

# Soon-Chun Jeong

## List of Publications by Year in descending order

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74  
papers

2,424  
citations

201674

27  
h-index

214800

47  
g-index

78  
all docs

78  
docs citations

78  
times ranked

2256  
citing authors

#	ARTICLE	IF	CITATIONS
1	The discovery of novel SNPs associated with group A soyasaponin biosynthesis from Korea soybean core collection. <i>Genomics</i> , 2022, 114, 110432.	2.9	4
2	Environmental risk assessment of glufosinate-resistant soybean by pollen-mediated gene flow under field conditions in the region of the genetic origin. <i>Science of the Total Environment</i> , 2021, 762, 143073.	8.0	6
3	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , 2021, 12, 97.	12.8	49
4	Fine-mapping and candidate gene analysis for the foxglove aphid resistance gene <i>Raso2</i> from wild soybean PI 366121. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2687-2698.	3.6	6
5	Genome assembly of the popular Korean soybean cultivar Hwangkeum. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5
6	Elucidation of genomic organizations of transgenic soybean plants through de novo genome assembly with short paired-end reads. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	6
7	Chromosomal features revealed by comparison of genetic maps of <i>Glycine max</i> and <i>Glycine soja</i> . <i>Genomics</i> , 2020, 112, 1481-1489.	2.9	8
8	Performance of hybrids between abiotic stress-tolerant transgenic rice and its weedy relatives under water-stressed conditions. <i>Scientific Reports</i> , 2020, 10, 9319.	3.3	5
9	Genome Resequencing, Improvement of Variant Calling, and Population Genomic Analyses Provide Insights into the Seedlessness in the Genus <i>Vitis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3365-3377.	1.8	6
10	Gene Flow from Transgenic PPO-inhibiting Herbicide-resistant Rice to Weedy Rice, and Agronomic Performance by Their Hybrids. <i>Journal of Plant Biology</i> , 2019, 62, 286-296.	2.1	4
11	Korean soybean core collection: Genotypic and phenotypic diversity population structure and genome-wide association study. <i>PLoS ONE</i> , 2019, 14, e0224074.	2.5	56
12	GmBRC1 is a Candidate Gene for Branching in Soybean ( <i>Glycine max</i> (L.) Merrill). <i>International Journal of Molecular Sciences</i> , 2019, 20, 135.	4.1	23
13	Genetic diversity patterns and domestication origin of soybean. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1179-1193.	3.6	44
14	Genetic analysis of the <i>Lf1</i> gene that controls leaflet number in soybean. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1685-1692.	3.6	5
15	Differences in the metabolic profiles and antioxidant activities of wild and cultivated black soybeans evaluated by correlation analysis. <i>Food Research International</i> , 2017, 100, 166-174.	6.2	25
16	GenoCore: A simple and fast algorithm for core subset selection from large genotype datasets. <i>PLoS ONE</i> , 2017, 12, e0181420.	2.5	41
17	Molecular Genetic Analysis of a Novel Recessive White Flower Gene in Wild Soybean. <i>Crop Science</i> , 2017, 57, 3027-3034.	1.8	1
18	Identification of haplotypes at the <i>Rsv4</i> genomic region in soybean associated with durable resistance to soybean mosaic virus. <i>Theoretical and Applied Genetics</i> , 2016, 129, 453-468.	3.6	37

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19	Development, validation and genetic analysis of a large soybean SNP genotyping array. <i>Plant Journal</i> , 2015, 81, 625-636.	5.7	125
20	Genetic diversity and population structure of wild soybean ( <i>Glycine soja</i> Sieb. and Zucc.) accessions in Korea. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S45-S48.	0.8	5
21	Multiple genes confer resistance to soybean mosaic virus in the soybean cultivar Hwangkeum. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S41-S44.	0.8	7
22	Population Structure and Domestication Revealed by High-Depth Resequencing of Korean Cultivated and Wild Soybean Genomes. <i>DNA Research</i> , 2014, 21, 153-167.	3.4	92
23	Effects of transgenic poplars expressing increased levels of cellular cytokinin on rhizosphere microbial communities. <i>European Journal of Soil Biology</i> , 2014, 63, 78-82.	3.2	5
24	Drought stress-induced compositional changes in tolerant transgenic rice and its wild type. <i>Food Chemistry</i> , 2014, 153, 145-150.	8.2	32
25	Cross-Family Translational Genomics of Abiotic Stress-Responsive Genes between <i>Arabidopsis</i> and <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2014, 9, e91721.	2.5	19
26	Effects of Bt Cabbage ( <i>Brassica oleracea</i> ) on the Host Preference and Performance of the Green Peach Aphid, <i>Myzus persicae</i> Sulzer (Hemiptera: Aphididae). <i>Korean Journal of Applied Entomology</i> , 2014, 53, 193-197.	0.3	4
27	Gene Flow from GM Cabbage to Non-GM Control. <i>Korean Journal of Agricultural Science</i> , 2014, 41, 157-161.	0.1	0
28	Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1103-1119.	3.6	21
29	Characterization of SMV resistance of soybean produced by genetic transformation of SMV-CP gene in RNAi. <i>Plant Biotechnology Reports</i> , 2013, 7, 425-433.	1.5	33
30	Comparative analysis of key nutrient composition between drought-tolerant transgenic rice and its non-transgenic counterpart. <i>Food Science and Biotechnology</i> , 2013, 22, 1-7.	2.6	7
31	Transgenic poplar trees expressing yeast cadmium factor 1 exhibit the characteristics necessary for the phytoremediation of mine tailing soil. <i>Chemosphere</i> , 2013, 90, 1478-1486.	8.2	111
32	<i>Ln</i> is a Key Regulator of Leaflet Shape and Number of Seeds per Pod in Soybean. <i>Plant Cell</i> , 2013, 24, 4807-4818.	6.6	90
33	Fitness cost and competitive ability of transgenic herbicide-tolerant rice expressing a protoporphyrinogen oxidase gene. <i>Journal of Ecology and Environment</i> , 2013, 36, 39-47.	1.6	4
34	A molecular framework for risk assessment of a virus-tolerant transgenic pepper line. <i>Journal of Crop Science and Biotechnology</i> , 2012, 15, 107-115.	1.5	2
35	Two-year field study shows little evidence that PPO-transgenic rice affects the structure of soil microbial communities. <i>Biology and Fertility of Soils</i> , 2012, 48, 453-461.	4.3	15
36	Expression of the <i>Arabidopsis AtMYB44</i> gene confers drought/salt-stress tolerance in transgenic soybean. <i>Molecular Breeding</i> , 2012, 29, 601-608.	2.1	73

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37	Do transgenic chili pepper plants producing viral coat protein affect the structure of a soil microbial community?. <i>Applied Soil Ecology</i> , 2011, 51, 130-138.	4.3	12
38	Gene flow from herbicide-tolerant GM rice and the heterosis of GM rice-weed F2 progeny. <i>Planta</i> , 2011, 233, 807-815.	3.2	20
39	Fine genetic mapping of the genomic region controlling leaflet shape and number of seeds per pod in the soybean. <i>Theoretical and Applied Genetics</i> , 2011, 122, 865-874.	3.6	52
40	Glycine max non-nodulation locus <i>rgj1</i> : a recombinogenic region encompassing a SNP in a lysine motif receptor-like kinase ( <i>GmNFR1<math>\pm</math></i> ). <i>Theoretical and Applied Genetics</i> , 2011, 122, 875-884.	3.6	7
41	Novel major quantitative trait loci regulating the content of isoflavone in soybean seeds. <i>Genes and Genomics</i> , 2011, 33, 685-692.	1.4	38
42	The <i>Rsv3</i> Locus Conferring Resistance to Soybean Mosaic Virus is Associated with a Cluster of Coiled-Coil Nucleotide-Binding Leucine-Rich Repeat Genes. <i>Plant Genome</i> , 2011, 4, .	2.8	50
43	Genetic Analysis of Genes Controlling Natural Variation of Seed Coat and Flower Colors in Soybean. <i>Journal of Heredity</i> , 2010, 101, 757-768.	2.4	84
44	Monitoring the occurrence of genetically modified maize at a grain receiving port and along transportation routes in the Republic of Korea. <i>Food Control</i> , 2010, 21, 456-461.	5.5	42
45	Whole-genome sequencing and intensive analysis of the undomesticated soybean ( <i>Glycine soja</i> ) in America, 2010, 107, 22032-22037.	7.1	299
46	Validation and Interaction of the Soybean Mosaic Virus Lethal Necrosis Allele, <i>Rsv1</i> , in PI 507389. <i>Crop Science</i> , 2009, 49, 1277-1283.	1.8	10
47	Marker-assisted identification of resistance genes to soybean mosaic virus in soybean lines. <i>Euphytica</i> , 2009, 169, 375-385.	1.2	16
48	Assessment of Gene Flow from Genetically Modified Anthracnose-Resistant Chili Pepper ( <i>Capsicum</i> ) in America, 2010, 107, 22032-22037.	2.1	9
49	Monitoring the occurrence of genetically modified soybean and maize in cultivated fields and along the transportation routes of the Incheon Port in South Korea. <i>Food Control</i> , 2009, 20, 250-254.	5.5	68
50	Gene flow from genetically modified to conventional chili pepper ( <i>Capsicum annum</i> L.). <i>Plant Science</i> , 2009, 176, 406-412.	3.6	15
51	A framework for molecular genetic assessment of a transgenic watermelon rootstock line. <i>Plant Science</i> , 2009, 176, 805-811.	3.6	10
52	Development of genetically modified crops based on considerations of risk assessment and management. <i>Journal of Plant Biotechnology</i> , 2009, 36, 360-365.	0.4	6
53	Detection of gene flow from GM to non-GM watermelon in a field trial. <i>Journal of Plant Biology</i> , 2008, 51, 74-77.	2.1	8
54	Genome structure in soybean revealed by a genomewide genetic map constructed from a single population. <i>Genomics</i> , 2008, 92, 52-59.	2.9	18

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55	Genetic Linkage Map of the Nucleolus Organizer Region in the Soybean. <i>Genetics</i> , 2008, 178, 605-608.	2.9	5
56	Pyramiding of Soybean Mosaic Virus Resistance Genes by Marker-Assisted Selection. <i>Crop Science</i> , 2008, 48, 517-526.	1.8	96
57	Molecular analysis and quantitative detection of a transgenic rice line expressing a bifunctional fusion TPSP. <i>Food Control</i> , 2007, 18, 1434-1442.	5.5	23
58	Genetic discrimination between <i>Catharanthus roseus</i> cultivars by metabolic fingerprinting using <sup>1</sup> H NMR spectra of aromatic compounds. <i>Biotechnology and Bioprocess Engineering</i> , 2007, 12, 646-652.	2.6	21
59	The Effect of the Anthracnose Resistant Chili Pepper (PepEST gene) on the Non-target Insects, Green Peach Aphids ( <i>Myzus persicae</i> Sulzer, Homoptera). <i>Korean Journal of Applied Entomology</i> , 2007, 46, 343-348.	0.3	3
60	The characterization of bacterial community structure in the rhizosphere of watermelon ( <i>Citrullus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 (T-RFLP). <i>Applied Soil Ecology</i> , 2006, 33, 79-86.	4.3	9
61	Structure, expression, and mapping of two nodule-specific genes identified by mining public soybean EST databases. <i>Gene</i> , 2006, 383, 71-80.	2.2	9
62	Application of comparative genomics in developing molecular markers tightly linked to the virus resistance gene Rsv4 in soybean. <i>Genome</i> , 2006, 49, 380-388.	2.0	54
63	Monitoring the occurrence of genetically modified soybean and maize around cultivated fields and at a grain receiving port in Korea. <i>Journal of Plant Biology</i> , 2006, 49, 218-223.	2.1	43
64	Principal component analysis and discriminant analysis (PCA-DA) for discriminating profiles of terminal restriction fragment length polymorphism (T-RFLP) in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2006, 38, 2344-2349.	8.8	36
65	Environmental Risk Assessment of Watermelon Grafted onto Transgenic Rootstock Resistant to Cucumber Green Mottle Mosaic Virus (CGMMV) on Non-Target Insects in Conventional Agro-Ecosystem. <i>Journal of Ecology and Environment</i> , 2006, 29, 323-330.	1.6	2
66	Recombination Within a Nucleotide-Binding-Site/Leucine-Rich-Repeat Gene Cluster Produces New Variants Conditioning Resistance to Soybean Mosaic Virus in Soybeans. <i>Genetics</i> , 2004, 166, 493-503.	2.9	139
67	Detection and genotyping of SNPs tightly linked to two disease resistance loci, Rsv1 and Rsv3, of soybean. <i>Plant Breeding</i> , 2004, 123, 305-310.	1.9	74
68	Recent Progress in the Evolution and Ecology of Actinorhizal Symbioses. <i>Plant Pathology Journal</i> , 2003, 19, 1-8.	1.7	1
69	Population size and diversity of <i>Frankia</i> in soils of <i>Ceanothus velutinus</i> and Douglas-fir stands. <i>Soil Biology and Biochemistry</i> , 2001, 33, 931-941.	8.8	27
70	Diversity and evolution of a non-TIR-NBS sequence family that clusters to a chromosomal "hotspot" for disease resistance genes in soybean. <i>Theoretical and Applied Genetics</i> , 2001, 103, 406-414.	3.6	39
71	Genomic fingerprinting of <i>Frankia</i> microsymbionts from <i>Ceanothus</i> copopulations using repetitive sequences and polymerase chain reactions. <i>Canadian Journal of Botany</i> , 1999, 77, 1220-1230.	1.1	4
72	Molecular Phylogenies of Plants and <i>Frankia</i> Support Multiple Origins of Actinorhizal Symbioses. <i>Molecular Phylogenetics and Evolution</i> , 1999, 13, 493-503.	2.7	48

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73	Genomic fingerprinting of <i>Frankia</i> microsymbionts from <i>Ceanothus</i> copopulations using repetitive sequences and polymerase chain reactions. <i>Canadian Journal of Botany</i> , 1999, 77, 1220-1230.	1.1	25
74	Molecular phylogeny of the genus <i>Ceanothus</i> (Rhamnaceae) using <i>rbc L</i> and <i>ndh F</i> sequences. <i>Theoretical and Applied Genetics</i> , 1997, 94, 852-857.	3.6	23