

Avinash Sreedasyam

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

2,238
citations

361413

20
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

3208
citing authors

#	ARTICLE	IF	CITATIONS
1	Soybean (<i>Glycine max</i>) Haplotype Map (GmHapMap): a universal resource for soybean translational and functional genomics. <i>Plant Biotechnology Journal</i> , 2021, 19, 324-334.	8.3	48
2	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
3	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
4	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
5	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
6	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
7	PEATmoss (<i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	5.7	74
8	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
9	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , 2020, 38, 1203-1210.	17.5	103
10	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
11	Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	3.6	13
12	Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. <i>Frontiers in Genetics</i> , 2019, 10, 487.	2.3	11
13	Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. <i>Frontiers in Genetics</i> , 2019, 10, 417.	2.3	20
14	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
15	Engineering Tree Seasonal Cycles of Growth Through Chromatin Modification. <i>Frontiers in Plant Science</i> , 2019, 10, 412.	3.6	17
16	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , 2018, 95, 168-182.	5.7	115
17	Molecular and phenotypic diversity of ICARDA spring barley (<i>Hordeum vulgare</i> L.) collection. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 255-269.	1.6	25
18	Flaxseed Consumption Inhibits Chemically Induced Lung Tumorigenesis and Modulates Expression of Phase II Enzymes and Inflammatory Cytokines in A/J Mice. <i>Cancer Prevention Research</i> , 2018, 11, 27-37.	1.5	22

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19	The <i>Sorghum bicolor</i> reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. <i>Plant Journal</i> , 2018, 93, 338-354.	5.7	431
20	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	12.8	101
21	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , 2018, 11, 170.	6.2	30
22	Piperlongumine potentiates the effects of gemcitabine in <i>in vitro</i> and <i>in vivo</i> human pancreatic cancer models. <i>Oncotarget</i> , 2018, 9, 10457-10469.	1.8	21
23	PlantSEED enables automated annotation and reconstruction of plant primary metabolism with improved compartmentalization and comparative consistency. <i>Plant Journal</i> , 2018, 95, 1102-1113.	5.7	25
24	Drought responsive gene expression regulatory divergence between upland and lowland ecotypes of a perennial C ₄ grass. <i>Genome Research</i> , 2016, 26, 510-518.	5.5	52
25	Using Deep RNA Sequencing for the Structural Annotation of the <i>Laccaria Bicolor</i> Mycorrhizal Transcriptome. <i>PLoS ONE</i> , 2010, 5, e9780.	2.5	32