

# Atsushi J Nagano

## List of Publications by Year in descending order

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161  
papers

3,445  
citations

172457

29  
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206112

48  
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192  
all docs

192  
docs citations

192  
times ranked

4206  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering and Prediction of Transcriptome Dynamics under Fluctuating Field Conditions. <i>Cell</i> , 2012, 151, 1358-1369.	28.9	219
2	Os- <i>GIGANTEA</i> Confers Robust Diurnal Rhythms on the Global Transcriptome of Rice in the Field. <i>Plant Cell</i> , 2011, 23, 1741-1755.	6.6	184
3	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	12.8	138
4	A key metabolic gene for recurrent freshwater colonization and radiation in fishes. <i>Science</i> , 2019, 364, 886-889.	12.6	109
5	Annual transcriptome dynamics in natural environments reveals plant seasonal adaptation. <i>Nature Plants</i> , 2019, 5, 74-83.	9.3	109
6	RNA-Seq reveals virus-virus and virus-plant interactions in nature. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw176.	2.7	96
7	Antagonistic Jacalin-Related Lectins Regulate the Size of ER Body-Type $\beta$ -Glucosidase Complexes in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2008, 49, 969-980.	3.1	85
8	Northern glacial refugia and altitudinal niche divergence shape genome-wide differentiation in the emerging plant model <i>Arabidopsis arenosa</i> . <i>Molecular Ecology</i> , 2016, 25, 3929-3949.	3.9	83
9	Microbial communities on flower surfaces act as signatures of pollinator visitation. <i>Scientific Reports</i> , 2015, 5, 8695.	3.3	80
10	Activation of an ER-body-localized $\beta$ -Glucosidase via a Cytosolic Binding Partner in Damaged Tissues of <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2005, 46, 1140-1148.	3.1	72
11	High-throughput linkage mapping of Australian white cypress pine ( <i>Callitris glaucophylla</i> ) and map transferability to related species. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	70
12	H3K27me3 demethylases alter HSP22 and HSP17.6C expression in response to recurring heat in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2021, 12, 3480.	12.8	68
13	A Genome Scan for Genes Underlying Microgeographic-Scale Local Adaptation in a Wild <i>Arabidopsis</i> Species. <i>PLoS Genetics</i> , 2015, 11, e1005361.	3.5	63
14	NAI2 Is an Endoplasmic Reticulum Body Component That Enables ER Body Formation in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2008, 20, 2529-2540.	6.6	62
15	Detection of Diurnal Variation of Tomato Transcriptome through the Molecular Timetable Method in a Sunlight-Type Plant Factory. <i>Frontiers in Plant Science</i> , 2016, 7, 87.	3.6	60
16	Identification of Two Novel Endoplasmic Reticulum Body-Specific Integral Membrane Proteins. <i>Plant Physiology</i> , 2012, 161, 108-120.	4.8	51
17	FAMA Is an Essential Component for the Differentiation of Two Distinct Cell Types, Myrosin Cells and Guard Cells, in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 4039-4052.	6.6	50
18	High-yielding rice Takanari has superior photosynthetic response to a commercial rice Koshihikari under fluctuating light. <i>Journal of Experimental Botany</i> , 2019, 70, 5287-5297.	4.8	49

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19	Detection of Plant Viruses in Natural Environments by Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2015, 1236, 89-98.	0.9	48
20	Genetic distance of inbred lines of Chinese cabbage and its relationship to heterosis. <i>Plant Gene</i> , 2016, 5, 1-7.	2.3	48
21	Lasy-Seq: a high-throughput library preparation method for RNA-Seq and its application in the analysis of plant responses to fluctuating temperatures. <i>Scientific Reports</i> , 2019, 9, 7091.	3.3	48
22	Oxidative rearrangement of (+)-sesamin by CYP92B14 co-generates twin dietary lignans in sesame. <i>Nature Communications</i> , 2017, 8, 2155.	12.8	45
23	Seasonality of interactions between a plant virus and its host during persistent infection in a natural environment. <i>ISME Journal</i> , 2020, 14, 506-518.	9.8	45
24	Gene regulatory network and its constituent transcription factors that control nitrogen deficiency responses in rice. <i>New Phytologist</i> , 2020, 227, 1434-1452.	7.3	45
25	Mutation in the putative ketoacyl-ACP reductase CaKR1 induces loss of pungency in Capsicum. <i>Theoretical and Applied Genetics</i> , 2019, 132, 65-80.	3.6	43
26	Truncated yet functional viral protein produced via RNA polymerase slippage implies underestimated coding capacity of RNA viruses. <i>Scientific Reports</i> , 2016, 6, 21411.	3.3	41
27	Iron deficiency-inducible peptide-coding genes <i>OsIMA1</i> and <i>OsIMA2</i> positively regulate a major pathway of iron uptake and translocation in rice. <i>Journal of Experimental Botany</i> , 2021, 72, 2196-2211.	4.8	41
28	Unfolded protein response transducer IRE1-mediated signaling independent of XBP1 mRNA splicing is not required for growth and development of medaka fish. <i>ELife</i> , 2017, 6, .	6.0	39
29	Simultaneous evaluation of the effects of geographic, environmental and temporal isolation in ecotypic populations of <i>Solidago virgaurea</i> . <i>New Phytologist</i> , 2017, 216, 1268-1280.	7.3	36
30	Genome editing reveals fitness effects of a gene for sexual dichromatism in Sulawesian fishes. <i>Nature Communications</i> , 2021, 12, 1350.	12.8	36
31	Ecogenomics of cleistogamous and chasmogamous flowering: genome-wide gene expression patterns from cross-species microarray analysis in <i>Cardamine kokaiensis</i> (Brassicaceae). <i>Journal of Ecology</i> , 2008, 96, 1086-1097.	4.0	32
32	Genome-wide patterns of divergence and introgression after secondary contact between <i>Pungitius</i> sticklebacks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190548.	4.0	32
33	Quantitative Analysis of ER Body Morphology in an Arabidopsis Mutant. <i>Plant and Cell Physiology</i> , 2009, 50, 2015-2022.	3.1	29
34	Plant trichomes and a single gene GLABRA1 contribute to insect community composition on field-grown <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2019, 19, 163.	3.6	28
35	RAD-Seq analysis of typical and minor Citrus accessions, including Bhutanese varieties. <i>Breeding Science</i> , 2016, 66, 797-807.	1.9	27
36	A recessive gene pepy-1 encoding Pelota confers resistance to begomovirus isolates of PepYLCIV and PepYLCAV in <i>Capsicum annum</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 2947-2964.	3.6	27

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37	Endoplasmic reticulum-derived bodies enable a single-cell chemical defense in Brassicaceae plants. <i>Communications Biology</i> , 2020, 3, 21.	4.4	26
38	Phylogenetic relationships of Aurantioideae (Rutaceae) based on RAD-Seq. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	24
39	Niche conservatism promotes speciation in cycads: the case of <i>Dioon merolae</i> (Zamiaceae) in Mexico. <i>New Phytologist</i> , 2020, 227, 1872-1884.	7.3	24
40	The ER body, a new organelle in <i>Arabidopsis thaliana</i> , requires NAI2 for its formation and accumulates specific $\beta$ -glucosidases. <i>Plant Signaling and Behavior</i> , 2009, 4, 849-852.	2.4	23
41	Circadian Oscillation of the Lettuce Transcriptome under Constant Light and Light-Dark Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1114.	3.6	23
42	Evidence for sympatric speciation in a Wallacean ancient lake. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1898-1915.	2.3	23
43	ERMO3/MVP1/GOLD36 Is Involved in a Cell Type-Specific Mechanism for Maintaining ER Morphology in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e49103.	2.5	22
44	The population genomic signature of environmental association and gene flow in an ecologically divergent tree species <i>Metrosideros polymorpha</i> (Myrtaceae). <i>Molecular Ecology</i> , 2017, 26, 1515-1532.	3.9	22
45	Seasonal plasticity and diel stability of H3K27me3 in natural fluctuating environments. <i>Nature Plants</i> , 2020, 6, 1091-1097.	9.3	21
46	Maintaining higher leaf photosynthesis after heading stage could promote biomass accumulation in rice. <i>Scientific Reports</i> , 2021, 11, 7579.	3.3	21
47	Genetic Properties Responsible for the Transgressive Segregation of Days to Heading in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1655-1662.	1.8	20
48	Characterization and quantitative trait locus mapping of late-flowering from a Thai soybean cultivar introduced into a photoperiod-insensitive genetic background. <i>PLoS ONE</i> , 2019, 14, e0226116.	2.5	20
49	Genomic predictions and genome-wide association studies based on RAD-seq of quality-related metabolites for the genomics-assisted breeding of tea plants. <i>Scientific Reports</i> , 2020, 10, 17480.	3.3	20
50	Repressive chromatin modification underpins the long-term expression trend of a perennial flowering gene in nature. <i>Nature Communications</i> , 2020, 11, 2065.	12.8	20
51	Heap: a highly sensitive and accurate SNP detection tool for low-coverage high-throughput sequencing data. <i>DNA Research</i> , 2017, 24, 397-405.	3.4	19
52	Analyses of single nucleotide polymorphisms identified by ddRAD-seq reveal genetic structure of tea germplasm and Japanese landraces for tea breeding. <i>PLoS ONE</i> , 2019, 14, e0220981.	2.5	19
53	Diurnal metabolic regulation of isoflavones and soyasaponins in soybean roots. <i>Plant Direct</i> , 2020, 4, e00286.	1.9	19
54	From the laboratory to the field: assaying histone methylation at <i>FLOWERING LOCUS C</i> in naturally growing <i>Arabidopsis halleri</i> . <i>Genes and Genetic Systems</i> , 2016, 91, 15-26.	0.7	18

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55	Identification of quantitative trait loci for increased $\hat{\alpha}$ -tocopherol biosynthesis in wild soybean using a high-density genetic map. <i>BMC Plant Biology</i> , 2019, 19, 510.	3.6	18
56	Genomic reconstruction of 100 000-year grassland history in a forested country: population dynamics of specialist forbs. <i>Biology Letters</i> , 2019, 15, 20180577.	2.3	17
57	Mitochondrial introgression by ancient admixture between two distant lacustrine fishes in Sulawesi Island. <i>PLoS ONE</i> , 2021, 16, e0245316.	2.5	17
58	Arabidopsis mutants affecting oxylipin signaling in photo-oxidative stress responses. <i>Plant Physiology and Biochemistry</i> , 2014, 81, 90-95.	5.8	16
59	Does genomic variation in a foundation species predict arthropod community structure in a riparian forest?. <i>Molecular Ecology</i> , 2018, 27, 1284-1295.	3.9	15
60	Phylogeographic analysis of the East Asian goldenrod ( <i>Solidago virgaurea</i> complex, Asteraceae) reveals hidden ecological diversification with recurrent formation of ecotypes. <i>Annals of Botany</i> , 2018, 121, 489-500.	2.9	14
61	Assessment of genetic diversity in Coho salmon ( <i>Oncorhynchus kisutch</i> ) populations with no family records using ddRAD-seq. <i>BMC Research Notes</i> , 2018, 11, 548.	1.4	14
62	Construction of High-Resolution RAD-Seq Based Linkage Map, Anchoring Reference Genome, and QTL Mapping of the Sex Chromosome in the Marine Medaka <i>Oryzias melastigma</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3537-3545.	1.8	14
63	Field multi-omics analysis reveals a close association between bacterial communities and mineral properties in the soybean rhizosphere. <i>Scientific Reports</i> , 2021, 11, 8878.	3.3	14
64	Using a two-stage convolutional neural network to rapidly identify tiny herbivorous beetles in the field. <i>Ecological Informatics</i> , 2021, 66, 101466.	5.2	14
65	A Survey on Plant Viruses in Natural Brassicaceae Communities Using RNA-Seq. <i>Microbial Ecology</i> , 2019, 78, 113-121.	2.8	13
66	Genetic isolation by distance in the yellowfin goby populations revealed by RAD sequencing. <i>Ichthyological Research</i> , 2020, 67, 98-104.	0.8	13
67	Radiation history of Asian <i>Asarum</i> (sect. <i>Heterotropa</i> , Aristolochiaceae) resolved using a phylogenomic approach based on double-digested RAD-seq data. <i>Annals of Botany</i> , 2020, 126, 245-260.	2.9	13
68	Species divergence and repeated ancient hybridization in a Sulawesi lake system. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1767-1780.	1.7	13
69	Phylogeographic testing of alternative histories of single origin versus parallel evolution of early flowering serpentine populations of <i>Picris hieracioides</i> L. (Asteraceae) in Japan. <i>Ecological Research</i> , 2018, 33, 537-547.	1.5	12
70	Auxin Contributes to the Intraorgan Regulation of Gene Expression in Response to Shade. <i>Plant Physiology</i> , 2018, 177, 847-862.	4.8	12
71	Noise plasticity correlations of gene expression in the multicellular organism <i>Arabidopsis thaliana</i> . <i>Journal of Theoretical Biology</i> , 2015, 387, 13-22.	1.7	11
72	A <i>GLABRA1</i> ortholog on LG A9 controls trichome number in the Japanese leafy vegetables Mizuna and Mibuna ( <i>Brassica rapa</i> L. subsp. <i>nipposinica</i> L. H. Bailey): evidence from QTL analysis. <i>Journal of Plant Research</i> , 2017, 130, 539-550.	2.4	11

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73	Construction of a high-density linkage map for bronze loquat using RAD-Seq. <i>Scientia Horticulturae</i> , 2019, 251, 59-64.	3.6	11
74	A spinach genome assembly with remarkable completeness, and its use for rapid identification of candidate genes for agronomic traits. <i>DNA Research</i> , 2021, 28, .	3.4	11
75	Transcriptome Analysis of Plant Hormone-Related Tomato ( <i>Solanum lycopersicum</i> ) Genes in a Sunlight-Type Plant Factory. <i>PLoS ONE</i> , 2015, 10, e0143412.	2.5	11
76	Effect of differences in light source environment on transcriptome of leaf lettuce ( <i>Lactuca sativa</i> L.) to optimize cultivation conditions. <i>PLoS ONE</i> , 2022, 17, e0265994.	2.5	11
77	AtMap1: a DNA microarray for genomic deletion mapping in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2008, 56, 1058-1065.	5.7	10
78	Transcriptional Variation in Glucosinolate Biosynthetic Genes and Inducible Responses to Aphid Herbivory on Field-Grown <i>Arabidopsis thaliana</i> . <i>Frontiers in Genetics</i> , 2019, 10, 787.	2.3	10
79	Neighbor GWAS: incorporating neighbor genotypic identity into genome-wide association studies of field herbivory. <i>Heredity</i> , 2021, 126, 597-614.	2.6	10
80	Analysis of Genetic Diversity and Population Structure of <i>Orobancha foetida</i> Populations From Tunisia Using RADseq. <i>Frontiers in Plant Science</i> , 2021, 12, 618245.	3.6	10
81	Fillable and unfillable gaps in plant transcriptome under field and controlled environments. <i>Plant, Cell and Environment</i> , 2022, 45, 2410-2427.	5.7	10
82	Genetic diversity of loquat ( <i>Eriobotrya japonica</i> ) revealed using RAD-Seq SNP markers. <i>Scientific Reports</i> , 2022, 12, .	3.3	10
83	Functional divergence of duplicate genes several million years after gene duplication in <i>Arabidopsis</i> . <i>DNA Research</i> , 2018, 25, 327-339.	3.4	9
84	Genet assignment and population structure analysis in a clonal forest-floor herb, <i>Cardamine leucantha</i> , using RAD-seq. <i>AoB PLANTS</i> , 2020, 12, plz080.	2.3	9
85	Genomic Basis of Transcriptome Dynamics in Rice under Field Conditions. <i>Plant and Cell Physiology</i> , 2021, 62, 1436-1445.	3.1	9
86	Combination of genetic analysis and ancient literature survey reveals the divergence of traditional <i>Brassica rapa</i> varieties from Kyoto, Japan. <i>Horticulture Research</i> , 2021, 8, 132.	6.3	9
87	An efficient early pooling protocol for environmental DNA metabarcoding. <i>Environmental DNA</i> , 2022, 4, 1212-1228.	5.8	9
88	Broad distribution spectrum from Gaussian to power law appears in stochastic variations in RNA-seq data. <i>Scientific Reports</i> , 2018, 8, 8339.	3.3	8
89	Classification of tea ( <i>Camellia sinensis</i> ) landraces and cultivars in Kyoto, Japan and other regions, based on simple sequence repeat markers and restriction site-associated DNA sequencing analysis. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 441-451.	1.6	8
90	Genomic and phenotypic consequences of two independent secondary contact zones between allopatric lineages of the anadromous ice goby <i>Leucopsarion petersii</i> . <i>Heredity</i> , 2020, 124, 223-235.	2.6	8

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91	Fluorescent protein-based imaging and tissue-specific RNA-seq analysis of <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 1260-1270.	4.8	8
92	Inferring historical survivals of climate relicts: the effects of climate changes, geography, and population-specific factors on herbaceous hydrangeas. <i>Heredity</i> , 2021, 126, 615-629.	2.6	8
93	PepYLCIV and PepYLCAV resistance gene Pepy-2 encodes DFDGD-Class RNA-dependent RNA polymerase in <i>Capsicum</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 2437-2452.	3.6	8
94	Genetic mapping of local adaptation along the altitudinal gradient in <i>Abies sachalinensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	7
95	ddRAD-seq based phylogeographic study of <i>Sargassum thunbergii</i> (Phaeophyceae, Heterokonta) around Japanese coast. <i>Marine Environmental Research</i> , 2018, 140, 104-113.	2.5	7
96	Frequent chloroplast capture among <i>Isodon</i> (Lamiaceae) species in Japan revealed by phylogenies based on variation in chloroplast and nuclear DNA. <i>Plant Species Biology</i> , 2019, 34, 127-137.	1.0	7
97	Genetic Architecture of Innate Fear Behavior in Chickens. <i>Behavior Genetics</i> , 2020, 50, 411-422.	2.1	7
98	A ddRAD-based population genetics and phylogenetics of an endangered freshwater fish from Japan. <i>Conservation Genetics</i> , 2020, 21, 641-652.	1.5	7
99	Integrative genomic phylogeography reveals signs of mitonuclear incompatibility in a natural hybrid goby population. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 176-194.	2.3	7
100	Elucidation of Japanese pepper ( <i>Zanthoxylum piperitum</i> De Candolle) domestication using RAD-Seq. <i>Scientific Reports</i> , 2021, 11, 6464.	3.3	7
101	Phylogeography of the East Asian grassland plant, <i>Viola orientalis</i> (Violaceae), inferred from plastid and nuclear restriction site-associated DNA sequencing data. <i>Journal of Plant Research</i> , 2021, 134, 1181-1198.	2.4	7
102	FIT: statistical modeling tool for transcriptome dynamics under fluctuating field conditions. <i>Bioinformatics</i> , 2017, 33, 1672-1680.	4.1	6
103	A first genetic map in the genus <i>Streptocarpus</i> generated with RAD sequencing based SNP markers. <i>South African Journal of Botany</i> , 2018, 117, 158-168.	2.5	6
104	Profiling SNP and Nucleotide Diversity to Characterize Mekong Delta Rice Landraces in Southeast Asian Populations. <i>Plant Genome</i> , 2019, 12, 190042.	2.8	6
105	Multiple waves of freshwater colonization of the three-spined stickleback in the Japanese Archipelago. <i>BMC Evolutionary Biology</i> , 2020, 20, 143.	3.2	6
106	Memory of Temperature in the Seasonal Control of Flowering Time: An Unexplored Link Between Meteorology and Molecular Biology. , 2013, , 195-215.		6
107	New taxa of <i>Rhododendron tschonoskii</i> alliance (Ericaceae) from East Asia. <i>PhytoKeys</i> , 2019, 134, 97-114.	1.0	6
108	Identification of QTLs conferring resistance to begomovirus isolate of PepYLCIV in <i>Capsicum chinense</i> . <i>Euphytica</i> , 2022, 218, 1.	1.2	6



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109	Genetic basis for the evolution of pelvic fin brooding, a new mode of reproduction, in a Sulawesi fish. <i>Molecular Ecology</i> , 2022, 31, 3798-3811.	3.9	6
110	First report of Pelargonium zonate spot virus from wild Brassicaceae plants in Japan. <i>Journal of General Plant Pathology</i> , 2017, 83, 329-332.	1.0	5
111	Quantitative trait loci mapping for the shear force value in breast muscle of F2 chickens. <i>Poultry Science</i> , 2019, 98, 1096-1101.	3.4	5
112	Mapping of QTLs controlling epicotyl length in adzuki bean (<i>Vigna angularis</i>). <i>Breeding Science</i> , 2021, 71, 208-216.	1.9	5
113	Neighbor QTL: an interval mapping method for quantitative trait loci underlying plant neighborhood effects. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	5
114	Evolutionary effects of geographic and climatic isolation between <i>Rhododendron tsusiophyllum</i> populations on the Izu Islands and mainland Honshu of Japan. <i>Heredity</i> , 2021, 126, 859-868.	2.6	5
115	Geographic and subsequent biotic isolations led to a diversity anomaly of section <i>Heterotropa</i> (genus <i>Asarum</i>: Aristolochiaceae) in insular versus continental regions of the Sino-Japanese Floristic Region. <i>Journal of Biogeography</i> , 2021, 48, 1917-1929.	3.0	5
116	Speciation along a latitudinal gradient: The origin of the Neotropical cycad sister pair <i>Dioon sonorense</i> <i>D. vovidesii</i> (Zamiaceae). <i>Ecology and Evolution</i> , 2021, 11, 6962-6976.	1.9	5
117	Genetic structure of Pacific crown-of-thorns starfish ( <i>Acanthaster cf. solaris</i> ) in southern Japan based on genome-wide RADseq analysis. <i>Coral Reefs</i> , 2021, 40, 1379-1385.	2.2	5
118	Phylogeographic analysis of <i>Saxifraga fortunei</i> complex (Saxifragaceae) reveals multiple origins of morphological and ecological variations in the Japanese Archipelago. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107230.	2.7	5
119	Transcriptome Analysis of a Cultivar of Green Perilla (<i>Perilla frutescens</i>) Using Genetic Similarity with Other Plants via Public Databases. <i>Environmental Control in Biology</i> , 2017, 55, 77-83.	0.7	5
120	Visualization of phosphorus retranslocation and phosphate transporter expression profiles in a shortened annual cycle system of poplar. <i>Plant, Cell and Environment</i> , 2022, 45, 1749-1764.	5.7	5
121	The basic leucine zipper transcription factor <sc>OsZIP83</sc> and the glutaredoxins <sc>OsGRX6</sc> and <sc>OsGRX9</sc> facilitate rice iron utilization under the control of <sc>OsHRZ</sc> ubiquitin ligases. <i>Plant Journal</i> , 2022, , .	5.7	5
122	Deeply divergent freshwater fish species within a single river system in central Sulawesi. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107519.	2.7	5
123	Mapping of Quantitative Trait Loci for Growth and Carcass-Related Traits in Chickens Using a Restriction-Site Associated DNA Sequencing Method. <i>Journal of Poultry Science</i> , 2019, 56, 166-176.	1.6	4
124	Pepper vein yellows virus 9: a novel polerovirus isolated from chili pepper in Indonesia. <i>Archives of Virology</i> , 2020, 165, 3017-3021.	2.1	4
125	Characterization of rhizome transcriptome and identification of a rhizomatous ER body in the clonal plant <i>Cardamine leucantha</i> . <i>Scientific Reports</i> , 2020, 10, 13291.	3.3	4
126	Genetic analysis of body weight in wild populations of medaka fish from different latitudes. <i>PLoS ONE</i> , 2020, 15, e0234803.	2.5	4



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127	Mapping of Quantitative Trait Loci Controlling Egg-Quality and -Production Traits in Japanese Quail ( <i>Coturnix japonica</i> ) Using Restriction-Site Associated DNA Sequencing. <i>Genes</i> , 2021, 12, 735.	2.4	4
128	Quantitative trait loci for growth-related traits in Japanese quail ( <i>Coturnix japonica</i> ) using restriction-site associated DNA sequencing. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1147-1159.	2.1	4
129	Do colour-morphs of an amphidromous goby represent different species? Taxonomy of <i>Lentipes</i> (Gobiiformes) from Japan and Palawan, Philippines, with phylogenomic approaches. <i>Systematics and Biodiversity</i> , 0, , 1-33.	1.2	4
130	Genetic consequences of being a dwarf: do evolutionary changes in life-history traits influence gene flow patterns in populations of the world's smallest goldenrod?. <i>Annals of Botany</i> , 2020, 126, 163-177.	2.9	3
131	Selection of transcripts related to low-temperature tolerance using RNA sequencing from F2 plants between japonica and indica rice ( <i>Oryza sativa</i> L.) cultivars. <i>Functional Plant Biology</i> , 2021, 48, 984.	2.1	3
132	Resource partitioning is not coupled with assortative mating in sympatrically divergent ricefish in a Wallacean ancient lake. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1133-1143.	1.7	3
133	Gudgeon fish with and without genetically determined countershading coexist in heterogeneous littoral environments of an ancient lake. <i>Ecology and Evolution</i> , 2021, 11, 13283-13294.	1.9	3
134	Mapping of quantitative trait loci underlying a magic trait in ongoing ecological speciation. <i>BMC Genomics</i> , 2021, 22, 615.	2.8	3
135	Hydrometeorology for plant omics: Potential evaporation as a key index for transcriptome in rice. <i>Environmental and Experimental Botany</i> , 2022, 196, 104724.	4.2	3
136	Microevolution of <i>Pieris</i> butterfly genes involved in host plant adaptation along a host plant community cline. <i>Molecular Ecology</i> , 2022, 31, 3083-3097.	3.9	3
137	Selection of Transcripts Affecting Initial Growth Rate of Rice Backcrossed Inbred Lines Using RNA Sequencing Data. <i>Frontiers in Plant Science</i> , 2018, 9, 1880.	3.6	2
138	Estimation of the Circadian Phase by Oscillatory Analysis of the Transcriptome in Plants. <i>Environmental Control in Biology</i> , 2018, 56, 67-72.	0.7	2
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