

# Su Ryun Choi

## List of Publications by Year in descending order

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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	The <i>Plasmodiophora brassicae</i> genome reveals insights in its life cycle and ancestry of chitin synthases. <i>Scientific Reports</i> , 2015, 5, 11153.	3.3	202
2	The reference genetic linkage map for the multinational <i>Brassica rapa</i> genome sequencing project. <i>Theoretical and Applied Genetics</i> , 2007, 115, 777-792.	3.6	160
3	Genic Microsatellite Markers in <i>Brassica rapa</i> : Development, Characterization, Mapping, and Their Utility in Other Cultivated and Wild <i>Brassica</i> Relatives. <i>DNA Research</i> , 2011, 18, 305-320.	3.4	77
4	Fine genetic and physical mapping of the CRb gene conferring resistance to clubroot disease in <i>Brassica rapa</i> . <i>Molecular Breeding</i> , 2014, 34, 1173-1183.	2.1	66
5	Genomic and Post-Translational Modification Analysis of Leucine-Rich-Repeat Receptor-Like Kinases in <i>Brassica rapa</i> . <i>PLoS ONE</i> , 2015, 10, e0142255.	2.5	56
6	Development of a high density integrated reference genetic linkage map for the multinational <i>Brassica rapa</i> 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". <i>Genome</i> , 2010, 53, 939-947.	2.0	43
7	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> ). <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 6772-6778.	5.2	41
8	Integrating Omics and Gene Editing Tools for Rapid Improvement of Traditional Food Plants for Diversified and Sustainable Food Security. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8093.	4.1	33
9	Genome-Wide Analysis and Characterization of Aux/IAA Family Genes in <i>Brassica rapa</i> . <i>PLoS ONE</i> , 2016, 11, e0151522.	2.5	29
10	Development and characterization of new microsatellite markers in <i>Panax ginseng</i> (C.A. Meyer) from BAC end sequences. <i>Conservation Genetics</i> , 2010, 11, 1223-1225.	1.5	26
11	Mapping quantitative trait loci for leaf and heading-related traits in Chinese cabbage ( <i>Brassica rapa</i> L.) Tj ETQq1 1 0,784314 rgBT /Over	2.1	22
12	Red Chinese Cabbage Transcriptome Analysis Reveals Structural Genes and Multiple Transcription Factors Regulating Reddish Purple Color. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2901.	4.1	21
13	Comparative mapping of <i>Raphanus sativus</i> genome using <i>Brassica</i> markers and quantitative trait loci analysis for the <i>Fusarium</i> wilt resistance trait. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2553-2562.	3.6	18
14	Genome-wide identification and characterization of NBS-encoding genes in <i>Raphanus sativus</i> L. and their roles related to <i>Fusarium oxysporum</i> resistance. <i>BMC Plant Biology</i> , 2021, 21, 47.	3.6	18
15	Sequence Variations Among 17 New Radish Isolates of Turnip mosaic virus Showing Differential Pathogenicity and Infectivity in <i>Nicotiana benthamiana</i> , <i>Brassica rapa</i> , and <i>Raphanus sativus</i> . <i>Phytopathology</i> , 2019, 109, 904-912.	2.2	14
16	Development of a leafy <i>Brassica rapa</i> fixed line collection for genetic diversity and population structure analysis. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	13
17	Quantitative Trait Loci for Morphological Traits and their Association with Functional Genes in <i>Raphanus sativus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 255.	3.6	13
18	Starch content changes and metabolism-related gene regulation of Chinese cabbage synergistically induced by <i>Plasmodiophora brassicae</i> infection. <i>Horticulture Research</i> , 2022, 9, .	6.3	12

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19	Mapping QTLs of resistance to head splitting in cabbage ( <i>Brassica oleracea</i> L.var. <i>capitata</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	11
20	Quantitative Trait Locus Mapping of Clubroot Resistance and Plasmodiophora brassicae Pathotype Banglim-Specific Marker Development in <i>Brassica rapa</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4157.	4.1	9
21	MiR1885 Regulates Disease Tolerance Genes in <i>Brassica rapa</i> during Early Infection with <i>Plasmodiophora brassicae</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 9433.	4.1	9
22	Integrated analysis of leaf morphological and color traits in different populations of Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1617-1634.	3.6	9
23	Toward unraveling the structure of <i>Brassica rapa</i> genome. <i>Physiologia Plantarum</i> , 2006, 126, 060307071539002-???	5.2	8
24	Genome-wide identification, characterization, and comparative phylogeny analysis of MADS-box transcription factors in <i>Brassica rapa</i> . <i>Genes and Genomics</i> , 2014, 36, 509-525.	1.4	8
25	Identification of QTLs and Candidate Genes Related to Flower Traits and Bolting Time in Radish ( <i>Raphanus sativus</i> L.). <i>Agronomy</i> , 2021, 11, 1623.	3.0	8
26	Genome-Wide Identification, Evolution, and Comparative Analysis of B-Box Genes in <i>Brassica rapa</i> , <i>B. oleracea</i> , and <i>B. napus</i> and Their Expression Profiling in <i>B. rapa</i> in Response to Multiple Hormones and Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10367.	4.1	8
27	Genetic and physiological analyses of root cracking in radish ( <i>Raphanus sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 3425-3437.	3.6	7
28	Development of SNP markers for marker-assisted breeding in Chinese cabbage using Fluidigm genotyping assays. <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 327-338.	2.1	7
29	Anatomic Characteristics Associated with Head Splitting in Cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo 2.5	2.5	6
30	Comprehensive analysis of CCCH zinc-finger-type transcription factors in the <i>Brassica rapa</i> genome. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 729-747.	2.1	6
31	Genome wide identification and functional prediction of long non-coding RNAs in <i>Brassica rapa</i> . <i>Genes and Genomics</i> , 2016, 38, 547-555.	1.4	5
32	F-Box Genes in <i>Brassica rapa</i> : Genome-Wide Identification, Structural Characterization, Expressional Validation, and Comparative Analysis. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 500-517.	1.8	5
33	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. <i>Phytopathology</i> , 2019, 109, 1638-1647.	2.2	5
34	Fine-mapping of a major QTL (Fwr1) for fusarium wilt resistance in radish. <i>Theoretical and Applied Genetics</i> , 2020, 133, 329-340.	3.6	5
35	L-Cysteine Increases the Transformation Efficiency of Chinese Cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 767140.	3.6	5
36	Development of EST database and transcriptome analysis in the leaves of <i>Brassica rapa</i> using a newly developed pipeline. <i>Genes and Genomics</i> , 2012, 34, 671-679.	1.4	4

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37	Isolation and characterization of fusarium wilt resistance gene analogs in radish. 3 Biotech, 2018, 8, 255.	2.2	4
38	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
39	Identification of candidate genes involved in the biosynthesis of carotenoids in Brassica rapa. Horticulture Environment and Biotechnology, 2014, 55, 342-351.	2.1	3
40	Molecular Mapping of Disease Resistance Genes. Compendium of Plant Genomes, 2017, , 165-175.	0.5	2
41	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