

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	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
2	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
3	Impacts of genetic bottlenecks on soybean genome diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16666-16671.	7.1	633
4	Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) in East Asia. <i>PLoS ONE</i> , 2010, 5, e122032-22037.	7.1	299
5	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.	2.9	285
6	A High Density Integrated Genetic Linkage Map of Soybean and the Development of a 1536 Universal Soy Linkage Panel for Quantitative Trait Locus Mapping. <i>Crop Science</i> , 2010, 50, 960-968.	1.8	247
7	Fungal and plant gene expression during the colonization of cacao seedlings by endophytic isolates of four <i>Trichoderma</i> species. <i>Planta</i> , 2006, 224, 1449-1464.	3.2	226
8	High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. <i>Theoretical and Applied Genetics</i> , 2008, 116, 945-952.	3.6	210
9	Highly Variable Patterns of Linkage Disequilibrium in Multiple Soybean Populations. <i>Genetics</i> , 2007, 175, 1937-1944.	2.9	182
10	High-throughput SNP discovery and assay development in common bean. <i>BMC Genomics</i> , 2010, 11, 475.	2.8	134
11	Precision genome engineering with programmable DNA-nicking enzymes. <i>Genome Research</i> , 2012, 22, 1327-1333.	5.5	127
12	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
13	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010, 11, R94.	9.6	66
14	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
15	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
16	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
17	The genome of the freshwater monogonont rotifer <i>Brachionus calyciflorus</i> . <i>Molecular Ecology Resources</i> , 2018, 18, 646-655.	4.8	52
18	Whole Spectrum of Cytochrome P450 Genes and Molecular Responses to Water-Accommodated Fractions Exposure in the Marine Medaka. <i>Environmental Science & Technology</i> , 2013, 47, 4804-4812.	10.0	50

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19	Complete Genome Sequence of <i>Burkholderia gladioli</i> BSR3. <i>Journal of Bacteriology</i> , 2011, 193, 3149-3149.	2.2	47
20	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
21	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
22	Application of machine learning in SNP discovery. <i>BMC Bioinformatics</i> , 2006, 7, 4.	2.6	43
23	A bioinformatics approach for identifying transgene insertion sites using whole genome sequencing data. <i>BMC Biotechnology</i> , 2017, 17, 67.	3.3	42
24	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
25	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
26	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
27	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
28	BARCSoySNP23: a panel of 23 selected SNPs for soybean cultivar identification. <i>Theoretical and Applied Genetics</i> , 2007, 114, 885-899.	3.6	36
29	Characterization of wild <i>Prunus yedoensis</i> analyzed by inter-simple sequence repeat and chloroplast DNA. <i>Scientia Horticulturae</i> , 2007, 114, 121-128.	3.6	35
30	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
31	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
32	The genome of the marine medaka <i>Oryzias melastigma</i> . <i>Molecular Ecology Resources</i> , 2018, 18, 656-665.	4.8	31
33	SNP-PHAGE–High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006, 7, 468.	2.6	29
34	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
35	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
36	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

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37	Complete Genome Sequence of <i>Mycobacterium intracellulare</i> Strain ATCC 13950T. <i>Journal of Bacteriology</i> , 2012, 194, 2750-2750.	2.2	25
38	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.. <i>Genes and Genetic Systems</i> , 1999, 74, 169-177.	0.7	24
39	Defining the genome structure of 'Tongil' rice, an important cultivar in the Korean "Green Revolution". <i>Rice</i> , 2014, 7, 22.	4.0	24
40	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
41	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
42	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
43	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
44	Marine medaka ATP-binding cassette (ABC) superfamily and new insight into teleost Abch nomenclature. <i>Scientific Reports</i> , 2015, 5, 15409.	3.3	22
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	Shotgun proteomic analysis for detecting differentially expressed proteins in the reduced culm number rice. <i>Proteomics</i> , 2011, 11, 455-468.	2.2	18
53	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
54	Complete Genome Sequence of <i>Mycobacterium intracellulare</i> Clinical Strain MOTT-02. <i>Journal of Bacteriology</i> , 2012, 194, 2771-2771.	2.2	17

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55	Complete Genome Sequence of Mycobacterium intracellulare Clinical Strain MOTT-64, Belonging to the INT1 Genotype. <i>Journal of Bacteriology</i> , 2012, 194, 3268-3268.	2.2	17
56	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
57	Variation block-based genomics method for crop plants. <i>BMC Genomics</i> , 2014, 15, 477.	2.8	15
58	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
59	Complete Genome Sequence of Mycobacterium intracellulare Clinical Strain MOTT-36Y, Belonging to the INT5 Genotype. <i>Journal of Bacteriology</i> , 2012, 194, 4141-4142.	2.2	13
60	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
61	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
62	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
63	Complete Genome Sequence of Mycobacterium bovis BCG Korea, the Korean Vaccine Strain for Substantial Production. <i>Genome Announcements</i> , 2013, 1, e0006913.	0.8	11
64	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
65	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
66	Generation of albino via SLC45a2 gene targeting by CRISPR/Cas9 in the marine medaka <i>Oryzias melastigma</i> . <i>Marine Pollution Bulletin</i> , 2020, 154, 111038.	5.0	11
67	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
68	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
69	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
70	Survey of the Applications of NGS to Whole-Genome Sequencing and Expression Profiling. <i>Genomics and Informatics</i> , 2012, 10, 1.	0.8	9
71	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
72	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

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73	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
74	RNA-Seq De Novo Assembly and Differential Transcriptome Analysis of Korean Medicinal Herb <i>Cirsium japonicum</i> var. <i>spinossimum</i> . <i>Genomics and Informatics</i> , 2018, 16, e34.	0.8	8
75	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
76	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
77	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
78	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
79	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
80	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
81	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
82	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
83	Identification of Hydrangeaceae accessions of wild origin from Jeju, Korea, using molecular markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2010, 8, 235-241.	0.8	4
84	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
85	Characterization of chloroplast genomes of <i>Alnus rubra</i> and <i>Betula cordifolia</i> , and their use in phylogenetic analyses in Betulaceae. <i>Genes and Genomics</i> , 2019, 41, 305-316.	1.4	4
86	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
87	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
88	Characterization of Gene Isoforms Related to Cellulose and Lignin Biosynthesis in Kenaf (<i>Hibiscus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.5	3
89	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
90	Abnormal leaf formation in soybean: genetic and environmental effects. <i>Theoretical and Applied Genetics</i> , 2006, 113, 137-146.	3.6	2

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91	The complete chloroplast genome of a rare species in Korea, <i>Lilium Dauricum</i> Ker Gawl. Mitochondrial DNA Part B: Resources, 2019, 4, 3591-3592.	0.4	2
92	Detection of mPing mobilization in transgenic rice plants. Genes and Genomics, 2020, 42, 47-54.	1.4	2
93	Editor's introduction to this issue (Genomics and Informatics, 2021, 19, e1).	0.8	2
94	Analysis of genome variants in dwarf soybean lines obtained in F6 derived from cross of normal parents (cultivated and wild soybean). Genomics and Informatics, 2021, 19, e19.	0.8	2
95	Characterization of transcription factor genes related to cold tolerance in Brassica napus. Genomics and Informatics, 2021, 19, e45.	0.8	2
96	Alternative Splicing (AS) Dynamics in Dwarf Soybean Derived from Cross of Glycine max and Glycine soja. Agronomy, 2022, 12, 1685.	3.0	2
97	Genomics-Assisted Breeding. , 2015, , 145-173.		1
98	The complete chloroplast genome of a Korean endemic species <i>Sophora koreensis</i> , Nakai. Mitochondrial DNA Part B: Resources, 2020, 5, 3067-3068.	0.4	1
99	The complete chloroplast genome of a Woodwardia japonica. Mitochondrial DNA Part B: Resources, 2020, 5, 102-103.	0.4	1
100	The complete chloroplast genome of a fern genus Thelypteris interrupta. Mitochondrial DNA Part B: Resources, 2020, 5, 572-573.	0.4	1
101	Comparative Gene Expression Analysis of Seed Development in Waxy and Dent Corn (Zea mays L.). Plant Breeding and Biotechnology, 2018, 6, 337-353.	0.9	1
102	Comparison of Metabolite Levels and Antioxidant Activity Among Pepper Cultivars. Han'guk Yukchong Hakhoe Chi, 2019, 51, 326-340.	0.5	1
103	Identification and Characterization of Key Genes Responsible for Weedy and Cultivar Growth Types in Soybean. Frontiers in Genetics, 2022, 13, 805347.	2.3	1
104	Genetic characterization of popcorn hybrids based on SNP genotyping and development of rapid ARMS based primers. Journal of Crop Science and Biotechnology, 2021, 24, 319-325.	1.5	0
105	EVALUATION, CHARACTERIZATION, AND IDENTIFICATION OF WOODY LANDSCAPE PLANTS. Acta Horticulturae, 2008, , 327-338.	0.2	0
106	The comparative gene expression concern to the seed pigmentation in maize (Zea mays L.). Genomics and Informatics, 2020, 18, e29.	0.8	0
107	Identification of novel haplotype of a cyst nematode resistance gene, GmSNAP18 in soybean [Glycine max (L.) Merr.]. Indian Journal of Genetics and Plant Breeding, 2020, 80, .	0.5	0
108	Genome-wide identification of 194 G protein-coupled receptor (GPCR) genes from the water flea Daphnia magna. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 42, 100983.	1.0	0