

Babu Valliyodan

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

10,119
citations

76326

40
h-index

71685

76
g-index

87
all docs

87
docs citations

87
times ranked

10509
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	2.8	53
2	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	9.5	20
3	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus <i>cqProt-003</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 1443-1455.	3.6	13
4	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction. <i>BMC Plant Biology</i> , 2022, 22, 180.	3.6	15
5	Mapping of partial resistance to <i>Phytophthora sojae</i> in soybean PIs using whole-genome sequencing reveals a major QTL. <i>Plant Genome</i> , 2022, 15, e20184.	2.8	11
6	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
7	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
8	The importance of slow canopy wilting in drought tolerance in soybean. <i>Journal of Experimental Botany</i> , 2020, 71, 642-652.	4.8	49
9	Whole-genome resequencing identifies quantitative trait loci associated with mycorrhizal colonization of soybean. <i>Theoretical and Applied Genetics</i> , 2020, 133, 409-417.	3.6	19
10	Mapping Quantitative Trait Loci for Soybean Seedling Shoot and Root Architecture Traits in an Inter-Specific Genetic Population. <i>Frontiers in Plant Science</i> , 2020, 11, 1284.	3.6	19
11	Molecular and genetic bases of heat stress responses in crop plants and breeding for increased resilience and productivity. <i>Journal of Experimental Botany</i> , 2020, 71, 3780-3802.	4.8	186
12	The renoprotective effects of soy protein in the aging kidney. <i>Medical Research Archives</i> , 2020, 8, .	0.2	4
13	Understanding genetic control of root system architecture in soybean: Insights into the genetic basis of lateral root number. <i>Plant, Cell and Environment</i> , 2019, 42, 212-229.	5.7	36
14	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
15	Genome-wide transcriptional profiling for elucidating the effects of brassinosteroids on <i>Glycine max</i> during early vegetative development. <i>Scientific Reports</i> , 2019, 9, 16085.	3.3	12
16	Whole-genome resequencing reveals the impact of the interaction of copy number variants of the <i>Rhg1</i> and <i>Rhg4</i> genes on broad-based resistance to soybean cyst nematode. <i>Plant Biotechnology Journal</i> , 2019, 17, 1595-1611.	8.3	65
17	Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. <i>BMC Genomics</i> , 2019, 20, 318.	2.8	46
18	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	12.8	183

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19	GmBZL3 acts as a major BR signaling regulator through crosstalk with multiple pathways in Glycine max. BMC Plant Biology, 2019, 19, 86.	3.6	10
20	Adapting legume crops to climate change using genomic approaches. Plant, Cell and Environment, 2019, 42, 6-19.	5.7	74
21	Nutritional Composition of the Green Leaves of Quinoa (Chenopodium quinoa Willd.). Journal of Food Research, 2019, 8, 55.	0.3	27
22	Genetic diversity of root system architecture in response to drought stress in grain legumes. Journal of Experimental Botany, 2018, 69, 3267-3277.	4.8	124
23	A major natural genetic variation associated with root system architecture and plasticity improves waterlogging tolerance and yield in soybean. Plant, Cell and Environment, 2018, 41, 2169-2182.	5.7	47
24	Dissecting genomic hotspots underlying seed protein, oil, and sucrose content in an interspecific mapping population of soybean using high-density linkage mapping. Plant Biotechnology Journal, 2018, 16, 1939-1953.	8.3	93
25	Comparative genome analysis to identify SNPs associated with high oleic acid and elevated protein content in soybean. Genome, 2018, 61, 217-222.	2.0	6
26	Prediction of Soybean Root Response in the Field Using Nondestructive Seedling Three-Dimensional Root Features. The Plant Phenome Journal, 2018, 1, 1-15.	2.0	6
27	Characterization of the XTH Gene Family: New Insight to the Roles in Soybean Flooding Tolerance. International Journal of Molecular Sciences, 2018, 19, 2705.	4.1	47
28	Advances in Genetics and Breeding of Salt Tolerance in Soybean. , 2018, , 217-237.		4
29	Genetic diversity and genomic strategies for improving drought and waterlogging tolerance in soybeans. Journal of Experimental Botany, 2017, 68, erw433.	4.8	118
30	Root xylem plasticity to improve water use and yield in water-stressed soybean. Journal of Experimental Botany, 2017, 68, erw472.	4.8	81
31	Sequencing, Assembly, and Annotation of the Soybean Genome. Compendium of Plant Genomes, 2017, , 73-82.	0.5	5
32	From Hype to Hope: Genome-Wide Association Studies in Soybean. Compendium of Plant Genomes, 2017, , 95-109.	0.5	0
33	Comprehensive Analysis of the Soybean (Glycine max) GmLAX Auxin Transporter Gene Family. Frontiers in Plant Science, 2016, 7, 282.	3.6	18
34	Identification and Comparative Analysis of Differential Gene Expression in Soybean Leaf Tissue under Drought and Flooding Stress Revealed by RNA-Seq. Frontiers in Plant Science, 2016, 7, 1044.	3.6	116
35	Soybean TIP Gene Family Analysis and Characterization of GmTIP1;5 and GmTIP2;5 Water Transport Activity. Frontiers in Plant Science, 2016, 7, 1564.	3.6	30
36	Evaluation of high yielding soybean germplasm under water limitation. Journal of Integrative Plant Biology, 2016, 58, 475-491.	8.5	29

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37	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	3.3	151
38	Small RNA profiles in soybean primary root tips under water deficit. <i>BMC Systems Biology</i> , 2016, 10, 126.	3.0	33
39	Genomic-assisted haplotype analysis and the development of high-throughput SNP markers for salinity tolerance in soybean. <i>Scientific Reports</i> , 2016, 6, 19199.	3.3	161
40	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. <i>BMC Genomics</i> , 2016, 17, 57.	2.8	99
41	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	8.3	221
42	Neglecting legumes has compromised human health and sustainable food production. <i>Nature Plants</i> , 2016, 2, 16112.	9.3	529
43	PGen: large-scale genomic variations analysis workflow and browser in SoyKB. <i>BMC Bioinformatics</i> , 2016, 17, 337.	2.6	27
44	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. <i>BMC Genomics</i> , 2016, 17, 110.	2.8	43
45	Genomic-assisted phylogenetic analysis and marker development for next generation soybean cyst nematode resistance breeding. <i>Plant Science</i> , 2016, 242, 342-350.	3.6	78
46	Application of Digital PCR in the Analysis of Transgenic Soybean Plants. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2016, 07, 403-417.	0.7	17
47	Genome-wide analysis and expression profiling of the PIN auxin transporter gene family in soybean (<i>Glycine max</i>). <i>BMC Genomics</i> , 2015, 16, 951.	2.8	55
48	A Bayesian model for detection of high-order interactions among genetic variants in genome-wide association studies. <i>BMC Genomics</i> , 2015, 16, 1011.	2.8	31
49	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	3.6	243
50	Expanding Omics Resources for Improvement of Soybean Seed Composition Traits. <i>Frontiers in Plant Science</i> , 2015, 6, 1021.	3.6	105
51	A Simple Analytical Method for High-Throughput Screening of Major Sugars from Soybean by Normal-Phase HPLC with Evaporative Light Scattering Detection. <i>Chromatography Research International</i> , 2015, 2015, 1-8.	0.4	19
52	Genome-wide expression analysis of soybean NF-Y genes reveals potential function in development and drought response. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1095-1115.	2.1	85
53	Genetic variants in root architecture-related genes in a <i>Glycine soja</i> accession, a potential resource to improve cultivated soybean. <i>BMC Genomics</i> , 2015, 16, 132.	2.8	67
54	Soybean (<i>Glycine max</i>) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. <i>BMC Genomics</i> , 2015, 16, 520.	2.8	173

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55	Identification and characterization of a stachyose synthase gene controlling reduced stachyose content in soybean. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2167-2176.	3.6	28
56	Soybean transcription factor ORFeome associated with drought resistance: a valuable resource to accelerate research on abiotic stress resistance. <i>BMC Genomics</i> , 2015, 16, 596.	2.8	17
57	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. <i>Plant Science</i> , 2015, 240, 65-78.	3.6	53
58	Understanding abiotic stress tolerance mechanisms in soybean: A comparative evaluation of soybean response to drought and flooding stress. <i>Plant Physiology and Biochemistry</i> , 2015, 86, 109-120.	5.8	156
59	A Sweetpotato Geranylgeranyl Pyrophosphate Synthase Gene, IbGGPS, Increases Carotenoid Content and Enhances Osmotic Stress Tolerance in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2015, 10, e0137623.	2.5	48
60	Functional Analysis of Water Stress-Responsive Soybean GmNAC003 and GmNAC004 Transcription Factors in Lateral Root Development in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2014, 9, e84886.	2.5	46
61	Expression of Root-Related Transcription Factors Associated with Flooding Tolerance of Soybean (<i>Glycine max</i>). <i>International Journal of Molecular Sciences</i> , 2014, 15, 17622-17643.	4.1	55
62	Integrating omic approaches for abiotic stress tolerance in soybean. <i>Frontiers in Plant Science</i> , 2014, 5, 244.	3.6	213
63	Overexpression of AtDREB1D transcription factor improves drought tolerance in soybean. <i>Molecular Biology Reports</i> , 2014, 41, 7995-8008.	2.3	56
64	Genomic differences between cultivated soybean, <i>G. max</i> and its wild relative <i>G. soja</i> . <i>BMC Genomics</i> , 2013, 14, S5.	2.8	30
65	Molecular characterization of <i>Glycine max</i> squalene synthase genes in seed phytosterol biosynthesis. <i>Plant Physiology and Biochemistry</i> , 2013, 73, 23-32.	5.8	30
66	Evaluation of Candidate Reference Genes for Normalization of Quantitative RT-PCR in Soybean Tissues under Various Abiotic Stress Conditions. <i>PLoS ONE</i> , 2012, 7, e46487.	2.5	115
67	Biological Mechanisms that Influence Soy Protein Concentration and Composition. , 2012, , 129-157.		2
68	Soybean Knowledge Base (SoyKB): a web resource for soybean translational genomics. <i>BMC Genomics</i> , 2012, 13, S15.	2.8	93
69	Metabolic engineering of soybean affords improved phytosterol seed traits. <i>Plant Biotechnology Journal</i> , 2012, 10, 12-19.	8.3	13
70	SoyDB: a knowledge database of soybean transcription factors. <i>BMC Plant Biology</i> , 2010, 10, 14.	3.6	104
71	Regulation of growth response to water stress in the soybean primary root. I. Proteomic analysis reveals region-specific regulation of phenylpropanoid metabolism and control of free iron in the elongation zone. <i>Plant, Cell and Environment</i> , 2010, 33, 223-243.	5.7	158
72	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854

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73	SoyMetDB: The soybean metabolome database. , 2010, , .		12
74	Molecular characterization of stress-inducible GmNAC genes in soybean. Molecular Genetics and Genomics, 2009, 281, 647-664.	2.1	138
75	Cloning, functional expression and phylogenetic analysis of plant sterol 24C-methyltransferases involved in sitosterol biosynthesis. Phytochemistry, 2009, 70, 1982-1998.	2.9	40
76	Spatial distribution of transcript changes in the maize primary root elongation zone at low water potential. BMC Plant Biology, 2008, 8, 32.	3.6	94
77	Genomics of Abiotic Stress in Soybean. , 2008, , 343-372.		10
78	Genomics Approaches To Soybean Improvement. , 2007, , 243-279.		10
79	Single Feature Polymorphism Discovery in Rice. PLoS ONE, 2007, 2, e284.	2.5	57
80	Understanding regulatory networks and engineering for enhanced drought tolerance in plants. Current Opinion in Plant Biology, 2006, 9, 189-195.	7.1	695
81	The MsPRP2 promoter enables strong heterologous gene expression in a root-specific manner and is enhanced by overexpression of Alfalfa. Planta, 2004, 219, 925-935.	3.2	31