

# Su Ryun Choi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3066646/publications.pdf>

Version: 2024-02-01

41  
papers

1,004  
citations

623734

14  
h-index

454955

30  
g-index

47  
all docs

47  
docs citations

47  
times ranked

930  
citing authors

#	ARTICLE	IF	CITATIONS
1	Starch content changes and metabolism-related gene regulation of Chinese cabbage synergistically induced by <i>Plasmodiophora brassicae</i> infection. Horticulture Research, 2022, 9, .	6.3	12
2	Identification of accession-specific variants and development of KASP markers for assessing the genetic makeup of Brassica rapa seeds. BMC Genomics, 2022, 23, 326.	2.8	2
3	Genome-wide identification and characterization of NBS-encoding genes in Raphanus sativus L. and their roles related to Fusarium oxysporum resistance. BMC Plant Biology, 2021, 21, 47.	3.6	18
4	Integrating Omics and Gene Editing Tools for Rapid Improvement of Traditional Food Plants for Diversified and Sustainable Food Security. International Journal of Molecular Sciences, 2021, 22, 8093.	4.1	33
5	QTL mapping for Fusarium wilt resistance based on the whole-genome resequencing and their association with functional genes in Raphanus sativus. Theoretical and Applied Genetics, 2021, 134, 3925-3940.	3.6	4
6	MiR1885 Regulates Disease Tolerance Genes in Brassica rapa during Early Infection with Plasmodiophora brassicae. International Journal of Molecular Sciences, 2021, 22, 9433.	4.1	9
7	Identification of QTLs and Candidate Genes Related to Flower Traits and Bolting Time in Radish (Raphanus sativus L.). Agronomy, 2021, 11, 1623.	3.0	8
8	Genome-Wide Identification, Evolution, and Comparative Analysis of B-Box Genes in Brassica rapa, B. oleracea, and B. napus and Their Expression Profiling in B. rapa in Response to Multiple Hormones and Abiotic Stresses. International Journal of Molecular Sciences, 2021, 22, 10367.	4.1	8
9	L-Cysteine Increases the Transformation Efficiency of Chinese Cabbage (Brassica rapa ssp. pekinensis). Frontiers in Plant Science, 2021, 12, 767140.	3.6	5
10	Fine-mapping of a major QTL (Fwr1) for fusarium wilt resistance in radish. Theoretical and Applied Genetics, 2020, 133, 329-340.	3.6	5
11	Quantitative Trait Locus Mapping of Clubroot Resistance and Plasmodiophora brassicae Pathotype Banglim-Specific Marker Development in Brassica rapa. International Journal of Molecular Sciences, 2020, 21, 4157.	4.1	9
12	Development of SNP markers for marker-assisted breeding in Chinese cabbage using Fluidigm genotyping assays. Horticulture Environment and Biotechnology, 2020, 61, 327-338.	2.1	7
13	Red Chinese Cabbage Transcriptome Analysis Reveals Structural Genes and Multiple Transcription Factors Regulating Reddish Purple Color. International Journal of Molecular Sciences, 2020, 21, 2901.	4.1	21
14	Genetic and physiological analyses of root cracking in radish (Raphanus sativus L.). Theoretical and Applied Genetics, 2019, 132, 3425-3437.	3.6	7
15	A Turnip Mosaic Virus Determinant of Systemic Necrosis in <i>Nicotiana benthamiana</i> and a Novel Resistance-Breaking Determinant in Chinese Cabbage Identified from Chimeric Infectious Clones. Phytopathology, 2019, 109, 1638-1647.	2.2	5
16	Sequence Variations Among 17 New Radish Isolates of Turnip mosaic virus Showing Differential Pathogenicity and Infectivity in Nicotiana benthamiana, Brassica rapa, and Raphanus sativus. Phytopathology, 2019, 109, 904-912.	2.2	14
17	Isolation and characterization of fusarium wilt resistance gene analogs in radish. 3 Biotech, 2018, 8, 255.	2.2	4
18	F-Box Genes in Brassica rapa: Genome-Wide Identification, Structural Characterization, Expressional Validation, and Comparative Analysis. Plant Molecular Biology Reporter, 2018, 36, 500-517.	1.8	5

#	ARTICLE	IF	CITATIONS
19	Comprehensive analysis of CCCH zinc-finger-type transcription factors in the Brassica rapa genome. Horticulture Environment and Biotechnology, 2018, 59, 729-747.	2.1	6
20	Molecular Mapping of Disease Resistance Genes. Compendium of Plant Genomes, 2017, , 165-175.	0.5	2
21	Integrated analysis of leaf morphological and color traits in different populations of Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). Theoretical and Applied Genetics, 2017, 130, 1617-1634.	3.6	9
22	Quantitative Trait Loci for Morphological Traits and their Association with Functional Genes in <i>Raphanus sativus</i> . Frontiers in Plant Science, 2016, 7, 255.	3.6	13
23	Genome wide identification and functional prediction of long non-coding RNAs in Brassica rapa. Genes and Genomics, 2016, 38, 547-555.	1.4	5
24	Genome-Wide Analysis and Characterization of Aux/IAA Family Genes in Brassica rapa. PLoS ONE, 2016, 11, e0151522.	2.5	29
25	The Plasmodiophora brassicae genome reveals insights in its life cycle and ancestry of chitin synthases. Scientific Reports, 2015, 5, 11153.	3.3	202
26	Anatomic Characteristics Associated with Head Splitting in Cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.5	6
27	Development of a leafy Brassica rapa fixed line collection for genetic diversity and population structure analysis. Molecular Breeding, 2015, 35, 1.	2.1	13
28	Accumulation of Phenylpropanoids by White, Blue, and Red Light Irradiation and Their Organ-Specific Distribution in Chinese Cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). Journal of Agricultural and Food Chemistry, 2015, 63, 6772-6778.	5.2	41
29	Mapping QTLs of resistance to head splitting in cabbage ( <i>Brassica oleracea</i> L.var. <i>capitata</i> L.). Molecular Breeding, 2015, 35, 1.	2.1	11
30	Genomic and Post-Translational Modification Analysis of Leucine-Rich-Repeat Receptor-Like Kinases in Brassica rapa. PLoS ONE, 2015, 10, e0142255.	2.5	56
31	Identification of candidate genes involved in the biosynthesis of carotenoids in Brassica rapa. Horticulture Environment and Biotechnology, 2014, 55, 342-351.	2.1	3
32	Genome-wide identification, characterization, and comparative phylogeny analysis of MADS-box transcription factors in Brassica rapa. Genes and Genomics, 2014, 36, 509-525.	1.4	8
33	Fine genetic and physical mapping of the CRb gene conferring resistance to clubroot disease in Brassica rapa. Molecular Breeding, 2014, 34, 1173-1183.	2.1	66
34	Comparative mapping of <i>Raphanus sativus</i> genome using Brassica markers and quantitative trait loci analysis for the Fusarium wilt resistance trait. Theoretical and Applied Genetics, 2013, 126, 2553-2562.	3.6	18
35	Development of EST database and transcriptome analysis in the leaves of Brassica rapa using a newly developed pipeline. Genes and Genomics, 2012, 34, 671-679.	1.4	4
36	Mapping quantitative trait loci for leaf and heading-related traits in Chinese cabbage ( <i>Brassica rapa</i> L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.1	22

#	ARTICLE	IF	CITATIONS
37	Genic Microsatellite Markers in Brassica rapa: Development, Characterization, Mapping, and Their Utility in Other Cultivated and Wild Brassica Relatives. DNA Research, 2011, 18, 305-320.	3.4	77
38	Development and characterization of new microsatellite markers in Panax ginseng (C.A. Meyer) from BAC end sequences. Conservation Genetics, 2010, 11, 1223-1225.	1.5	26
39	Development of a high density integrated reference genetic linkage map for the multinational Brassica rapa Genome Sequencing Project This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". Genome, 2010, 53, 939-947.	2.0	43
40	The reference genetic linkage map for the multinational Brassica rapa genome sequencing project. Theoretical and Applied Genetics, 2007, 115, 777-792.	3.6	160
41	Toward unraveling the structure of Brassica rapa genome. Physiologia Plantarum, 2006, 126, 060307071539002-???	5.2	8