

Kashmir Singh

List of Publications by Year in descending order

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103
papers

3,246
citations

136885

32
h-index

175177

52
g-index

112
all docs

112
docs citations

112
times ranked

3498
citing authors

#	ARTICLE	IF	CITATIONS
1	An RNA isolation system for plant tissues rich in secondary metabolites. BMC Research Notes, 2011, 4, 85.	0.6	214
2	Phenylalanine ammonia-lyase (PAL) and cinnamate 4-hydroxylase (C4H) and catechins (flavan-3-ols) accumulation in tea. Functional and Integrative Genomics, 2009, 9, 125-134.	1.4	161
3	Association of a Novel DNA Virus with the Grapevine Vein-Clearing and Vine Decline Syndrome. Phytopathology, 2011, 101, 1081-1090.	1.1	117
4	Survey of High Throughput RNA-Seq Data Reveals Potential Roles for lncRNAs during Development and Stress Response in Bread Wheat. Frontiers in Plant Science, 2017, 8, 1019.	1.7	111
5	Microbial degradation of herbicides. Critical Reviews in Microbiology, 2016, 42, 1-17.	2.7	107
6	26S rRNA-based internal control gene primer pair for reverse transcription-polymerase chain reaction-based quantitative expression studies in diverse plant species. Analytical Biochemistry, 2004, 335, 330-333.	1.1	94
7	Genome-wide identification and characterization of abiotic-stress responsive SOD (superoxide) Tj ETQq1 1 0.784314rgBT /Oyerlock 10	1.2	94
8	The liverwort <i>Pellia endiviifolia</i> shares microtranscriptomic traits that are common to green algae and land plants. New Phytologist, 2015, 206, 352-367.	3.5	84
9	Biodegradation of malathion by <i>Brevibacillus</i> sp. strain KB2 and <i>Bacillus cereus</i> strain PU. World Journal of Microbiology and Biotechnology, 2012, 28, 1133-1141.	1.7	79
10	An early gene of the flavonoid pathway, flavanone 3-hydroxylase, exhibits a positive relationship with the concentration of catechins in tea (<i>Camellia sinensis</i>). Tree Physiology, 2008, 28, 1349-1356.	1.4	78
11	p-Coumarate:CoA ligase as a key gene in the yield of catechins in tea [<i>Camellia sinensis</i> (L.) O. Kuntze]. Functional and Integrative Genomics, 2009, 9, 271-275.	1.4	76
12	Molecular Characterization and Global Expression Analysis of Lectin Receptor Kinases in Bread Wheat (<i>Triticum aestivum</i>). PLoS ONE, 2016, 11, e0153925.	1.1	73
13	Genomic Dissection and Expression Profiling Revealed Functional Divergence in <i>Triticum aestivum</i> Leucine Rich Repeat Receptor Like Kinases (TaLRRKs). Frontiers in Plant Science, 2016, 7, 1374.	1.7	68
14	De Novo Transcriptome Sequencing Reveals Important Molecular Networks and Metabolic Pathways of the Plant, <i>Chlorophytum borivilium</i> . PLoS ONE, 2013, 8, e83336.	1.1	65
15	Molecular regulation of catechins biosynthesis in tea [<i>Camellia sinensis</i> (L.) O. Kuntze]. Gene, 2012, 495, 205-210.	1.0	63
16	Molecular characterization of ascorbate peroxidase (APX) and APX-related (APX-R) genes in <i>Triticum aestivum</i> L.. Genomics, 2020, 112, 4208-4223.	1.3	56
17	Molecular characterization revealed the role of catalases under abiotic and arsenic stress in bread wheat (<i>Triticum aestivum</i> L.). Journal of Hazardous Materials, 2021, 403, 123585.	6.5	56
18	A root-specific wall-associated kinase gene, HvWAK1, regulates root growth and is highly divergent in barley and other cereals. Functional and Integrative Genomics, 2013, 13, 167-177.	1.4	54

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19	Microbial degradation of an organophosphate pesticide, malathion. <i>Critical Reviews in Microbiology</i> , 2014, 40, 146-154.	2.7	53
20	An Improved Protocol for the Isolation of RNA from Roots of Tea (<i>Camellia sinensis</i> (L.) O. Kuntze). <i>Molecular Biotechnology</i> , 2012, 52, 82-88.	1.3	51
21	Present Scenario of Long Non-Coding RNAs in Plants. <i>Non-coding RNA</i> , 2017, 3, 16.	1.3	51
22	Small RNA profiling of virus-infected grapevines: evidences for virus infection-associated and variety-specific miRNAs. <i>Functional and Integrative Genomics</i> , 2012, 12, 659-669.	1.4	50
23	Genomic dissection and transcriptional profiling of Cysteine-rich receptor-like kinases in five cereals and functional characterization of TaCRK68-A. <i>International Journal of Biological Macromolecules</i> , 2019, 134, 316-329.	3.6	50
24	Genome-wide characterization revealed role of NBS-LRR genes during powdery mildew infection in <i>Vitis vinifera</i> . <i>Genomics</i> , 2020, 112, 312-322.	1.3	50
25	Microbial remediation of explosive waste. <i>Critical Reviews in Microbiology</i> , 2012, 38, 152-167.	2.7	49
26	Genome-wide investigation of regulatory roles of lncRNAs in response to heat and drought stress in <i>Brassica juncea</i> (Indian mustard). <i>Environmental and Experimental Botany</i> , 2020, 171, 103922.	2.0	46
27	Exploration of glutathione reductase for abiotic stress response in bread wheat (<i>Triticum aestivum</i>) Tj ETQq1 1 0.784314 rgBT ₄₄ /Overl	2.8	44
28	Characterization of dihydroflavonol 4-reductase cDNA in tea [<i>Camellia sinensis</i> (L.) O. Kuntze]. <i>Plant Biotechnology Reports</i> , 2009, 3, 95-101.	0.9	43
29	Differential display mediated cloning of anthocyanidin reductase gene from tea (<i>Camellia sinensis</i>) and its relationship with the concentration of epicatechins. <i>Tree Physiology</i> , 2009, 29, 837-846.	1.4	43
30	Cloning, expression and characterization of a metagenome derived thermoactive/thermostable pectinase. <i>Molecular Biology Reports</i> , 2012, 39, 8353-8361.	1.0	39
31	Thaumatococin-like protein kinases: Molecular characterization and transcriptional profiling in five cereal crops. <i>Plant Science</i> , 2020, 290, 110317.	1.7	37
32	Microplastics in soil: Impacts and microbial diversity and degradation. <i>Pedosphere</i> , 2022, 32, 49-60.	2.1	34
33	Characterization of a thermostable lipase showing loss of secondary structure at ambient temperature. <i>Molecular Biology Reports</i> , 2012, 39, 2795-2804.	1.0	32
34	Production of Biodiesel From Used Mustard Oil and Its Performance Analysis in Internal Combustion Engine. <i>Journal of Energy Resources Technology, Transactions of the ASME</i> , 2010, 132, .	1.4	31
35	Characterization of Squalene synthase Gene from <i>Chlorophytum borivilianum</i> (Sant. and Fernand.). <i>Molecular Biotechnology</i> , 2013, 54, 944-953.	1.3	31
36	Long Non-coding RNAs Coordinate Developmental Transitions and Other Key Biological Processes in Grapevine. <i>Scientific Reports</i> , 2019, 9, 3552.	1.6	31

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37	Differential expression of Histone H3 gene in tea (<i>Camellia sinensis</i> (L.) O. Kuntze) suggests its role in growing tissue. <i>Molecular Biology Reports</i> , 2009, 36, 537-542.	1.0	29
38	Characterization of a novel esterase Rv1497 of <i>Mycobacterium tuberculosis</i> H37Rv demonstrating β -lactamase activity. <i>Enzyme and Microbial Technology</i> , 2016, 82, 180-190.	1.6	29
39	Characterization of an acid inducible lipase Rv3203 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Molecular Biology Reports</i> , 2014, 41, 285-296.	1.0	28
40	Soft and Hard Textured Wheat Differ in Starch Properties as Indicated by Trimodal Distribution, Morphology, Thermal and Crystalline Properties. <i>PLoS ONE</i> , 2016, 11, e0147622.	1.1	28
41	Insights into the miRNA-mediated response of maize leaf to arsenate stress. <i>Environmental and Experimental Botany</i> , 2017, 137, 96-109.	2.0	27
42	LysM domain-containing proteins modulate stress response and signalling in <i>Triticum aestivum</i> L.. <i>Environmental and Experimental Botany</i> , 2021, 189, 104558.	2.0	27
43	Compendium of Plant-Specific CRISPR Vectors and Their Technical Advantages. <i>Life</i> , 2021, 11, 1021.	1.1	26
44	Cloning and differential expression of QM like protein homologue from tea [<i>Camellia sinensis</i> (L.) O. Kuntze]. <i>Molecular Biology Reports</i> , 2009, 36, 921-927.	1.0	24
45	De novo Transcriptome Analysis Revealed Genes Involved in Flavonoid and Vitamin C Biosynthesis in <i>Phyllanthus emblica</i> (L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1610.	1.7	24
46	Genome-wide characterization and expression analysis suggested diverse functions of the mechanosensitive channel of small conductance-like (MSL) genes in cereal crops. <i>Scientific Reports</i> , 2020, 10, 16583.	1.6	24
47	Transformation of malathion by <i>Lysinibacillus</i> sp. isolated from soil. <i>Biotechnology Letters</i> , 2012, 34, 863-867.	1.1	23
48	2C-methyl- d- erythritol 2,4-cyclodiphosphate synthase from <i>Stevia rebaudiana</i> Bertoni is a functional gene. <i>Molecular Biology Reports</i> , 2012, 39, 10971-10978.	1.0	22
49	RNA-Seq mediated root transcriptome analysis of <i>Chlorophytum borivilianum</i> for identification of genes involved in saponin biosynthesis. <i>Functional and Integrative Genomics</i> , 2016, 16, 37-55.	1.4	22
50	mesT, a unique epoxide hydrolase, is essential for optimal growth of <i>Mycobacterium tuberculosis</i> in the presence of styrene oxide. <i>Future Microbiology</i> , 2017, 12, 527-546.	1.0	22
51	Investigation of long non-coding RNAs as regulatory players of grapevine response to powdery and downy mildew infection. <i>BMC Plant Biology</i> , 2021, 21, 265.	1.6	21
52	Small RNA profiling for identification of miRNAs involved in regulation of saponins biosynthesis in <i>Chlorophytum borivilianum</i> . <i>BMC Plant Biology</i> , 2017, 17, 265.	1.6	20
53	Comparative metatranscriptome analysis revealed broad response of microbial communities in two soil types, agriculture versus organic soil. <i>Journal of Genetic Engineering and Biotechnology</i> , 2019, 17, 6.	1.5	20
54	Comparative analysis of maize root sRNA transcriptome unveils the regulatory roles of miRNAs in submergence stress response mechanism. <i>Environmental and Experimental Botany</i> , 2020, 171, 103924.	2.0	20

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55	Elucidating genes involved in sesquiterpenoid and flavonoid biosynthetic pathways in <i>Saussurea lappa</i> by de novo leaf transcriptome analysis. <i>Genomics</i> , 2019, 111, 1474-1482.	1.3	19
56	CsNAM-like protein encodes a nuclear localized protein and responds to varied cues in tea [<i>Camellia sinensis</i> (L.) O. Kuntze]. <i>Gene</i> , 2012, 502, 69-74.	1.0	18
57	smRNAome profiling to identify conserved and novel microRNAs in <i>Stevia rebaudiana</i> Bertoni. <i>BMC Plant Biology</i> , 2012, 12, 197.	1.6	18
58	Characterization of APX and APX-R gene family in <i>Brassica juncea</i> and <i>B. rapa</i> for tolerance against abiotic stresses. <i>Plant Cell Reports</i> , 2022, 41, 571-592.	2.8	18
59	Long Non-Coding RNAs as Emerging Regulators of Pathogen Response in Plants. <i>Non-coding RNA</i> , 2022, 8, 4.	1.3	18
60	Differentially expressed transcripts from leaf and root tissue of <i>Chlorophytum borivilianum</i> : A plant with high medicinal value. <i>Gene</i> , 2012, 511, 79-87.	1.0	17
61	Functional characterization of flavanone 3-hydroxylase gene from <i>Phyllanthus emblica</i> (L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2015, 24, 453-460.	0.9	17
62	Puroindoline allelic diversity in Indian wheat germplasm and identification of new allelic variants. <i>Breeding Science</i> , 2015, 65, 319-326.	0.9	16
63	De novo assembly and characterization of transcriptomes of early-stage fruit from two genotypes of <i>Annona squamosa</i> L. with contrast in seed number. <i>BMC Genomics</i> , 2015, 16, 86.	1.2	14
64	Bioremediation of malathion in soil by mixed <i>Bacillus</i> culture. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2013, 04, 674-678.	0.3	14
65	Genome-Wide Analysis and Expression Profiling of Rice Hybrid Proline-Rich Proteins in Response to Biotic and Abiotic Stresses, and Hormone Treatment. <i>Plants</i> , 2019, 8, 343.	1.6	13
66	Fabrication of iron oxide nanocolloids using metallosurfactant-based microemulsions: antioxidant activity, cellular, and genotoxicity toward <i>Vitis vinifera</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 892-909.	2.0	13
67	Comparative transcriptomics reveals candidate transcription factors involved in costunolide biosynthesis in medicinal plant- <i>Saussurea lappa</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 150, 52-67.	3.6	13
68	2,4,6-Trinitrophenol degradation by <i>Bacillus cereus</i> isolated from a firing range. <i>Biotechnology Letters</i> , 2011, 33, 2411-2415.	1.1	12
69	Isolation of High Quality RNA from <i>Phyllanthus emblica</i> and Its Evaluation by Downstream Applications. <i>Molecular Biotechnology</i> , 2012, 52, 269-275.	1.3	12
70	Delineating bacterial community structure of polluted soil samples collected from cancer prone belt of Punjab, India. <i>3 Biotech</i> , 2015, 5, 727-734.	1.1	11
71	Amino acids flanking the central core of Cu,Zn superoxide dismutase are important in retaining enzyme activity after autoclaving. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 475-485.	2.0	11
72	Molecular Design, Synthesis, Computational Screening, Antimicrobial Evaluation and Molecular Docking Study of Acetylinic Isatin Hybrids. <i>ChemistrySelect</i> , 2018, 3, 1942-1952.	0.7	11

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73	New Virus Discovery by Deep Sequencing of Small RNAs. <i>Methods in Molecular Biology</i> , 2012, 883, 177-191.	0.4	10
74	Insight into the Roles of Proline-Rich Extensin-like Receptor Protein Kinases of Bread Wheat (Triticum) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	1.1	9
75	Transportation of Drug-(Polystyrene Bead) Conjugate by Actomyosin Motor System. <i>Journal of Biomedical Nanotechnology</i> , 2010, 6, 279-286.	0.5	8
76	Identification of defense related gene families and their response against powdery and downy mildew infections in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2021, 22, 776.	1.2	8
77	Low-intensity magnetic fields assisted alignment of actin filaments. <i>International Journal of Biological Macromolecules</i> , 2010, 47, 371-374.	3.6	7
78	Characterization and expression analysis of chalcone synthase and chalcone isomerase genes in <i>Phyllanthus emblica</i> (L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 105-113.	0.9	7
79	<i>Vitis vinifera</i> (grapevine) lncRNAs are potential regulators of response to necrotrophic fungus, <i>Botrytis cinerea</i> infection. <i>Physiological and Molecular Plant Pathology</i> , 2020, 112, 101553.	1.3	7
80	Eco-friendly and Cost-effective Use of Rice Straw in the Form of Fixed Bed Column to Remove Water Pollutants. <i>Journal of Bioremediation & Biodegradation</i> , 2016, 07, .	0.5	6
81	mbtj: an iron stress-induced acetyl hydrolase/esterase of <i>Mycobacterium tuberculosis</i> helps bacteria to survive during iron stress. <i>Future Microbiology</i> , 2018, 13, 547-564.	1.0	6
82	Synthesis and Immobilization of Benzothiazole-Appended Triazole-Silane: Biological Evaluation and Molecular Docking Approach. <i>ChemistrySelect</i> , 2018, 3, 1609-1614.	0.7	5
83	Understanding role of Glutathione Reductase gene family in drought and heat stresses in <i>Brassica juncea</i> and <i>B. rapa</i> . <i>Environmental and Experimental Botany</i> , 2021, 190, 104595.	2.0	5
84	New Insight into Old <i>Bacillus</i> Lipase: Solvent Stable Mesophilic Lipase Demonstrating Enzyme Activity towards Cold. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015, 25, 340-348.	1.0	4
85	Molecular analysis of squalene epoxidase gene from <i>Chlorophytum borivillianum</i> (Sant. and Fernand.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2015, 24, 417-424.	0.9	4
86	Regeneration and Genetic Fidelity Analysis of <i>Chlorophytum borivillianum</i> ; Using Flower Stalk as Explant Source. <i>Advances in Bioscience and Biotechnology</i> (Print), 2021, 12, 95-107.	0.3	4
87	Gauging the trends of pseudogenes in plants. <i>Critical Reviews in Biotechnology</i> , 2021, 41, 1114-1129.	5.1	4
88	Divalent cation induced actin ring formation. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 793-797.	3.6	3
89	Transportation of drug-gold nanocomposites by actinomyosin motor system. <i>Journal of Nanoparticle Research</i> , 2011, 13, 2295-2303.	0.8	3
90	Differential expression of two members of Rv1922-LipD operon in <i>Mycobacterium tuberculosis</i> : Does rv1923 qualify for membership?. <i>Pathogens and Disease</i> , 2015, 73, .	0.8	3

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91	Degradation of TNP, RDX, and CL-20 Explosives by Microbes. Environmental Science and Engineering, 2014, , 87-111.	0.1	3
92	Bacillus: As Bioremediator Agent of Major Environmental Pollutants. , 2016, , 35-55.		2
93	Characterization of cold responsive uncoupling protein1 (UCP1) gene from Brassica juncea L. (Czern.) Tj ETQq1 1 0.784314 rgBT /Over	0.9	2
94	Identification of novel microRNAs and their targets in Chlorophytum borivilianum by small RNA and degradome sequencing. Non-coding RNA Research, 2019, 4, 141-154.	2.4	2
95	Identification and characterization of SlbHLH, SIDof and SIWRKY transcription factors interacting with SIDPD gene involved in costunolide biosynthesis in Saussurea lappa. International Journal of Biological Macromolecules, 2021, 173, 146-159.	3.6	2
96	In-Vitro Transportation of Drug Molecule by Actin Myosin Motor System. IFMBE Proceedings, 2009, , 902-905.	0.2	1
97	Revisiting plant response to fungal stress in view of long noncoding RNAs. , 2021, , 293-311.		1
98	Biodegradation of Cladinafop Propargyl by Aeromonas sp. Isolated from Field Crop. Frontiers of Biological and Life Sciences, 2014, 2, 67.	0.3	1
99	DISSECTION OF DEFENSE PATHWAYS IN THE GRAPEVINE-POWDERY MILDEW INTERACTION BY EMPLOYING ARABIDOPSIS DEFENSE-RELATED MUTANTS. Acta Horticulturae, 2014, , 85-89.	0.1	0
100	Characterization of nuclear cap binding complex protein genes (CBP20 and CBP80) from Brassica juncea. Plant Gene, 2016, 5, 87-99.	1.4	0
101	Molecular cloning and characterization of farnesyl pyrophosphate synthase gene from Panax sokpayensis, a new Panax species from Sikkim Himalaya. Journal of Applied Research on Medicinal and Aromatic Plants, 2019, 14, 100215.	0.9	0
102	Targeted Metabolite Profiling of Five Cultivars of Vitis vinifera L. Fruits. ACS Food Science & Technology, 2021, 1, 653-659.	1.3	0
103	Applications of Landscape Genetics to Study the Effect of Varying Landscapes and Environmental Challenges in Plant Populations. Energy, Environment, and Sustainability, 2019, , 171-187.	0.6	0