

Suk-Yoon Kwon

List of Publications by Year in descending order

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122
papers

5,164
citations

136740

32
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95083

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123
all docs

123
docs citations

123
times ranked

5757
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. <i>Nature Genetics</i> , 2014, 46, 270-278.	9.4	867
2	Simultaneous overexpression of both CuZn superoxide dismutase and ascorbate peroxidase in transgenic tall fescue plants confers increased tolerance to a wide range of abiotic stresses. <i>Journal of Plant Physiology</i> , 2007, 164, 1626-1638.	1.6	310
3	Enhanced drought tolerance of transgenic rice plants expressing a pea manganese superoxide dismutase. <i>Journal of Plant Physiology</i> , 2005, 162, 465-472.	1.6	305
4	Enhanced tolerance to oxidative stress in transgenic tobacco plants expressing three antioxidant enzymes in chloroplasts. <i>Plant Cell Reports</i> , 2007, 26, 591-598.	2.8	214
5	Enhanced tolerance of transgenic potato plants expressing both superoxide dismutase and ascorbate peroxidase in chloroplasts against oxidative stress and high temperature. <i>Plant Cell Reports</i> , 2006, 25, 1380-1386.	2.8	212
6	Enhanced tolerances of transgenic tobacco plants expressing both superoxide dismutase and ascorbate peroxidase in chloroplasts against methyl viologen-mediated oxidative stress. <i>Plant, Cell and Environment</i> , 2002, 25, 873-882.	2.8	194
7	Enhanced stress-tolerance of transgenic tobacco plants expressing a human dehydroascorbate reductase gene. <i>Journal of Plant Physiology</i> , 2003, 160, 347-353.	1.6	158
8	A novel oxidative stress-inducible peroxidase promoter from sweetpotato: molecular cloning and characterization in transgenic tobacco plants and cultured cells. <i>Plant Molecular Biology</i> , 2003, 51, 831-838.	2.0	150
9	The Activated SA and JA Signaling Pathways Have an Influence on flg22-Triggered Oxidative Burst and Callose Deposition. <i>PLoS ONE</i> , 2014, 9, e88951.	1.1	135
10	Stress-induced expression of choline oxidase in potato plant chloroplasts confers enhanced tolerance to oxidative, salt, and drought stresses. <i>Plant Cell Reports</i> , 2008, 27, 687-698.	2.8	133
11	Overexpression of sweetpotato swpa4 peroxidase results in increased hydrogen peroxide production and enhances stress tolerance in tobacco. <i>Planta</i> , 2008, 227, 867-881.	1.6	123
12	Enhanced tolerance of transgenic sweetpotato plants that express both CuZnSOD and APX in chloroplasts to methyl viologen-mediated oxidative stress and chilling. <i>Molecular Breeding</i> , 2007, 19, 227-239.	1.0	101
13	Tobacco seeds simultaneously over-expressing Cu/Zn-superoxide dismutase and ascorbate peroxidase display enhanced seed longevity and germination rates under stress conditions. <i>Journal of Experimental Botany</i> , 2010, 61, 2499-2506.	2.4	98
14	Glycine betaine: a versatile compound with great potential for gene pyramiding to improve crop plant performance against environmental stresses. <i>Plant Biotechnology Reports</i> , 2013, 7, 49-57.	0.9	94
15	Rice Transcription Factor OsDOF11 Modulates Sugar Transport by Promoting Expression of Sucrose Transporter and SWEET Genes. <i>Molecular Plant</i> , 2018, 11, 833-845.	3.9	90
16	Enhanced tolerance of transgenic potato plants overexpressing nucleoside diphosphate kinase 2 against multiple environmental stresses. <i>Transgenic Research</i> , 2008, 17, 705-715.	1.3	89
17	Enhanced tolerance to methyl viologen-induced oxidative stress and high temperature in transgenic potato plants overexpressing the CuZnSOD, APX and NDPK2 genes. <i>Physiologia Plantarum</i> , 2010, 140, 153-162.	2.6	85
18	Simultaneous expression of choline oxidase, superoxide dismutase and ascorbate peroxidase in potato plant chloroplasts provides synergistically enhanced protection against various abiotic stresses. <i>Physiologia Plantarum</i> , 2010, 138, 520-533.	2.6	82

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19	Chloroplast Cu/Zn-superoxide dismutase is a highly sensitive site in cucumber leaves chilled in the light. <i>Planta</i> , 2002, 216, 315-324.	1.6	80
20	Molecular characterization of cDNAs for two anionic peroxidases from suspension cultures of sweet potato. <i>Molecular Genetics and Genomics</i> , 1999, 261, 941-947.	2.4	58
21	Overexpression of 2-cysteine peroxiredoxin enhances tolerance to methyl viologen-mediated oxidative stress and high temperature in potato plants. <i>Plant Physiology and Biochemistry</i> , 2011, 49, 891-897.	2.8	58
22	Biocontrol activity of <i>Paenibacillus polymyxa</i> AC-1 against <i>Pseudomonas syringae</i> and its interaction with <i>Arabidopsis thaliana</i> . <i>Microbiological Research</i> , 2016, 185, 13-21.	2.5	51
23	Small RNA and transcriptome deep sequencing proffers insight into floral gene regulation in <i>Rosa</i> cultivars. <i>BMC Genomics</i> , 2012, 13, 657.	1.2	49
24	Expression of <i>Arabidopsis</i> NDPK2 increases antioxidant enzyme activities and enhances tolerance to multiple environmental stresses in transgenic sweetpotato plants. <i>Molecular Breeding</i> , 2009, 24, 233-244.	1.0	47
25	Evolution of ribosomal DNA-derived satellite repeat in tomato genome. <i>BMC Plant Biology</i> , 2009, 9, 42.	1.6	46
26	A Genome-Wide Comparison of NB-LRR Type of Resistance Gene Analogs (RGA) in the Plant Kingdom. <i>Molecules and Cells</i> , 2012, 33, 385-392.	1.0	46
27	Differential expression of 10 sweetpotato peroxidases in response to sulfur dioxide, ozone, and ultraviolet radiation. <i>Plant Physiology and Biochemistry</i> , 2007, 45, 908-914.	2.8	44
28	Use of Heat Stress Responsive Gene Expression Levels for Early Selection of Heat Tolerant Cabbage (<i>Brassica oleracea</i> L.). <i>International Journal of Molecular Sciences</i> , 2013, 14, 11871-11894.	1.8	39
29	High-Throughput Sequencing and De Novo Assembly of <i>Brassica oleracea</i> var. <i>Capitata</i> L. for Transcriptome Analysis. <i>PLoS ONE</i> , 2014, 9, e92087.	1.1	38
30	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017, 24, dsw049.	1.5	38
31	Differential expression of 10 sweetpotato peroxidase genes in response to bacterial pathogen, <i>Pectobacterium chrysanthemi</i> . <i>Plant Physiology and Biochemistry</i> , 2004, 42, 451-455.	2.8	36
32	Genome Sequence of the Plant Growth-Promoting Rhizobacterium <i>Bacillus</i> sp. Strain JS. <i>Journal of Bacteriology</i> , 2012, 194, 3760-3761.	1.0	35
33	High expression of a human lactoferrin in transgenic tobacco cell cultures. <i>Biotechnology Letters</i> , 2003, 25, 213-218.	1.1	32
34	Changes of net photosynthesis, antioxidant enzyme activities, and antioxidant contents of <i>Liriodendron tulipifera</i> under elevated ozone. <i>Photosynthetica</i> , 2009, 47, 19-25.	0.9	32
35	A novel pepper (<i>Capsicum annum</i>) receptor-like kinase functions as a negative regulator of plant cell death via accumulation of superoxide anions. <i>New Phytologist</i> , 2010, 185, 701-715.	3.5	32
36	RNA-Seq Analysis and De Novo Transcriptome Assembly of Jerusalem Artichoke (<i>Helianthus tuberosus</i>) Tj ETQq0 0 Q rgBT /Overlock 10 T	1.1	31

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37	Current status of genetic transformation technology developed in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Integrative Agriculture</i> , 2015, 14, 469-482.	1.7	31
38	Transcriptome analysis of the oriental melon (<i>Cucumis melo</i> L. var. <i>makuwa</i>) during fruit development. <i>PeerJ</i> , 2017, 5, e2834.	0.9	31
39	Isolation of novel leaf-inhabiting endophytic bacteria in <i>Arabidopsis thaliana</i> and their antagonistic effects on phytopathogens. <i>Plant Biotechnology Reports</i> , 2015, 9, 451-458.	0.9	30
40	Molecular characterization of a cDNA encoding copper/zinc superoxide dismutase from cultured cells of <i>Manihot esculenta</i> . <i>Plant Physiology and Biochemistry</i> , 2005, 43, 55-60.	2.8	28
41	Development of tobacco ringspot virus-based vectors for foreign gene expression and virus-induced gene silencing in a variety of plants. <i>Virology</i> , 2016, 492, 166-178.	1.1	27
42	NPR1 is Instrumental in Priming for the Enhanced flg22-induced MPK3 and MPK6 Activation. <i>Plant Pathology Journal</i> , 2015, 31, 192-194.	0.7	27
43	An insight into the tomato spotted wilt virus (TSWV), tomato and thrips interaction. <i>Plant Biotechnology Reports</i> , 2018, 12, 157-163.	0.9	26
44	Production of taxadiene from cultured ginseng roots transformed with taxadiene synthase gene. <i>BMB Reports</i> , 2012, 45, 589-594.	1.1	26
45	Construction of SARS-CoV-2 virus-like particles in plant. <i>Scientific Reports</i> , 2022, 12, 1005.	1.6	26
46	Molecular Cloning of a cDNA Encoding Ribosome Inactivating Protein from <i>Amaranthus viridis</i> and Its Expression in <i>E. coli</i> . <i>Molecules and Cells</i> , 2000, 10, 8-12.	1.0	25
47	Differential Resistance to Methyl Viologen in Transgenic Tobacco Plants that Express Sweet Potato Peroxidases. <i>Journal of Plant Physiology</i> , 2000, 156, 504-509.	1.6	25
48	Transgenic Ginseng Cell Lines That Produce High levels of a Human Lactoferrin. <i>Planta Medica</i> , 2003, 69, 1005-1008.	0.7	24
49	Differential expression of four sweet potato peroxidase genes in response to abscisic acid and ethephon. <i>Phytochemistry</i> , 2000, 54, 19-22.	1.4	23
50	Alterations in intracellular and extracellular activities of antioxidant enzymes during suspension culture of sweetpotato. <i>Phytochemistry</i> , 2004, 65, 2471-2476.	1.4	23
51	A novel WD40 protein, BnSWD1, is involved in salt stress in <i>Brassica napus</i> . <i>Plant Biotechnology Reports</i> , 2010, 4, 165-172.	0.9	23
52	Screening of Tissue-Specific Genes and Promoters in Tomato by Comparing Genome Wide Expression Profiles of <i>Arabidopsis</i> Orthologues. <i>Molecules and Cells</i> , 2012, 34, 53-60.	1.0	22
53	Transgenic cucumber fruits that produce elevated level of an anti-aging superoxide dismutase. <i>Molecular Breeding</i> , 2003, 11, 213-220.	1.0	20
54	Ectopic Expression of a Cold-Responsive CuZn Superoxide Dismutase Gene, SodCc1, in Transgenic Rice (<i>Oryza sativa</i> L.). <i>Journal of Plant Biology</i> , 2009, 52, 154-160.	0.9	20

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55	Rpi-blb2-Mediated Hypersensitive Cell Death Caused by <i>Phytophthora infestans</i> AVRblb2 Requires SGT1, but not EDS1, NDR1, Salicylic Acid-, Jasmonic Acid-, or Ethylene-Mediated Signaling. <i>Plant Pathology Journal</i> , 2014, 30, 254-260.	0.7	20
56	<i>Capsicum annuum</i> homeobox 1 (CaHB1) is a nuclear factor that has roles in plant development, salt tolerance, and pathogen defense. <i>Biochemical and Biophysical Research Communications</i> , 2013, 442, 116-121.	1.0	19
57	Comparative genomic analysis of mitogen activated protein kinase gene family in grapevine. <i>Genes and Genomics</i> , 2010, 32, 275-281.	0.5	18
58	High-yield production of functional human lactoferrin in transgenic cell cultures of siberian ginseng (<i>Acanthopanax senticosus</i>). <i>Biotechnology and Bioprocess Engineering</i> , 2006, 11, 442-448.	1.4	16
59	Molecular characterization of a cDNA encoding DRE-binding transcription factor from dehydration-treated fibrous roots of sweetpotato. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 196-204.	2.8	16
60	<i>Agrobacterium</i> -mediated transformation of reed (<i>Phragmites communis</i> Trinius) using mature seed-derived calli. <i>GCB Bioenergy</i> , 2013, 5, 73-80.	2.5	16
61	Silencing of SIFTR-c, the catalytic subunit of ferredoxin:thioredoxin reductase, induces pathogenesis-related genes and pathogen resistance in tomato plants. <i>Biochemical and Biophysical Research Communications</i> , 2010, 399, 750-754.	1.0	15
62	A TMT-Based Quantitative Proteome Analysis to Elucidate the TSWV Induced Signaling Cascade in Susceptible and Resistant Cultivars of <i>Solanum lycopersicum</i> . <i>Plants</i> , 2020, 9, 290.	1.6	15
63	Development of selection marker-free transgenic potato plants with enhanced tolerance to oxidative stress. <i>Journal of Plant Biology</i> , 2008, 51, 401-407.	0.9	14
64	Responses of MxPPO overexpressing transgenic tall fescue plants to two diphenyl-ether herbicides, oxyfluorfen and acifluorfen. <i>Acta Physiologiae Plantarum</i> , 2008, 30, 745-754.	1.0	14
65	Improvement of biomass accumulation of potato plants by transformation of cyanobacterial photorespiratory glycolate catabolism pathway genes. <i>Plant Biotechnology Reports</i> , 2016, 10, 269-276.	0.9	14
66	How does SA signaling link the Flg22 responses?. <i>Plant Signaling and Behavior</i> , 2014, 9, e972806.	1.2	13
67	Draft genome sequences of two oriental melons, <i>Cucumis melo</i> L. var. <i>makuwa</i> . <i>Scientific Data</i> , 2019, 6, 220.	2.4	13
68	Characterization of full-length enriched expressed sequence tags of dehydration-treated white fibrous roots of sweetpotato. <i>BMB Reports</i> , 2009, 42, 271-276.	1.1	13
69	Antioxidant enzymes in <i>Nicotiana</i> cells containing an <i>Ipomoea</i> peroxidase gene. <i>Phytochemistry</i> , 1998, 48, 1287-1290.	1.4	11
70	Cucumber Pti1-L is a cytoplasmic protein kinase involved in defense responses and salt tolerance. <i>Journal of Plant Physiology</i> , 2014, 171, 817-822.	1.6	11
71	Comparative proteomic analysis of host responses to <i>Plasmodiophora brassicae</i> infection in susceptible and resistant <i>Brassica oleracea</i> . <i>Plant Biotechnology Reports</i> , 2020, 14, 263-274.	0.9	11
72	Genome-wide Analysis of Alternative Splicing in An Inbred Cabbage (<i>Brassica oleracea</i> L.) Line 'HO'™ in Response to Heat Stress. <i>Current Genomics</i> , 2017, 19, 12-20.	0.7	10

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73	Temporally distinct regulatory pathways coordinate thermo-responsive storage organ formation in potato. <i>Cell Reports</i> , 2022, 38, 110579.	2.9	10
74	The Arabidopsis cyclophilin CYP18-1 facilitates PRP18 dephosphorylation and the splicing of introns retained under heat stress. <i>Plant Cell</i> , 2022, 34, 2383-2403.	3.1	10
75	The development of herbicide-resistant maize: stable <i>Agrobacterium</i> -mediated transformation of maize using explants of type II embryogenic calli. <i>Plant Biotechnology Reports</i> , 2009, 3, 277-283.	0.9	9
76	Molecular characterization of the sweet potato peroxidase <i>SWPA4</i> promoter which responds to abiotic stresses and pathogen infection. <i>Physiologia Plantarum</i> , 2009, 135, 390-399.	2.6	9
77	SLPMEI, a pollen-specific gene in tomato. <i>Canadian Journal of Plant Science</i> , 2014, 94, 73-83.	0.3	9
78	Comparative transcriptome profiling and SSR marker identification in three Jerusalem artichoke (<i>Helianthus tuberosus</i> L.) cultivars exhibiting phenotypic variation. <i>Plant Biotechnology Reports</i> , 2016, 10, 447-461.	0.9	9
79	Molecular cloning of peroxidase cDNAs from dehydration-treated fibrous roots of sweetpotato and their differential expression in response to stress. <i>BMB Reports</i> , 2008, 41, 259-265.	1.1	9
80	Microarray Analysis of bacterial blight resistance 1 mutant rice infected with <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Plant Breeding and Biotechnology</i> , 2013, 1, 354-365.	0.3	9
81	High frequency shoot induction and plant regeneration from cotyledonary hypocotyl explants of cucumber (<i>Cucumis sativus</i> L.) seedlings. <i>Journal of Plant Physiology</i> , 2000, 157, 136-139.	1.6	8
82	Genome-Wide Comparative Analysis of Flowering-Time Genes; Insights on the Gene Family Expansion and Evolutionary Perspective. <i>Frontiers in Plant Science</i> , 2021, 12, 702243.	1.7	8
83	Suppression of Phytochrome-Interacting Factors Enhances Photoresponses of Seedlings and Delays Flowering With Increased Plant Height in <i>Brachypodium distachyon</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 756795.	1.7	8
84	Genomic detection and molecular characterization of two distinct isolates of cycas necrotic stunt virus from <i>Paeonia suffruticosa</i> and <i>Daphne odora</i> . <i>Virus Genes</i> , 2019, 55, 734-737.	0.7	7
85	De Novo Transcriptome Analysis of <i>Cucumis melo</i> L. var. <i>makuwa</i> . <i>Molecules and Cells</i> , 2016, 39, 141-148.	1.0	7
86	The expression of cyanobacterial glycolate decarboxylation pathway genes improves biomass accumulation in <i>Arabidopsis thaliana</i> . <i>Plant Biotechnology Reports</i> , 2019, 13, 361-373.	0.9	6
87	The use of cotyledonary-node explants in <i>Agrobacterium tumefaciens</i> -mediated transformation of cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Plant Biotechnology</i> , 2011, 38, 198-202.	0.1	6
88	Identification of a pollen-specific gene, SICRK1 (RFK2) in tomato. <i>Genes and Genomics</i> , 2014, 36, 303-311.	0.5	5
89	Silencing of an Î± -dioxygenase gene, Ca-DOX, retards growth and suppresses basal disease resistance responses in <i>Capsicum annum</i> . <i>Plant Molecular Biology</i> , 2017, 93, 497-509.	2.0	5
90	Production of transgenic cucumber expressing phytoene synthase-2A carotene desaturase gene. <i>Journal of Plant Biotechnology</i> , 2016, 43, 341-346.	0.1	5

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91	Development of a Screening System for Plant Defense-Inducing Agent using Transgenic Tobacco Plant with PR-1a Promoter and GUS Gene. <i>Plant Pathology Journal</i> , 2005, 21, 288-292.	0.7	5
92	Complete genome sequence of a South Korean isolate of Brugmansia mosaic virus. <i>Archives of Virology</i> , 2013, 158, 2019-2022.	0.9	4
93	Complete genome sequence of artemisia virus B, a new polerovirus infecting <i>Artemisia princeps</i> in South Korea. <i>Archives of Virology</i> , 2021, 166, 1495-1499.	0.9	4
94	The development of transgenic maize expressing <i>Actinobacillus pleuropneumoniae</i> ApxIIA gene using <i>Agrobacterium</i> . <i>Journal of Plant Biotechnology</i> , 2010, 37, 313-318.	0.1	4
95	Development of transgenic cucumbers expressing <i>Arabidopsis</i> Nit gene. <i>Journal of Plant Biotechnology</i> , 2013, 40, 198-202.	0.1	4
96	Expression of Dengue virus EIII domain-coding gene in maize as an edible vaccine candidate. <i>Journal of Plant Biotechnology</i> , 2014, 41, 50-55.	0.1	4
97	First Report of <i>Impatiens flower break virus</i> Infecting <i>Impatiens walleriana</i> in South Korea. <i>Plant Disease</i> , 2017, 101, 394-394.	0.7	4
98	Alteration of floral organ identity by over-expression of IbMADS3-1 in tobacco. <i>Transgenic Research</i> , 2011, 20, 365-376.	1.3	3
99	RISA: a new web-tool for Rapid Identification of SSRs and Analysis of primers. <i>Genes and Genomics</i> , 2012, 34, 583-590.	0.5	3
100	Expression of cucumber LOX genes in response to powdery mildew and defense-related signal molecules. <i>Canadian Journal of Plant Science</i> , 2014, 94, 845-850.	0.3	3
101	Overexpression of ADP-glucose pyrophosphorylase (IbAGPaseS) affects expression of carbohydrate regulated genes in sweet potato [<i>Ipomoea batatas</i> (L.) Lam. cv. Yulmi]. <i>Genes and Genomics</i> , 2015, 37, 595-605.	0.5	3
102	The first complete sequence and genome structure of daphne virus Y. <i>Archives of Virology</i> , 2016, 161, 2905-2908.	0.9	3
103	The complete sequence and genome organization of ligustrum virus A, a novel carlavirus. <i>Archives of Virology</i> , 2016, 161, 3593-3596.	0.9	3
104	Complete genome sequence of a tentative new member of the genus Badnavirus identified in <i>Codonopsis lanceolata</i> . <i>Archives of Virology</i> , 2019, 164, 1733-1737.	0.9	3
105	Complete genome sequence and genome organization of <i>achyranthes virus A</i> , a novel member of the genus Potyvirus. <i>Archives of Virology</i> , 2020, 165, 2695-2698.	0.9	3
106	Comprehensive analysis of Translationally Controlled Tumor Protein (TCTP) provides insights for lineage-specific evolution and functional divergence. <i>PLoS ONE</i> , 2020, 15, e0232029.	1.1	3
107	Complete genome sequence of platycodon closterovirus 1, a novel putative member of the genus Closterovirus. <i>Archives of Virology</i> , 2021, 166, 2051-2054.	0.9	3
108	Enhanced Tolerance to Oxidative Stress of Transgenic Potato (cv. Superior) Plants Expressing Both SOD and APX in Chloroplasts. <i>Journal of Plant Biotechnology</i> , 2007, 34, 299-305.	0.1	3

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109	First Report of Cotton Leafroll Dwarf Virus Infecting <i>Hibiscus syriacus</i> in South Korea. Plant Disease, 2022, 106, 3003.	0.7	3

110 Molecular characterization and expression of a cDNA encoding copper/zinc superoxide dismutase