

# Kashmir Singh

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Exploration of glutathione reductase for abiotic stress response in bread wheat ( <i>Triticum aestivum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	2.8	44
2	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
3	Microplastics in soil: Impacts and microbial diversity and degradation. <i>Pedosphere</i> , 2022, 32, 49-60.	2.1	34
4	Long Non-Coding RNAs as Emerging Regulators of Pathogen Response in Plants. <i>Non-coding RNA</i> , 2022, 8, 4.	1.3	18
5	Insight into the Roles of Proline-Rich Extensin-like Receptor Protein Kinases of Bread Wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	9
6	Molecular characterization revealed the role of catalases under abiotic and arsenic stress in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Hazardous Materials</i> , 2021, 403, 123585.	6.5	56
7	Revisiting plant response to fungal stress in view of long noncoding RNAs. , 2021, , 293-311.		1
8	Regeneration and Genetic Fidelity Analysis of <i>Chlorophytum borivilianum</i> ; Using Flower Stalk as Explant Source. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2021, 12, 95-107.	0.3	4
9	Identification and characterization of SlbHLH, SlDof and SlWRKY transcription factors interacting with SlDPD gene involved in costunolide biosynthesis in <i>Saussurea lappa</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 173, 146-159.	3.6	2
10	Targeted Metabolite Profiling of Five Cultivars of <i>Vitis vinifera</i> L. Fruits. <i>ACS Food Science &amp; Technology</i> , 2021, 1, 653-659.	1.3	0
11	Gauging the trends of pseudogenes in plants. <i>Critical Reviews in Biotechnology</i> , 2021, 41, 1114-1129.	5.1	4
12	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
13	Compendium of Plant-Specific CRISPR Vectors and Their Technical Advantages. <i>Life</i> , 2021, 11, 1021.	1.1	26
14	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
15	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
16	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
17	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
18	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

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19	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
20	Thaumatin-like protein kinases: Molecular characterization and transcriptional profiling in five cereal crops. <i>Plant Science</i> , 2020, 290, 110317.	1.7	37
21	<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
22	Molecular characterization of ascorbate peroxidase (APX) and APX-related (APX-R) genes in <i>Triticum aestivum</i> L.. <i>Genomics</i> , 2020, 112, 4208-4223.	1.3	56
23	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
24	Comparative transcriptomics reveals candidate transcription factors involved in costunolide biosynthesis in medicinal plant-Saussurea lappa. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 52-67.	3.6	13
25	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
26	Molecular cloning and characterization of farnesyl pyrophosphate synthase gene from <i>Panax sokpayensis</i> , a new <i>Panax</i> species from Sikkim Himalaya. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2019, 14, 100215.	0.9	0
27	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
28	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
29	Genome-wide identification and characterization of abiotic-stress responsive SOD (superoxide) Tj ETQq1 1 0.784314,rgBT /Oyerlock 10	1.2	94
30	Long Non-coding RNAs Coordinate Developmental Transitions and Other Key Biological Processes in Grapevine. <i>Scientific Reports</i> , 2019, 9, 3552.	1.6	31
31	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
32	Identification of novel microRNAs and their targets in <i>Chlorophytum borivillanum</i> by small RNA and degradome sequencing. <i>Non-coding RNA Research</i> , 2019, 4, 141-154.	2.4	2
33	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
34	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
35	Applications of Landscape Genetics to Study the Effect of Varying Landscapes and Environmental Challenges in Plant Populations. <i>Energy, Environment, and Sustainability</i> , 2019, , 171-187.	0.6	0
36	Synthesis and Immobilization of Benzothiazole-Appended Triazole-Silane: Biological Evaluation and Molecular Docking Approach. <i>ChemistrySelect</i> , 2018, 3, 1609-1614.	0.7	5

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37	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
38	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
39	Characterization of cold responsive uncoupling protein1 (UCP1) gene from <i>Brassica juncea</i> L. (Czern.) Tj ETQq1 1 0.784314 rgBT /Over	0.9	2
40	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
41	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
42	Survey of High Throughput RNA-Seq Data Reveals Potential Roles for lncRNAs during Development and Stress Response in Bread Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 1019.	1.7	111
43	Present Scenario of Long Non-Coding RNAs in Plants. <i>Non-coding RNA</i> , 2017, 3, 16.	1.3	51
44	Small RNA profiling for identification of miRNAs involved in regulation of saponins biosynthesis in <i>Chlorophytum borivilium</i> . <i>BMC Plant Biology</i> , 2017, 17, 265.	1.6	20
45	Microbial degradation of herbicides. <i>Critical Reviews in Microbiology</i> , 2016, 42, 1-17.	2.7	107
46	Eco-friendly and Cost-effective Use of Rice Straw in the Form of Fixed Bed Column to Remove Water Pollutants. <i>Journal of Bioremediation &amp; Biodegradation</i> , 2016, 07, .	0.5	6
47	Molecular Characterization and Global Expression Analysis of Lectin Receptor Kinases in Bread Wheat ( <i>Triticum aestivum</i> ). <i>PLoS ONE</i> , 2016, 11, e0153925.	1.1	73
48	Genomic Dissection and Expression Profiling Revealed Functional Divergence in <i>Triticum aestivum</i> Leucine Rich Repeat Receptor Like Kinases (TaLRRKs). <i>Frontiers in Plant Science</i> , 2016, 7, 1374.	1.7	68
49	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
50	Bacillus: As Bioremediator Agent of Major Environmental Pollutants. , 2016, , 35-55.		2
51	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
52	Characterization of nuclear cap binding complex protein genes (CBP20 and CBP80) from <i>Brassica juncea</i> . <i>Plant Gene</i> , 2016, 5, 87-99.	1.4	0
53	Characterization of a novel esterase Rv1497 of <i>Mycobacterium tuberculosis</i> H37Rv demonstrating $\beta$ -lactamase activity. <i>Enzyme and Microbial Technology</i> , 2016, 82, 180-190.	1.6	29
54	RNA-Seq mediated root transcriptome analysis of <i>Chlorophytum borivilium</i> for identification of genes involved in saponin biosynthesis. <i>Functional and Integrative Genomics</i> , 2016, 16, 37-55.	1.4	22

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55	Soft and Hard Textured Wheat Differ in Starch Properties as Indicated by Trimodal Distribution, Morphology, Thermal and Crystalline Properties. PLoS ONE, 2016, 11, e0147622.	1.1	28
56	Puroindoline allelic diversity in Indian wheat germplasm and identification of new allelic variants. Breeding Science, 2015, 65, 319-326.	0.9	16
57	Differential expression of two members of Rv1922-LipD operon in Mycobacterium tuberculosis: Does rv1923 qualify for membership?. Pathogens and Disease, 2015, 73, .	0.8	3
58	New Insight into Old <i>Bacillus</i> Lipase: Solvent Stable Mesophilic Lipase Demonstrating Enzyme Activity towards Cold. Journal of Molecular Microbiology and Biotechnology, 2015, 25, 340-348.	1.0	4
59	Molecular analysis of squalene epoxidase gene from Chlorophytum borivilianum (Sant. and Fernand.). Journal of Plant Biochemistry and Biotechnology, 2015, 24, 417-424.	0.9	4
60	De novo assembly and characterization of transcriptomes of early-stage fruit from two genotypes of Annona squamosa L. with contrast in seed number. BMC Genomics, 2015, 16, 86.	1.2	14
61	Delineating bacterial community structure of polluted soil samples collected from cancer prone belt of Punjab, India. 3 Biotech, 2015, 5, 727-734.	1.1	11
62	Functional characterization of flavanone 3-hydroxylase gene from Phyllanthus emblica (L.). Journal of Plant Biochemistry and Biotechnology, 2015, 24, 453-460.	0.9	17
63	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
64	Microbial degradation of an organophosphate pesticide, malathion. Critical Reviews in Microbiology, 2014, 40, 146-154.	2.7	53
65	Characterization of an acid inducible lipase Rv3203 from Mycobacterium tuberculosis H37Rv. Molecular Biology Reports, 2014, 41, 285-296.	1.0	28
66	DISSECTION OF DEFENSE PATHWAYS IN THE GRAPEVINE-POWDERY MILDEW INTERACTION BY EMPLOYING ARABIDOPSIS DEFENSE-RELATED MUTANTS. Acta Horticulturae, 2014, , 85-89.	0.1	0
67	Degradation of TNP, RDX, and CL-20 Explosives by Microbes. Environmental Science and Engineering, 2014, , 87-111.	0.1	3
68	Biodegradation of Cladinafop Propargyl by Aeromonas sp. Isolated from Field Crop. Frontiers of Biological and Life Sciences, 2014, 2, 67.	0.3	1
69	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
70	Characterization of Squalene synthase Gene from Chlorophytum borivilianum (Sant. and Fernand.). Molecular Biotechnology, 2013, 54, 944-953.	1.3	31
71	De Novo Transcriptome Sequencing Reveals Important Molecular Networks and Metabolic Pathways of the Plant, Chlorophytum borivilianum. PLoS ONE, 2013, 8, e83336.	1.1	65
72	Bioremediation of malathion in soil by mixed Bacillus culture. Advances in Bioscience and Biotechnology (Print), 2013, 04, 674-678.	0.3	14

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73	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
74	Molecular regulation of catechins biosynthesis in tea [ <i>Camellia sinensis</i> (L.) O. Kuntze]. <i>Gene</i> , 2012, 495, 205-210.	1.0	63
75	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
76	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
77	Microbial remediation of explosive waste. <i>Critical Reviews in Microbiology</i> , 2012, 38, 152-167.	2.7	49
78	New Virus Discovery by Deep Sequencing of Small RNAs. <i>Methods in Molecular Biology</i> , 2012, 883, 177-191.	0.4	10
79	Differentially expressed transcripts from leaf and root tissue of <i>Chlorophytum borivilium</i> : A plant with high medicinal value. <i>Gene</i> , 2012, 511, 79-87.	1.0	17
80	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
81	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
82	Cloning, expression and characterization of a metagenome derived thermoactive/thermostable pectinase. <i>Molecular Biology Reports</i> , 2012, 39, 8353-8361.	1.0	39
83	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
84	Transformation of malathion by <i>Lysinibacillus</i> sp. isolated from soil. <i>Biotechnology Letters</i> , 2012, 34, 863-867.	1.1	23
85	Biodegradation of malathion by <i>Brevibacillus</i> sp. strain KB2 and <i>Bacillus cereus</i> strain PU. <i>World Journal of Microbiology and Biotechnology</i> , 2012, 28, 1133-1141.	1.7	79
86	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
87	Divalent cation induced actin ring formation. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 793-797.	3.6	3
88	Association of a Novel DNA Virus with the Grapevine Vein-Clearing and Vine Decline Syndrome. <i>Phytopathology</i> , 2011, 101, 1081-1090.	1.1	117
89	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
90	Transportation of drug-gold nanocomposites by actinomyosin motor system. <i>Journal of Nanoparticle Research</i> , 2011, 13, 2295-2303.	0.8	3

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91	An RNA isolation system for plant tissues rich in secondary metabolites. BMC Research Notes, 2011, 4, 85.	0.6	214
92	Transportation of Drug-(Polystyrene Bead) Conjugate by Actomyosin Motor System. Journal of Biomedical Nanotechnology, 2010, 6, 279-286.	0.5	8
93	Production of Biodiesel From Used Mustard Oil and Its Performance Analysis in Internal Combustion Engine. Journal of Energy Resources Technology, Transactions of the ASME, 2010, 132, .	1.4	31
94	Low-intensity magnetic fields assisted alignment of actin filaments. International Journal of Biological Macromolecules, 2010, 47, 371-374.	3.6	7
95	In-Vitro Transportation of Drug Molecule by Actin Myosin Motor System. IFMBE Proceedings, 2009, , 902-905.	0.2	1
96	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
97	p-Coumarate:CoA ligase as a key gene in the yield of catechins in tea [Camellia sinensis (L.) O. Kuntze]. Functional and Integrative Genomics, 2009, 9, 271-275.	1.4	76
98	Differential expression of Histone H3 gene in tea (Camellia sinensis (L.) O. Kuntze) suggests its role in growing tissue. Molecular Biology Reports, 2009, 36, 537-542.	1.0	29
99	Cloning and differential expression of QM like protein homologue from tea [Camellia sinensis (L.) O. Kuntze]. Molecular Biology Reports, 2009, 36, 921-927.	1.0	24
100	Characterization of dihydroflavonol 4-reductase cDNA in tea [Camellia sinensis (L.) O. Kuntze]. Plant Biotechnology Reports, 2009, 3, 95-101.	0.9	43
101	Differential display mediated cloning of anthocyanidin reductase gene from tea (Camellia sinensis) and its relationship with the concentration of epicatechins. Tree Physiology, 2009, 29, 837-846.	1.4	43
102	An early gene of the flavonoid pathway, flavanone 3-hydroxylase, exhibits a positive relationship with the concentration of catechins in tea (Camellia sinensis). Tree Physiology, 2008, 28, 1349-1356.	1.4	78
103	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