

Jong-Wook Chung

List of Publications by Year in descending order

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66
papers

1,297
citations

331670

21
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395702

33
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67
all docs

67
docs citations

67
times ranked

1265
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of polymorphic microsatellite markers in sesame (<i>Sesamum indicum</i> L.). <i>Molecular Ecology Notes</i> , 2005, 5, 736-738.	1.7	92
2	Population Dynamics Among six Major Groups of the <i>Oryza rufipogon</i> Species Complex, Wild Relative of Cultivated Asian Rice. <i>Rice</i> , 2016, 9, 56.	4.0	80
3	Characterization of new microsatellite markers in mung bean, <i>Vigna radiata</i> (L.). <i>Molecular Ecology Notes</i> , 2006, 6, 1132-1134.	1.7	62
4	Sequence Information on Simple Sequence Repeats and Single Nucleotide Polymorphisms through Transcriptome Analysis of Mungbean. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 63-73.	8.5	58
5	Development and characterization of twenty-five new polymorphic microsatellite markers in proso millet (<i>Panicum miliaceum</i> L.). <i>Genes and Genomics</i> , 2010, 32, 267-273.	1.4	57
6	Characterization of microsatellite loci developed for <i>Amaranthus hypochondriacus</i> and their cross-amplifications in wild species. <i>Conservation Genetics</i> , 2008, 9, 243-246.	1.5	50
7	Development of 65 Novel Polymorphic cDNA-SSR Markers in Common Vetch (<i>Vicia sativa</i> subsp. <i>sativa</i>) Using Next Generation Sequencing. <i>Molecules</i> , 2013, 18, 8376-8392.	3.8	44
8	Transcriptome analysis and SNP/SSR marker information of red pepper variety YCM334 and Taeon. <i>Scientia Horticulturae</i> , 2011, 129, 38-45.	3.6	42
9	Evaluation of the genetic diversity and population structure of sesame (<i>Sesamum indicum</i> L.) using microsatellite markers. <i>Genes and Genomics</i> , 2011, 33, 187-195.	1.4	42
10	Development of SSR markers to study diversity in the genus <i>Cymbidium</i> . <i>Biochemical Systematics and Ecology</i> , 2010, 38, 585-594.	1.3	38
11	Association analysis of physicochemical traits on eating quality in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2013, 191, 9-21.	1.2	38
12	Analysis of genetic diversity and population structure of rice cultivars from Korea, China and Japan using SSR markers. <i>Genes and Genomics</i> , 2009, 31, 283-292.	1.4	37
13	Genetic assessment of safflower (<i>Arthamus tinctorius</i> L.) collection with microsatellite markers acquired via pyrosequencing method. <i>Molecular Ecology Resources</i> , 2014, 14, 69-78.	4.8	37
14	Development of an allele-mining set in rice using a heuristic algorithm and SSR genotype data with least redundancy for the post-genomic era. <i>Molecular Breeding</i> , 2010, 26, 639-651.	2.1	36
15	Development and Molecular Characterization of 55 Novel Polymorphic cDNA-SSR Markers in Faba Bean (<i>Vicia faba</i> L.) Using 454 Pyrosequencing. <i>Molecules</i> , 2013, 18, 1844-1856.	3.8	34
16	Molecular genetic diversity and population structure in <i>Lycium</i> accessions using SSR markers. <i>Comptes Rendus - Biologies</i> , 2010, 333, 793-800.	0.2	30
17	Association Analysis of the Amino Acid Contents in Rice. <i>Journal of Integrative Plant Biology</i> , 2009, 51, 1126-1137.	8.5	26
18	Cross-Amplification of <i>Vicia sativa</i> subsp. <i>sativa</i> Microsatellites across 22 Other <i>Vicia</i> Species. <i>Molecules</i> , 2015, 20, 1543-1550.	3.8	26

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19	Phytochemicals and Antioxidant Activity of Korean Black Soybean (<i>Glycine max</i> L.) Landraces. <i>Antioxidants</i> , 2020, 9, 213.	5.1	26
20	The Complete Chloroplast Genome of <i>Capsicum annum</i> var. <i>glabriusculum</i> Using Illumina Sequencing. <i>Molecules</i> , 2015, 20, 13080-13088.	3.8	25
21	Anthocyanin and Isoflavone Contents in Korean Black Soybean Landraces and Their Antioxidant Activities. <i>Plant Breeding and Biotechnology</i> , 2016, 4, 441-452.	0.9	23
22	Development of SNP-based CAPS and dCAPS markers in eight different genes involved in starch biosynthesis in rice. <i>Molecular Breeding</i> , 2009, 24, 93-101.	2.1	22
23	Development of 44 Novel Polymorphic SSR Markers for Determination of Shiitake Mushroom (<i>Lentinula edodes</i>) Cultivars. <i>Genes</i> , 2017, 8, 109.	2.4	21
24	Transcriptome Analysis of Two <i>Vicia sativa</i> Subspecies: Mining Molecular Markers to Enhance Genomic Resources for Vetch Improvement. <i>Genes</i> , 2015, 6, 1164-1182.	2.4	19
25	De novo transcriptome assembly and the identification of gene-associated single-nucleotide polymorphism markers in Asian and American ginseng roots. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1055-1065.	2.1	18
26	Novel Microsatellite Markers Acquired from <i>Rubus coreanus</i> Miq. and Cross-Amplification in Other <i>Rubus</i> Species. <i>Molecules</i> , 2015, 20, 6432-6442.	3.8	17
27	Development of a Core Set from a Large Rice Collection using a Modified Heuristic Algorithm to Retain Maximum Diversity. <i>Journal of Integrative Plant Biology</i> , 2009, 51, 1116-1125.	8.5	16
28	The complete chloroplast genome of <i>Capsicum frutescens</i> (Solanaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1600002.	2.1	15
29	UPLC-ESI-Q-TOF-MS-Based Metabolite Profiling, Antioxidant and Anti-Inflammatory Properties of Different Organ Extracts of <i>Abeliophyllum distichum</i> . <i>Antioxidants</i> , 2021, 10, 70.	5.1	15
30	A study on relative abundance, composition and length variation of microsatellites in 18 underutilized crop species. <i>Genetic Resources and Crop Evolution</i> , 2009, 56, 237-246.	1.6	14
31	Genetic diversity and population structure analysis of strawberry (<i>Fragaria x ananassa</i> Duch.) using SSR markers. <i>Electronic Journal of Biotechnology</i> , 2012, 15, .	2.2	14
32	Assessment of molecular genetic diversity and population structure of sesame (<i>Sesamum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Resources: Characterisation and Utilisation, 2014, 12, 112-119.	0.8	14
33	Antioxidant Activity and Phytochemical Content of Nine <i>Amaranthus</i> Species. <i>Agronomy</i> , 2021, 11, 1032.	3.0	14
34	Characterization of 30 new microsatellite markers, developed from enriched genomic DNA library of zoysiagrass <i>Zoysia japonica</i> Steud.. <i>Molecular Ecology Notes</i> , 2007, 7, 1323-1325.	1.7	13
35	The Complete Chloroplast Genome Sequence of Korean Landrace "Subicho" Pepper (<i>Capsicum</i>) Tj ETQq1 1 0,784314 rgBT /Ove	0.9	11
36	New cDNA-SSR markers in the narrow-leaved vetch (<i>Vicia sativa</i> subsp. <i>nigra</i>) using 454 pyrosequencing. <i>Molecular Breeding</i> , 2014, 33, 749-754.	2.1	10

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37	Comparative efficacy of four candidate DNA barcode regions for identification of <i>Vicia</i> species. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 286-295.	0.8	10
38	Phytochemical distribution and antioxidant activities of Korean adzuki bean (<i>Vigna angularis</i>) landraces. <i>Journal of Crop Science and Biotechnology</i> , 2017, 20, 205-212.	1.5	10
39	The complete chloroplast genome sequence of <i>Glycyrrhiza lepidota</i> (Nutt.) Pursh - An American wild licorice. <i>Journal of Crop Science and Biotechnology</i> , 2017, 20, 295-303.	1.5	10
40	Complete Mitochondrial Genome and a Set of 10 Novel Kompetitive Allele-Specific PCR Markers in Ginseng (<i>Panax ginseng</i> C. A. Mey.). <i>Agronomy</i> , 2020, 10, 1868.	3.0	10
41	Analysis of genetic diversity and population structure of 135 dill (<i>Anethum graveolens</i> L.) accessions using RAPD markers. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 893-903.	1.6	9
42	Comparison of flavonoid contents and antioxidant activities of <i>Vicia</i> species. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 119-126.	0.8	9
43	Complete chloroplast genome sequence of <i>Capsicum baccatum</i> var. <i>baccatum</i> . <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	8
44	Development and Molecular Characterization of Novel Polymorphic Genomic DNA SSR Markers in <i>Lentinula edodes</i> . <i>Mycobiology</i> , 2017, 45, 105-109.	1.7	8
45	Genetic Diversity and Population Structure of Korean Soybean Collection Using 75 Microsatellite Markers. <i>Hang'uk Jakmul Hakhoe Chi</i> , 2014, 59, 492-497.	0.2	8
46	Development of peptide nucleic acid (PNA) microarray for identification of <i>Panax</i> species based on the nuclear ribosomal internal transcribed spacer (ITS) and 5.8S rDNA regions. <i>Genes and Genomics</i> , 2010, 32, 463-468.	1.4	7
47	Molecular Characterization of 170 New gDNA-SSR Markers for Genetic Diversity in Button Mushroom (<i>Agaricus bisporus</i>). <i>Mycobiology</i> , 2019, 47, 527-532.	1.7	7
48	Development of Polymorphic Simple Sequence Repeat Markers using High-Throughput Sequencing in Button Mushroom (<i>Agaricus bisporus</i>). <i>Mycobiology</i> , 2018, 46, 421-428.	1.7	6
49	Functional Analysis of a Novel ABL (Abnormal Browning Related to Light) Gene in Mycelial Brown Film Formation of <i>Lentinula edodes</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 272.	3.5	6
50	Establishment of a UPLC-PDA/ESI-Q-TOF/MS-Based Approach for the Simultaneous Analysis of Multiple Phenolic Compounds in Amaranth (<i>A. cruentus</i> and <i>A. tricolor</i>). <i>Molecules</i> , 2020, 25, 5674.	3.8	6
51	Analysis of Genetic Diversity and Population Structure of Wild Strains and Cultivars Using Genomic SSR Markers in <i>Lentinula edodes</i> . <i>Mycobiology</i> , 2020, 48, 115-121.	1.7	6
52	Microsatellite variations and population structure in an on-farm collection of Japanese apricot (<i>Prunus mume</i> Sieb. et Zucc.). <i>Biochemical Systematics and Ecology</i> , 2012, 42, 99-112.	1.3	5
53	Photosynthesis, Metabolite Composition and Anatomical Structure of <i>Oryza sativa</i> and Two Wild Relatives, <i>O. grandiglumis</i> and <i>O. alta</i> . <i>Rice Science</i> , 2017, 24, 218-227.	3.9	5
54	Genetic diversity and population structure of Chinese ginseng accessions using SSR markers. <i>Journal of Plant Biotechnology</i> , 2017, 44, 312-319.	0.4	5

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55	Complete Chloroplast Genome of the Inverted Repeat-Lacking Species <i>Vicia bungei</i> and Development of Polymorphic Simple Sequence Repeat Markers. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	5
56	Newly developed polymorphic microsatellite markers in Job's tears (<i>Coix lacryma-jobi</i> L.). <i>Molecular Ecology Notes</i> , 2006, 6, 689-691.	1.7	4
57	Transcriptome characterization and large-scale identification of SSR/SNP markers in symbiotic nitrogen fixation crop faba bean (<i>Vicia faba</i> L.). <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 459-469.	2.1	4
58	Development of CAPS Markers for Evaluation of Genetic Diversity and Population Structure in the Germplasm of Button Mushroom (<i>Agaricus bisporus</i>). <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 375.	3.5	4
59	Evaluation of the Nutrient Composition, In Vitro Fermentation Characteristics, and In Situ Degradability of <i>Amaranthus caudatus</i> , <i>Amaranthus cruentus</i> , and <i>Amaranthus hypochondriacus</i> in Cattle. <i>Animals</i> , 2021, 11, 18.	2.3	3
60	Evaluation of Genetic Diversity and Population Structure Analysis among Germplasm of <i>Agaricus bisporus</i> by SSR Markers. <i>Mycobiology</i> , 2021, 49, 376-384.	1.7	2
61	Development of genomic simple sequence repeat markers for <i>Glycyrrhiza lepidota</i> and cross-amplification of other <i>Glycyrrhiza</i> species. <i>PeerJ</i> , 2019, 7, e7479.	2.0	2
62	Comparison of eating quality and seed storage protein among Korean rice landraces. <i>Journal of Crop Science and Biotechnology</i> , 2016, 19, 241-247.	1.5	1
63	Evaluation of Phytochemical contents and antioxidant activity of Korean common bean (<i>Phaseolus vulgaris</i> L.) landraces. <i>Journal of the Korean Society of International Agriculture</i> , 2018, 30, 357-369.	0.4	1
64	Genetic Diversity and Phenetic Relationship of Dill (<i>Anethum graveolens</i> L.) by rps16-trnK DNA Sequences. <i>Journal of Life Science</i> , 2013, 23, 1305-1310.	0.2	0
65	Comparison of the antioxidant and anti-inflammatory activities of leaf extracts from grain amaranths (<i>Amaranthus</i> spp.). <i>Journal of Plant Biotechnology</i> , 2022, 49, 99-105.	0.4	0
66	Comparison of Antioxidant Activities in <i>Agastache</i> Species. <i>Journal of the Korean Society of Food Science and Nutrition</i> , 2022, 51, 389-394.	0.9	0