

# Won Cheol Yim

## List of Publications by Year in descending order

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Version: 2024-02-01

39  
papers

1,895  
citations

361388

20  
h-index

315719

38  
g-index

41  
all docs

41  
docs citations

41  
times ranked

2342  
citing authors

#	ARTICLE	IF	CITATIONS
1	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472
2	A roadmap for research on crassulacean acid metabolism (<sc>CAM</sc>) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	7.3	211
3	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
4	Disentangling Sources of Gene Tree Discordance in Phylogenomic Data Sets: Testing Ancient Hybridizations in <i>Amaranthaceae</i> s.l. <i>Systematic Biology</i> , 2021, 70, 219-235.	5.6	112
5	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga <i>Dunaliella salina</i> Strain CCAP19/18. <i>Genome Announcements</i> , 2017, 5, .	0.8	83
6	Temporal and spatial transcriptomic and micro<sc>RNA</sc> dynamics of <sc>CAM</sc> photosynthesis in pineapple. <i>Plant Journal</i> , 2017, 92, 19-30.	5.7	78
7	A gene family encoding RING finger proteins in rice: their expansion, expression diversity, and co-expressed genes. <i>Plant Molecular Biology</i> , 2010, 72, 369-380.	3.9	70
8	<i>Sporobolus stapfianus</i> : Insights into desiccation tolerance in the resurrection grasses from linking transcriptomics to metabolomics. <i>BMC Plant Biology</i> , 2017, 17, 67.	3.6	61
9	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	21.4	60
10	PLANEX: the plant co-expression database. <i>BMC Plant Biology</i> , 2013, 13, 83.	3.6	52
11	Evolution of <sc>DOPA</sc> 4,5- $\alpha$ -dioxygenase activity allows for recurrent specialisation to betalain pigmentation in Caryophyllales. <i>New Phytologist</i> , 2020, 227, 914-929.	7.3	48
12	Identification of Ice Plant ( <i>Mesembryanthemum crystallinum</i> L.) MicroRNAs Using RNA-Seq and Their Putative Roles in High Salinity Responses in Seedlings. <i>Frontiers in Plant Science</i> , 2016, 7, 1143.	3.6	47
13	Laying the Foundation for Crassulacean Acid Metabolism (CAM) Biodesign: Expression of the C4 Metabolism Cycle Genes of CAM in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 101.	3.6	45
14	Expression diversity and evolutionary dynamics of rice duplicate genes. <i>Molecular Genetics and Genomics</i> , 2009, 281, 483-493.	2.1	40
15	A <i>Vitis vinifera</i> basic helix- $\alpha$ -helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. <i>Plant Biotechnology Journal</i> , 2018, 16, 1595-1615.	8.3	39
16	Plant tissue succulence engineering improves water-use efficiency, water-deficit stress attenuation and salinity tolerance in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 103, 1049-1072.	5.7	36
17	Cas9-mediated gene editing in the black-legged tick, <i>Ixodes scapularis</i> , by embryo injection and ReMOT Control. <i>iScience</i> , 2022, 25, 103781.	4.1	35
18	Crassulacean Acid Metabolism Abiotic Stress-Responsive Transcription Factors: a Potential Genetic Engineering Approach for Improving Crop Tolerance to Abiotic Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 129.	3.6	28

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19	Identification of Genes Encoding Enzymes Catalyzing the Early Steps of Carrot Polyacetylene Biosynthesis. <i>Plant Physiology</i> , 2018, 178, 1507-1521.	4.8	26
20	Evolution of non-specific lipid transfer protein (nsLTP) genes in the Poaceae family: their duplication and diversity. <i>Molecular Genetics and Genomics</i> , 2008, 279, 481-497.	2.1	24
21	Transcriptional regulation of wound suberin deposition in potato cultivars with differential wound healing capacity. <i>Plant Journal</i> , 2021, 107, 77-99.	5.7	21
22	Expressional diversity of wheat nsLTP genes: evidence of subfunctionalization via cis-regulatory divergence. <i>Genetica</i> , 2010, 138, 843-852.	1.1	18
23	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	4.6	18
24	Divergence of genes encoding non-specific lipid transfer proteins in the poaceae family. <i>Molecules and Cells</i> , 2007, 24, 215-23.	2.6	18
25	Biosystems Design to Accelerate C <sub>3</sub> -to-CAM Progression. <i>Biodesign Research</i> , 2020, 2020, .	1.9	16
26	Cross experimental analysis of microarray gene expression data from volatile organic compounds treated targets. <i>Molecular and Cellular Toxicology</i> , 2011, 7, 233-241.	1.7	11
27	Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. <i>PeerJ</i> , 2017, 5, e3486.	2.0	10
28	Structural diversity, biosynthesis, and function of plant falcarin-type polyacetylenic lipids. <i>Journal of Experimental Botany</i> , 2022, 73, 2889-2904.	4.8	10
29	Identification of novel 17-estradiol (E2) target genes using cross-experiment gene expression datasets. <i>Toxicology and Environmental Health Sciences</i> , 2010, 2, 25-38.	2.1	9
30	Cross-experimental analysis of microarray gene expression datasets for in silico risk assessment of TiO <sub>2</sub> nano-particles. <i>Molecular and Cellular Toxicology</i> , 2012, 8, 229-239.	1.7	8
31	An rbcL mRNA-binding protein is associated with C3 to C4 evolution and light-induced production of Rubisco in <i>Flaveria</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 4635-4649.	4.8	7
32	Membrane Profiling by Free Flow Electrophoresis and SWATH-MS to Characterize Subcellular Compartment Proteomes in <i>Mesembryanthemum crystallinum</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 5020.	4.1	5
33	Mitochondrial haplotypes are not associated with mice selectively bred for high voluntary wheel running. <i>Mitochondrion</i> , 2019, 46, 134-139.	3.4	4
34	Characterization of a microbial consortium with potential for biological degradation of cactus pear biomass for biofuel production. <i>Heliyon</i> , 2021, 7, e07854.	3.2	4
35	Relationship of Transformation Efficiency and Metabolites Induced in Korean Soybean Cotyledons Treated with Sonication. <i>Hang'uk Jakmul Hakhoe Chi</i> , 2013, 58, 119-127.	0.2	4
36	Transcriptional network analysis of the tryptophan-accumulating rice mutant during grain filling. <i>Molecular Genetics and Genomics</i> , 2012, 287, 699-709.	2.1	1

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37	Characterization of Expressed Genes Under Ozone Stress in Soybean. <i>Plant Breeding and Biotechnology</i> , 2013, 1, 270-276.	0.9	1
38	Sexual Recombination and Selection During Domestication of Clonally Propagated Pineapple. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
39	Distribution of Genetic Variants in Korean Soybeans. <i>Hang'uk Jakmul Hakhoe Chi</i> , 2015, 60, 224-230.	0.2	0