

# Devinder Sandhu

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

5,374  
citations

394421

19  
h-index

144013

57  
g-index

63  
all docs

63  
docs citations

63  
times ranked

6240  
citing authors

#	ARTICLE	IF	CITATIONS
1	Morphological, physiological, biochemical, and transcriptome studies reveal the importance of transporters and stress signaling pathways during salinity stress in <i>Prunus</i> . <i>Scientific Reports</i> , 2022, 12, 1274.	3.3	15
2	Deciphering Molecular Mechanisms Involved in Salinity Tolerance in Guar ( <i>Cyamopsis tetragonoloba</i> ) Tj ETQq0 0 0 ggBT /Overlock 10 Tf 3.5 11	3.5	11
3	Transgenic Expression of <i>Prunus persica</i> Salt Overly Sensitive 2 ( <i>PpSOS2</i> ) in the <i>atsos2</i> Mutant Imparts Salt Tolerance in <i>Arabidopsis</i> . <i>ACS Agricultural Science and Technology</i> , 2022, 2, 153-164.	2.3	1
4	Comparative Transcriptome Analysis of <i>Agrobacterium tumefaciens</i> Reveals the Molecular Basis for the Recalcitrant Genetic Transformation of <i>Camellia sinensis</i> L. <i>Biomolecules</i> , 2022, 12, 688.	4.0	2
5	Isolation and characterization of Salt Overly Sensitive family genes in spinach. <i>Physiologia Plantarum</i> , 2021, 171, 520-532.	5.2	20
6	Transcript Analysis of Two Spinach Cultivars Reveals the Complexity of Salt Tolerance Mechanisms. <i>ACS Agricultural Science and Technology</i> , 2021, 1, 64-75.	2.3	5
7	Influence of Moderate to High Salinity on the Phytochemical Profiles of Two Salinity-Tolerant Spinach Genotypes. <i>ACS Food Science &amp; Technology</i> , 2021, 1, 205-214.	2.7	4
8	Transcriptional profiling of two contrasting genotypes uncovers molecular mechanisms underlying salt tolerance in alfalfa. <i>Scientific Reports</i> , 2021, 11, 5210.	3.3	13
9	Contrasting Responses of Guar Genotypes Shed Light on Multiple Component Traits of Salinity Tolerance Mechanisms. <i>Agronomy</i> , 2021, 11, 1068.	3.0	6
10	Linking genetic determinants with salinity tolerance and ion relationships in eggplant, tomato and pepper. <i>Scientific Reports</i> , 2021, 11, 16298.	3.3	8
11	Physiological, Morphological, Biochemical, and Genetic Responses of Alfalfa to Salinity. <i>Compendium of Plant Genomes</i> , 2021, , 145-157.	0.5	2
12	Characterization of natural genetic variation identifies multiple genes involved in salt tolerance in maize. <i>Functional and Integrative Genomics</i> , 2020, 20, 261-275.	3.5	17
13	Linking diverse salinity responses of 14 almond rootstocks with physiological, biochemical, and genetic determinants. <i>Scientific Reports</i> , 2020, 10, 21087.	3.3	11
14	Germination and Growth of Spinach under Potassium Deficiency and Irrigation with High-Salinity Water. <i>Plants</i> , 2020, 9, 1739.	3.5	9
15	Spinach Plants Favor the Absorption of K <sup>+</sup> over Na <sup>+</sup> Regardless of Salinity, and May Benefit from Na <sup>+</sup> When K <sup>+</sup> is Deficient in the Soil. <i>Plants</i> , 2020, 9, 507.	3.5	22
16	Grape Rootstock Response to Salinity, Water and Combined Salinity and Water Stresses. <i>Agronomy</i> , 2019, 9, 321.	3.0	19
17	Mutation in a PHD-finger protein MS4 causes male sterility in soybean. <i>BMC Plant Biology</i> , 2019, 19, 378.	3.6	19
18	Variable salinity responses and comparative gene expression in woodland strawberry genotypes. <i>Scientia Horticulturae</i> , 2019, 254, 61-69.	3.6	13

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19	Expression of the high-affinity K <sup>+</sup> transporter 1 (PpHKT1) gene from almond rootstock "Nemaguard"™ improved salt tolerance of transgenic Arabidopsis. PLoS ONE, 2019, 14, e0214473.	2.5	15
20	Molecular characterization and expression analysis of the Na <sup>+</sup> /H <sup>+</sup> exchanger gene family in Medicago truncatula. Functional and Integrative Genomics, 2018, 18, 141-153.	3.5	29
21	Spinach (Spinacea oleracea L.) Response to Salinity: Nutritional Value, Physiological Parameters, Antioxidant Capacity, and Gene Expression. Agriculture (Switzerland), 2018, 8, 163.	3.1	33
22	Dynamics of Salt Tolerance: Molecular Perspectives. , 2018, , 25-40.		11
23	Seasonal and Differential Sesquiterpene Accumulation in Artemisia annua Suggest Selection Based on Both Artemisinin and Dihydroartemisinic Acid may Increase Artemisinin in planta. Frontiers in Plant Science, 2018, 9, 1096.	3.6	13
24	Genetics and Physiology of the Nuclearly Inherited Yellow Foliar Mutants in Soybean. Frontiers in Plant Science, 2018, 9, 471.	3.6	10
25	Inheritance and Genetic Mapping of the Reduced Height (Rht18) Gene in Wheat. Plants, 2018, 7, 58.	3.5	13
26	Variable salinity responses of 12 alfalfa genotypes and comparative expression analyses of salt-response genes. Scientific Reports, 2017, 7, 42958.	3.3	91
27	Isolation and characterization of Aconitate hydratase 4 (Aco4) from soybean. Canadian Journal of Plant Science, 2017, , .	0.9	1
28	Transposon-Based Functional Characterization of Soybean Genes. Compendium of Plant Genomes, 2017, , 183-192.	0.5	0
29	The endogenous transposable element Tgm9 is suitable for generating knockout mutants for functional analyses of soybean genes and genetic improvement in soybean. PLoS ONE, 2017, 12, e0180732.	2.5	7
30	Soybean proteins GmTic110 and GmPsbP are crucial for chloroplast development and function. Plant Science, 2016, 252, 76-87.	3.6	16
31	Transposon Tagging of a Male-Sterility, Female-Sterility Gene, St8, Revealed that the Meiotic MER3 DNA Helicase Activity Is Essential for Fertility in Soybean. PLoS ONE, 2016, 11, e0150482.	2.5	8
32	Evolutionary, Comparative and Functional Analyses of the Brassinosteroid Receptor Gene, BRI1, in Wheat and Its Relation to Other Plant Genomes. PLoS ONE, 2015, 10, e0127544.	2.5	12
33	Molecular mapping of five soybean genes involved in male-sterility, female-sterility. Genome, 2015, 58, 143-149.	2.0	10
34	Evaluation of spontaneous generation of allelic variation in soybean in response to sexual hybridization and stress. Canadian Journal of Plant Science, 2015, 95, 405-415.	0.9	5
35	Candidate Gene Identification for a Lethal Chlorophyll-Deficient Mutant in Soybean. Agronomy, 2014, 4, 462-469.	3.0	12
36	Molecular mapping of three male-sterile, female-fertile mutants and generation of a comprehensive map of all known male sterility genes in soybean. Genome, 2014, 57, 155-160.	2.0	20

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37	A candidate male-fertility female-fertility gene tagged by the soybean endogenous transposon, Tgm9. <i>Functional and Integrative Genomics</i> , 2013, 13, 67-73.	3.5	13
38	Molecular Mapping of D1, D2 and ms5 Revealed Linkage between the Cotyledon Color Locus D2 and the Male-Sterile Locus ms5 in Soybean. <i>Plants</i> , 2013, 2, 441-454.	3.5	10
39	Segregation distortion in a region containing a male-sterility, female-sterility locus in soybean. <i>Plant Science</i> , 2012, 195, 151-156.	3.6	25
40	Arabidopsis nonhost resistance gene PSS1 confers immunity against an oomycete and a fungal pathogen but not a bacterial pathogen that cause diseases in soybean. <i>BMC Plant Biology</i> , 2012, 12, 87.	3.6	25
41	Mapping Eight Male-Sterile, Female-Sterile Soybean Mutants. <i>Crop Science</i> , 2011, 51, 231-236.	1.8	8
42	Using Microsatellites to Understand the Physical Distribution of Recombination on Soybean Chromosomes. <i>PLoS ONE</i> , 2011, 6, e22306.	2.5	27
43	Molecular Mapping of 2 Environmentally Sensitive Male-Sterile Mutants in Soybean. <i>Journal of Heredity</i> , 2011, 102, 11-16.	2.4	31
44	Dynamic nature of a wheat centromere with a functional gene. <i>Molecular Breeding</i> , 2010, 26, 177-187.	2.1	5
45	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
46	The Male Sterility Locus ms3 Is Present in a Fertility Controlling Gene Cluster in Soybean. <i>Journal of Heredity</i> , 2009, 100, 565-570.	2.4	19
47	Systemic acquired resistance in soybean is regulated by two proteins, Orthologous to Arabidopsis NPR1. <i>BMC Plant Biology</i> , 2009, 9, 105.	3.6	68
48	Enhanced Oleic Acid Content in the Soybean Mutant M23 Is Associated with the Deletion in the Fad2-1a Gene Encoding a Fatty Acid Desaturase. <i>JAOCS, Journal of the American Oil Chemists' Society</i> , 2007, 84, 229-235.	1.9	39
49	Phenotypic and Molecular Analysis of Oleate Content in the Mutant Soybean Line M23. <i>Crop Science</i> , 2005, 45, 1997-2000.	1.8	44
50	Demarcating the gene-rich regions of the wheat genome. <i>Nucleic Acids Research</i> , 2004, 32, 3546-3565.	14.5	181
51	Deletion of a Disease Resistance Nucleotide-Binding-Site Leucine-Rich-Repeat-like Sequence Is Associated With the Loss of the Phytophthora Resistance Gene Rps4 in Soybean. <i>Genetics</i> , 2004, 168, 2157-2167.	2.9	98
52	Identification of Wheat Chromosomal Regions Containing Expressed Resistance Genes. <i>Genetics</i> , 2004, 166, 461-481.	2.9	78
53	Construction and characterization of a soybean yeast artificial chromosome library and identification of clones for the Rps6 region. <i>Functional and Integrative Genomics</i> , 2003, 3, 153-159.	3.5	7
54	Gene-Containing Regions of Wheat and the Other Grass Genomes. <i>Plant Physiology</i> , 2002, 128, 803-811.	4.8	112

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55	Identification of Expressed Sequence Markers for a Major Gene-Rich Region of Wheat Chromosome Group <i>1S</i> Using RNA Fingerprintingâ€“Differential Display. <i>Crop Science</i> , 2002, 42, 1285-1290.	1.8	10
56	Genomic sequencing reveals gene content, genomic organization, and recombination relationships in barley. <i>Functional and Integrative Genomics</i> , 2002, 2, 51-59.	3.5	65
57	Structural and functional organization of the '1S0.8 gene-rich region' in the Triticeae. <i>Plant Molecular Biology</i> , 2002, 48, 791-804.	3.9	24
58	Erratum Structural and functional organization of the `1S0.8 gene-rich region' in the Triticeae. <i>Plant Molecular Biology</i> , 2002, 50, 151-153.	3.9	0
59	Identification and Physical Localization of Useful Genes and Markers to a Major Gene-Rich Region on Wheat Group <i>1S</i> Chromosomes. <i>Genetics</i> , 2001, 157, 1735-1747.	2.9	104
60	Title is missing!. <i>Euphytica</i> , 1997, 95, 109-113.	1.2	20
61	Microsatellites Based Genetic Linkage Map of the <i>Rht3</i> Locus in Bread Wheat. <i>Molecular Plant Breeding</i> , 0, , .	0.0	2