing datasets. FEBS Letters, 2013, 587, 2629-2634.	2.8	61
68	Quantitative analysis of the naringenin-inducible proteome in *Rhizobium leguminosarum* by isobaric tagging and mass spectrometry. Proteomics, 2013, 13, 1961-1972.	2.2	23
69	Expression patterns of photoperiod and temperature regulated heading date genes in Oryza sativa. Computational Biology and Chemistry, 2013, 45, 36-41.	2.3	5
70	Review: role of carbon sources for in vitro plant growth and development. Molecular Biology Reports, 2013, 40, 2837-2849.	2.3	157
71	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
72	Screening features to improve the class prediction of acute myeloid leukemia and myelodysplastic syndrome. Gene, 2013, 512, 348-354.	2.2	8

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73	High-Throughput RAD-SNP Genotyping for Characterization of Sugar Beet Genotypes. Plant Molecular Biology Reporter, 2013, 32, 691.	1.8	15
74	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
75	Genome-Wide Landscape of Alternative Splicing Events in Brachypodium distachyon. DNA Research, 2013, 20, 163-171.	3.4	69
76	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
77	ChloroMitoSSRDB: Open Source Repository of Perfect and Imperfect Repeats in Organelle Genomes for Evolutionary Genomics. DNA Research, 2013, 20, 127-133.	3.4	24
78	Clinical Effects of Xinmailong Therapy in Patients with Chronic Heart Failure. International Journal of Medical Sciences, 2013, 10, 624-633.	2.5	24
79	Next Generation Sequencing for Better Understanding Alternative Splicing: Way Ahead for Model and Non-Model Plants. Transcriptomics: Open Access, 2013, 01, .	0.2	1
80	Genome dynamics in three different geographical isolates of white spot syndrome virus (WSSV). Archives of Virology, 2012, 157, 2357-2362.	2.1	10
81	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
82	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
83	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
84	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
85	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