

# Ik-Young Choi

## List of Publications by Year in descending order

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108  
papers

6,439  
citations

159585

30  
h-index

74163

75  
g-index

110  
all docs

110  
docs citations

110  
times ranked

8799  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rice <i>microRNA171f/SCL6</i> module enhances drought tolerance by regulation of flavonoid biosynthesis genes. <i>Plant Direct</i> , 2022, 6, e374.	1.9	19
2	Identification and Characterization of Key Genes Responsible for Weedy and Cultivar Growth Types in Soybean. <i>Frontiers in Genetics</i> , 2022, 13, 805347.	2.3	1
3	Genome-wide identification of 194 G protein-coupled receptor (GPCR) genes from the water flea <i>Daphnia magna</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100983.	1.0	0
4	Comparison in Content of Total Polyphenol, Flavonoid, and Antioxidant Capacity from Different Organs and Extruded Condition of <i>Moringa oleifera</i> Lam. <i>Processes</i> , 2022, 10, 819.	2.8	3
5	Alternative Splicing (AS) Dynamics in Dwarf Soybean Derived from Cross of <i>Glycine max</i> and <i>Glycine soja</i> . <i>Agronomy</i> , 2022, 12, 1685.	3.0	2
6	Genetic characterization of popcorn hybrids based on SNP genotyping and development of rapid ARMS based primers. <i>Journal of Crop Science and Biotechnology</i> , 2021, 24, 319-325.	1.5	0
7	Editor's introduction to this issue (G&I 19:1, 2021). <i>Genomics and Informatics</i> , 2021, 19, e1.	0.8	2
8	Application of Upstream Open Reading Frames (uORFs) Editing for the Development of Stress-Tolerant Crops. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3743.	4.1	9
9	Analysis of genome variants in dwarf soybean lines obtained in F6 derived from cross of normal parents (cultivated and wild soybean). <i>Genomics and Informatics</i> , 2021, 19, e19.	0.8	2
10	Gene Expression and Isoform Identification of PacBio Full-Length cDNA Sequences for Berberine Biosynthesis in <i>Berberis koreana</i> . <i>Plants</i> , 2021, 10, 1314.	3.5	10
11	Mapping of QTL for agronomic traits using high-density SNPs with an RIL population in maize. <i>Genes and Genomics</i> , 2021, 43, 1403-1411.	1.4	7
12	Unraveling the complexity of faba bean ( <i>Vicia faba</i> L.) transcriptome to reveal cold-stress-responsive genes using long-read isoform sequencing technology. <i>Scientific Reports</i> , 2021, 11, 21094.	3.3	12
13	Identification of resurrection genes from the transcriptome of dehydrated and rehydrated <i>Selaginella tamariscina</i> . <i>Plant Signaling and Behavior</i> , 2021, 16, 1973703.	2.4	4
14	Characterization of transcription factor genes related to cold tolerance in <i>Brassica napus</i> . <i>Genomics and Informatics</i> , 2021, 19, e45.	0.8	2
15	Detection of mPing mobilization in transgenic rice plants. <i>Genes and Genomics</i> , 2020, 42, 47-54.	1.4	2
16	De novo assembly and characterization of transcriptome in the medicinal plant <i>Euphorbia jolkini</i> . <i>Genes and Genomics</i> , 2020, 42, 1011-1021.	1.4	3
17	Genomic analysis and a consensus chloroplast genome sequence of <i>Prunus yedoensis</i> for DNA marker development. <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 859-867.	2.1	5
18	The complete chloroplast genome of a Korean endemic species <i>Sophora koreensis</i> , Nakai. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3067-3068.	0.4	1

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19	Characterization of Gene Isoforms Related to Cellulose and Lignin Biosynthesis in Kenaf ( <i>Hibiscus</i> ) Tj ETQq1 1 0.784314 rgBT <sub>3</sub> /Overlook	3.5	3
20	The complete chloroplast genome of a <i>Woodwardia japonica</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 102-103.	0.4	1
21	The complete chloroplast genome of a fern genus <i>Thelypteris interrupta</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 572-573.	0.4	1
22	Effect of germination environment on the biochemical compounds and anti-inflammatory properties of soybean cultivars. <i>PLoS ONE</i> , 2020, 15, e0232159.	2.5	23
23	Generation of albino via <i>SLC45a2</i> gene targeting by CRISPR/Cas9 in the marine medaka <i>Oryzias melastigma</i> . <i>Marine Pollution Bulletin</i> , 2020, 154, 111038.	5.0	11
24	The C- and G-value paradox with polyploidy, repeatomes, introns, phenomes and cell economy. <i>Genes and Genomics</i> , 2020, 42, 699-714.	1.4	21
25	The comparative gene expression concern to the seed pigmentation in maize ( <i>Zea mays</i> L.). <i>Genomics and Informatics</i> , 2020, 18, e29.	0.8	0
26	Identification of novel haplotype of a cyst nematode resistance gene, <i>GmSNAP18</i> in soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Indian Journal of Genetics and Plant Breeding</i> , 2020, 80, .	0.5	0
27	Genome-wide transcriptome profiling of the medicinal plant <i>Zanthoxylum planispinum</i> using a single-molecule direct RNA sequencing approach. <i>Genomics</i> , 2019, 111, 973-979.	2.9	32
28	Comparative transcriptome analysis reveals higher expression of stress and defense responsive genes in dwarf soybeans obtained from the crossing of <i>G. max</i> and <i>G. soja</i> . <i>Genes and Genomics</i> , 2019, 41, 1315-1327.	1.4	8
29	Transcriptome analysis of <i>Asparagus officinalis</i> reveals genes involved in the biosynthesis of rutin and protodioscin. <i>PLoS ONE</i> , 2019, 14, e0219973.	2.5	20
30	The complete chloroplast genome of a rare species in Korea, <i>Lilium Dauricum</i> Ker Gawl. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3591-3592.	0.4	2
31	NGS sequencing reveals that many of the genetic variations in transgenic rice plants match the variations found in natural rice population. <i>Genes and Genomics</i> , 2019, 41, 213-222.	1.4	8
32	Characterization of chloroplast genomes of <i>Alnus rubra</i> and <i>Betula cordifolia</i> , and their use in phylogenetic analyses in <i>Betulaceae</i> . <i>Genes and Genomics</i> , 2019, 41, 305-316.	1.4	4
33	Comparison of Metabolite Levels and Antioxidant Activity Among Pepper Cultivars. <i>Han'guk Yukchong Hakhoe Chi</i> , 2019, 51, 326-340.	0.5	1
34	The genome of the marine medaka <i>Oryzias melastigma</i> . <i>Molecular Ecology Resources</i> , 2018, 18, 656-665.	4.8	31
35	The genome of the freshwater monogonont rotifer <i>Brachionus calyciflorus</i> . <i>Molecular Ecology Resources</i> , 2018, 18, 646-655.	4.8	52
36	Transcriptional profiling of antioxidant defense system and heat shock protein (Hsp) families in the cadmium- and copper-exposed marine ciliate <i>Euplotes crassus</i> . <i>Genes and Genomics</i> , 2018, 40, 85-98.	1.4	13

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37	Molecular identification of <i>Allium ochotense</i> and <i>Allium microdictyon</i> using multiplex-PCR based on single nucleotide polymorphisms. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 865-873.	2.1	5
38	Genetic diversity and population structure among accessions of <i>Perilla frutescens</i> (L.) Britton in East Asia using new developed microsatellite markers. <i>Genes and Genomics</i> , 2018, 40, 1319-1329.	1.4	44
39	RNA-Seq De Novo Assembly and Differential Transcriptome Analysis of Korean Medicinal Herb <i>Cirsium japonicum</i> var. <i>spinosissimum</i> . <i>Genomics and Informatics</i> , 2018, 16, e34.	0.8	8
40	Comparative Gene Expression Analysis of Seed Development in Waxy and Dent Corn ( <i>Zea mays</i> L.). <i>Plant Breeding and Biotechnology</i> , 2018, 6, 337-353.	0.9	1
41	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017, 24, dsw049.	3.4	38
42	A Comparative Study of Phenolic Antioxidant Activity and Flavonoid Biosynthesis-Related Gene Expression Between Summer and Winter Strawberry Cultivars. <i>Journal of Food Science</i> , 2017, 82, 341-349.	3.1	20
43	Diversity, distribution, and significance of transposable elements in the genome of the only selfing hermaphroditic vertebrate <i>Kryptolebias marmoratus</i> . <i>Scientific Reports</i> , 2017, 7, 40121.	3.3	28
44	Transcriptome response of the Pacific oyster, <i>Crassostrea gigas</i> susceptible to thermal stress: A comparison with the response of tolerant oyster. <i>Molecular and Cellular Toxicology</i> , 2017, 13, 105-113.	1.7	55
45	A bioinformatics approach for identifying transgene insertion sites using whole genome sequencing data. <i>BMC Biotechnology</i> , 2017, 17, 67.	3.3	42
46	Chloroplast genomes of <i>Lilium lancifolium</i> , <i>L. amabile</i> , <i>L. callosum</i> , and <i>L. philadelphicum</i> : Molecular characterization and their use in phylogenetic analysis in the genus <i>Lilium</i> and other allied genera in the order Liliales. <i>PLoS ONE</i> , 2017, 12, e0186788.	2.5	19
47	Alternative Splicing Profile and Sex-Preferential Gene Expression in the Female and Male Pacific Abalone <i>Haliotis discus hannai</i> . <i>Genes</i> , 2017, 8, 99.	2.4	39
48	Whole genome sequence and genome annotation of <i>Colletotrichum acutatum</i> , causal agent of anthracnose in pepper plants in South Korea. <i>Genomics Data</i> , 2016, 8, 45-46.	1.3	26
49	Thermal stress induces a distinct transcriptome profile in the Pacific oyster <i>Crassostrea gigas</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 19, 62-70.	1.0	35
50	Omics of the marine medaka ( <i>Oryzias melastigma</i> ) and its relevance to marine environmental research. <i>Marine Environmental Research</i> , 2016, 113, 141-152.	2.5	56
51	Transcriptome profiling of the Pacific oyster <i>Crassostrea gigas</i> by Illumina RNA-seq. <i>Genes and Genomics</i> , 2016, 38, 359-365.	1.4	9
52	The complete mitochondrial genome sequence of the ascomycete plant pathogen <i>Colletotrichum acutatum</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4547-4548.	0.7	8
53	The complete chloroplast genomes of three Korean <i>Echinochloa crus-galli</i> accessions. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4357-4358.	0.7	7
54	Marine medaka ATP-binding cassette (ABC) superfamily and new insight into teleost Abch nomenclature. <i>Scientific Reports</i> , 2015, 5, 15409.	3.3	22

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55	Multiple Genes Related to Muscle Identified through a Joint Analysis of a Two-stage Genome-wide Association Study for Racing Performance of 1,156 Thoroughbreds. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 771-781.	2.4	13
56	RNA-seq based whole transcriptome analysis of the cyclopoid copepod <i>Paracyclops nana</i> focusing on xenobiotics metabolism. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 15, 12-19.	1.0	21
57	Gene set by de novo assembly of <i>Perilla</i> species and expression profiling between <i>P. frutescens</i> (L.) var. <i>frutescens</i> and var. <i>crispa</i> . <i>Gene</i> , 2015, 559, 155-163.	2.2	18
58	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015, 16, 1.	2.8	1,445
59	Whole transcriptome analysis of the monogonont rotifer <i>Brachionus koreanus</i> provides molecular resources for developing biomarkers of carbohydrate metabolism. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 14, 33-41.	1.0	11
60	Genomics-Assisted Breeding. , 2015, , 145-173.		1
61	Transcriptome profiling of larvae of the marine medaka <i>Oryzias melastigma</i> by Illumina RNA-seq. <i>Marine Genomics</i> , 2015, 24, 255-258.	1.1	11
62	A Genome-wide Scan for Selective Sweeps in Racing Horses. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 1525-1531.	2.4	47
63	Variation block-based genomics method for crop plants. <i>BMC Genomics</i> , 2014, 15, 477.	2.8	15
64	Defining the genome structure of 'Tongil' rice, an important cultivar in the Korean "Green Revolution". <i>Rice</i> , 2014, 7, 22.	4.0	24
65	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014, 46, 270-278.	21.4	867
66	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
67	Understanding pathogenic <i>Burkholderia glumae</i> metabolic and signaling pathways within rice tissues through in vivo transcriptome analyses. <i>Gene</i> , 2014, 547, 77-85.	2.2	23
68	Transcriptome information of the Arctic green sea urchin and its use in environmental monitoring. <i>Polar Biology</i> , 2014, 37, 1133-1144.	1.2	4
69	Effects of benzo[a]pyrene on whole cytochrome P450-involved molecular responses in the marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2014, 152, 232-243.	4.0	38
70	miRAuto: An Automated User-Friendly MicroRNA Prediction Tool Utilizing Plant Small RNA Sequencing Data. <i>Molecules and Cells</i> , 2013, 35, 342-347.	2.6	5
71	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
72	Expression profile analysis of antioxidative stress and developmental pathway genes in the manganese-exposed intertidal copepod <i>Tigriopus japonicus</i> with 6K oligochip. <i>Chemosphere</i> , 2013, 92, 1214-1223.	8.2	22

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73	Whole Spectrum of Cytochrome P450 Genes and Molecular Responses to Water-Accommodated Fractions Exposure in the Marine Medaka. <i>Environmental Science &amp; Technology</i> , 2013, 47, 4804-4812.	10.0	50
74	Complete Genome Sequence of <i>Mycobacterium bovis</i> BCG Korea, the Korean Vaccine Strain for Substantial Production. <i>Genome Announcements</i> , 2013, 1, e0006913.	0.8	11
75	The Hot Pepper ( <i>Capsicum annuum</i> ) MicroRNA Transcriptome Reveals Novel and Conserved Targets: A Foundation for Understanding MicroRNA Functional Roles in Hot Pepper. <i>PLoS ONE</i> , 2013, 8, e64238.	2.5	55
76	Complete Genome Sequence of <i>Mycobacterium intracellulare</i> Clinical Strain MOTT-36Y, Belonging to the INT5 Genotype. <i>Journal of Bacteriology</i> , 2012, 194, 4141-4142.	2.2	13
77	Complete Genome Sequence of <i>Mycobacterium intracellulare</i> Clinical Strain MOTT-02. <i>Journal of Bacteriology</i> , 2012, 194, 2771-2771.	2.2	17
78	Complete Genome Sequence of <i>Mycobacterium intracellulare</i> Clinical Strain MOTT-64, Belonging to the INT1 Genotype. <i>Journal of Bacteriology</i> , 2012, 194, 3268-3268.	2.2	17
79	Complete Genome Sequence of <i>Mycobacterium intracellulare</i> Strain ATCC 13950T. <i>Journal of Bacteriology</i> , 2012, 194, 2750-2750.	2.2	25
80	Genome Sequence of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Strain PCC21, a Pathogen Causing Soft Rot in Chinese Cabbage. <i>Journal of Bacteriology</i> , 2012, 194, 6345-6346.	2.2	22
81	Identification and analysis of whole microcystin synthetase genes from two Korean strains of the cyanobacterium <i>Microcystis aeruginosa</i> . <i>Genes and Genomics</i> , 2012, 34, 435-439.	1.4	6
82	Precision genome engineering with programmable DNA-nicking enzymes. <i>Genome Research</i> , 2012, 22, 1327-1333.	5.5	127
83	The polychaete, <i>Perinereis nuntia</i> ESTs and its use to uncover potential biomarker genes for molecular ecotoxicological studies. <i>Environmental Research</i> , 2012, 112, 48-57.	7.5	17
84	HspA and HtpG Enhance Thermotolerance in the Cyanobacterium, <i>Microcystis aeruginosa</i> NIES-298. <i>Journal of Microbiology and Biotechnology</i> , 2012, 22, 118-125.	2.1	5
85	Draft Genome Database Construction from Four Strains (NIES-298, FCY- 26, -27, and -28) of the Cyanobacterium <i>Microcystis aeruginosa</i> . <i>Journal of Microbiology and Biotechnology</i> , 2012, 22, 1208-1213.	2.1	6
86	Survey of the Applications of NGS to Whole-Genome Sequencing and Expression Profiling. <i>Genomics and Informatics</i> , 2012, 10, 1.	0.8	9
87	Analysis of expressed sequence tags from the liver and ovary of the euryhaline hermaphroditic fish, <i>Kryptolebias marmoratus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 244-255.	1.0	14
88	Sequence analysis of genomic DNA (680 Mb) by GS-FLX-Titanium sequencer in the monogonont rotifer, <i>Brachionus ibericus</i> . <i>Hydrobiologia</i> , 2011, 662, 65-75.	2.0	39
89	Shotgun proteomic analysis for detecting differentially expressed proteins in the reduced culm number rice. <i>Proteomics</i> , 2011, 11, 455-468.	2.2	18
90	Complete Genome Sequence of Japanese <i>Erwinia</i> Strain Ejp617, a Bacterial Shoot Blight Pathogen of Pear. <i>Journal of Bacteriology</i> , 2011, 193, 586-587.	2.2	29

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91	Complete Genome Sequence of Burkholderia gladioli BSR3. Journal of Bacteriology, 2011, 193, 3149-3149.	2.2	47
92	High-throughput SNP discovery and assay development in common bean. BMC Genomics, 2010, 11, 475.	2.8	134
93	A High Density Integrated Genetic Linkage Map of Soybean and the Development of a 1536 Universal Soy Linkage Panel for Quantitative Trait Locus Mapping. Crop Science, 2010, 50, 960-968.	1.8	247
94	Identification of Hydrangeaceae accessions of wild origin from Jeju, Korea, using molecular markers. Plant Genetic Resources: Characterisation and Utilisation, 2010, 8, 235-241.	0.8	4
95	Sequence and structure of Brassica rapa chromosome A3. Genome Biology, 2010, 11, R94.	9.6	66
96	Whole-genome sequencing and intensive analysis of the undomesticated soybean ( <i>Glycine soja</i> ) in America, 2010, 107, 22032-22037.	7.1	299
97	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. Theoretical and Applied Genetics, 2008, 116, 945-952.	3.6	210
98	EVALUATION, CHARACTERIZATION, AND IDENTIFICATION OF WOODY LANDSCAPE PLANTS. Acta Horticulturae, 2008, , 327-338.	0.2	0
99	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. Genetics, 2007, 176, 685-696.	2.9	285
100	Highly Variable Patterns of Linkage Disequilibrium in Multiple Soybean Populations. Genetics, 2007, 175, 1937-1944.	2.9	182
101	Characterization of wild <i>Prunus yedoensis</i> analyzed by inter-simple sequence repeat and chloroplast DNA. Scientia Horticulturae, 2007, 114, 121-128.	3.6	35
102	BARCSoySNP23: a panel of 23 selected SNPs for soybean cultivar identification. Theoretical and Applied Genetics, 2007, 114, 885-899.	3.6	36
103	Fungal and plant gene expression during the colonization of cacao seedlings by endophytic isolates of four <i>Trichoderma</i> species. Planta, 2006, 224, 1449-1464.	3.2	226
104	Abnormal leaf formation in soybean: genetic and environmental effects. Theoretical and Applied Genetics, 2006, 113, 137-146.	3.6	2
105	Application of machine learning in SNP discovery. BMC Bioinformatics, 2006, 7, 4.	2.6	43
106	SNP-PHAGE--High throughput SNP discovery pipeline. BMC Bioinformatics, 2006, 7, 468.	2.6	29
107	Impacts of genetic bottlenecks on soybean genome diversity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16666-16671.	7.1	633
108	Genetic diversity measured by simple sequence repeat variations among the wild soybean, <i>Glycine soja</i> , collected along the riverside of five major rivers in Korea.. Genes and Genetic Systems, 1999, 74, 169-177.	0.7	24