

Shailendra Goel

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,362
citations

430874

18
h-index

345221

36
g-index

47
all docs

47
docs citations

47
times ranked

1522
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and validation of in silico mined polymorphic EST-SSR for genetic diversity and cross-species transferability studies in Safflower. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 168-177.	1.7	1
2	â€œOmicron mildâ€? Testing this narrative with the mutational landscape of its three lineages and response to existing vaccines and therapeutic antibodies. <i>Journal of Medical Virology</i> , 2022, 94, 3521-3539.	5.0	20
3	Contrasting Reproductive Strategies of Two <i>Nymphaea</i> Species Affect Existing Natural Genetic Diversity as Assessed by Microsatellite Markers: Implications for Conservation and Wetlands Restoration. <i>Frontiers in Plant Science</i> , 2022, 13, 773572.	3.6	7
4	Aberrant promoter hypermethylation regulates thrombomodulin in high altitude induced deep vein thrombosis. <i>Thrombosis Research</i> , 2022, 215, 5-13.	1.7	0
5	Identification of significant marker-trait associations for Fusarium wilt resistance in a genetically diverse core collection of safflower using AFLP and SSR markers. <i>Journal of Applied Genetics</i> , 2022, 63, 447-462.	1.9	5
6	Overview of developed core and mini core collections and their effective utilization in cultivated rice and its related species (<i>Oryza</i> sp.)â€”A review. <i>Plant Breeding</i> , 2022, 141, 501-512.	1.9	5
7	Mapping of SARS-CoV-2 spike protein evolution during the first and second waves of COVID-19 infections in India. <i>Future Virology</i> , 2022, 17, 557-575.	1.8	2
8	Long-read-based draft genome sequence of Indian black gram (<i>Uttara</i>): Insights into disease resistance and seed storage protein genes. <i>Plant Genome</i> , 2022, 15, .	2.8	3
9	Applicability of Start Codon Targeted (SCoT) and Inter Simple Sequence Repeat (ISSR) markers in assessing genetic diversity in <i>Crepidium acuminatum</i> (D. Don) Szlach.. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2021, 23, 100310.	1.5	6
10	Abiotic stress-mediated modulation of the chromatin landscape in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 5280-5293.	4.8	24
11	Dynamics of Eco-Evolutionary Forces in Shaping Dioecy. , 2020, , 173-196.		1
12	Deciphering species relationships and evolution in <i>Chenopodium</i> through sequence variations in nuclear internal transcribed spacer region and amplified fragment-length polymorphism in nuclear DNA. <i>Journal of Genetics</i> , 2019, 98, 1.	0.7	2
13	Karyo-morphological consistency and heterochromatin distribution pattern in diploid and colchitetraploids of <i>Vigna radiata</i> and <i>V. mungo</i> . <i>Meta Gene</i> , 2019, 21, 100569.	0.6	1
14	Analysis of genetic variation using ISSR and the development of SCAR marker in synthetic autotetraploids of <i>Vigna mungo</i> (L.) Hepper. <i>Vegetos</i> , 2019, 32, 48-57.	1.5	3
15	Prediction of upslope movement of <i>Rhododendron arboreum</i> in Western Himalaya. <i>Tropical Ecology</i> , 2019, 60, 518-524.	1.2	6
16	Occurrence of subdioecy and scarcity of gender-specific markers reveal an ongoing transition to dioecy in Himalayan seabuckthorn (<i>Hippophae rhamnoides</i> ssp. <i>turkestanica</i>). <i>Heredity</i> , 2019, 122, 120-132.	2.6	8
17	Transcriptome analysis of root-knot nematode (<i>Meloidogyne incognita</i>)-infected tomato (<i>Solanum lycopersicum</i>) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. <i>Molecular Plant Pathology</i> , 2018, 19, 615-633.	4.2	127
18	Association Mapping for Important Agronomic Traits in Safflower (<i>Carthamus tinctorius</i> L.) Core Collection Using Microsatellite Markers. <i>Frontiers in Plant Science</i> , 2018, 9, 402.	3.6	45

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19	Standardization of Hydroponics based procedure for High-Throughput Screening and its Application for identification of differential host response in Safflower against <i>Fusarium oxysporum carthamii</i> . <i>Vegetos</i> , 2018, 31, 5.	1.5	1
20	Cytogenetic and molecular evidences revealing genomic changes after autopolyploidization: a case study of synthetic autotetraploid <i>Phlox drummondii</i> Hook. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 641-650.	3.1	19
21	MicroRNA-145 Impedes Thrombus Formation via Targeting Tissue Factor in Venous Thrombosis. <i>EBioMedicine</i> , 2017, 26, 175-186.	6.1	56
22	ISSR markers for gender identification and genetic diagnosis of <i>Hippophae rhamnoides</i> ssp. <i>turkestanica</i> growing at high altitudes in Ladakh region (Jammu and Kashmir). <i>Protoplasma</i> , 2017, 254, 1063-1077.	2.1	13
23	Genome-wide identification and characterization of miRNAome from tomato (<i>Solanum lycopersicum</i>) roots and root-knot nematode (<i>Meloidogyne incognita</i>) during susceptible interaction. <i>PLoS ONE</i> , 2017, 12, e0175178.	2.5	42
24	Evaluation of Different Hosts and Laboratory Conditions for Rearing of the Mustard Aphid (<i>Lipaphis</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 juncea</i> (Indian Mustard). <i>Vegetos</i> , 2017, 30, 185.	1.5	1
25	Utilization of Molecular, Phenotypic, and Geographical Diversity to Develop Compact Composite Core Collection in the Oilseed Crop, Safflower (<i>Carthamus tinctorius</i> L.) through Maximization Strategy. <i>Frontiers in Plant Science</i> , 2016, 7, 1554.	3.6	65
26	Facultative apomixis and development of fruit in a deciduous shrub with medicinal and nutritional uses. <i>AoB PLANTS</i> , 2015, 7, plv098.	2.3	14
27	De novo transcriptome profiling of cold-stressed siliques during pod filling stages in Indian mustard (<i>Brassica juncea</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 932.	3.6	33
28	Assessment of Genetic Diversity and Population Structure in a Global Reference Collection of 531 Accessions of <i>Carthamus tinctorius</i> L. (Safflower) Using AFLP Markers. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1299-1313.	1.8	33
29	Global insights into high temperature and drought stress regulated genes by RNA-Seq in economically important oilseed crop <i>Brassica juncea</i> . <i>BMC Plant Biology</i> , 2015, 15, 9.	3.6	128
30	Generation of silver stained TE-AFLP markers in tea (<i>Camellia sinensis</i>) and their assessment in filling gaps with construction of a genetic linkage map. <i>Scientia Horticulturae</i> , 2015, 192, 293-301.	3.6	3
31	Construction of a genetic linkage map and mapping of drought tolerance trait in Indian beverage tea. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	18
32	Development of Genomic Microsatellite Markers in <i>Carthamus tinctorius</i> L. (Safflower) Using Next Generation Sequencing and Assessment of Their Cross-Species Transferability and Utility for Diversity Analysis. <i>PLoS ONE</i> , 2015, 10, e0135443.	2.5	45
33	A Genome-Wide Perspective of miRNAome in Response to High Temperature, Salinity and Drought Stresses in <i>Brassica juncea</i> (Czern) L. <i>PLoS ONE</i> , 2014, 9, e92456.	2.5	70
34	Identification and characterization of miRNAome in root, stem, leaf and tuber developmental stages of potato (<i>Solanum tuberosum</i> L.) by high-throughput sequencing. <i>BMC Plant Biology</i> , 2014, 14, 6.	3.6	105
35	Significance of Satellite DNA Revealed by Conservation of a Widespread Repeat DNA Sequence Among Angiosperms. <i>Applied Biochemistry and Biotechnology</i> , 2014, 173, 1790-1801.	2.9	8
36	Development of a set of genomic microsatellite markers in tea (<i>Camellia</i> L.) (<i>Camelliaceae</i>). <i>Molecular Breeding</i> , 2013, 32, 735-741.	2.1	15

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37	Molecular analysis of genomic changes in synthetic autotetraploid <i>Phlox drummondii</i> Hook. Biological Journal of the Linnean Society, 2013, 110, 591-605.	1.6	23
38	Sequence Analysis of KpnI Repeat Sequences to Revisit the Phylogeny of the Genus <i>Carthamus</i> L.. Applied Biochemistry and Biotechnology, 2013, 169, 1109-1125.	2.9	6
39	Structural organization of the gynoecium and pollen tube path in Himalayan sea buckthorn, <i>Hippophae rhamnoides</i> (Elaeagnaceae). AoB PLANTS, 2013, 5, .	2.3	6
40	Evolution of the apomixis transmitting chromosome in <i>Pennisetum</i> . BMC Evolutionary Biology, 2011, 11, 289.	3.2	53
41	Sequence Analysis of Bacterial Artificial Chromosome Clones from the Apospory-Specific Genomic Region of <i>Pennisetum</i> and <i>Cenchrus</i> . Plant Physiology, 2008, 147, 1396-1411.	4.8	107
42	<i>Pennisetum squamulatum</i> : Is the Predominant Cytotype Hexaploid or Octaploid?. Journal of Heredity, 2006, 97, 521-524.	2.4	10
43	Comparative Physical Mapping of the Apospory-Specific Genomic Region in Two Apomictic Grasses: <i>Pennisetum squamulatum</i> and <i>Cenchrus ciliaris</i> . Genetics, 2006, 173, 389-400.	2.9	42
44	High-Resolution Physical Mapping in <i>Pennisetum squamulatum</i> Reveals Extensive Chromosomal Heteromorphism of the Genomic Region Associated with Apomixis. Plant Physiology, 2004, 134, 1733-1741.	4.8	109
45	Delineation by Fluorescence <i>in Situ</i> Hybridization of a Single Hemizygous Chromosomal Region Associated With Aposporous Embryo Sac Formation in <i>Pennisetum squamulatum</i> and <i>Cenchrus ciliaris</i> . Genetics, 2003, 163, 1069-1082.	2.9	67
46	Establishment of a correlation between pistil size and female gametophyte developmental stages in apomictic and sexual lines of <i>Cenchrus americanus</i> (L.) Morrone. Vegetos, 0, , 1.	1.5	0
47	A comprehensive account of SARS-CoV-2 genome structure, incurred mutations, lineages and COVID-19 vaccination program. Future Virology, 0, , .	1.8	4