

# Atsushi J Nagano

## List of Publications by Year in descending order

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Version: 2024-02-01

161  
papers

3,445  
citations

172457

29  
h-index

206112

48  
g-index

192  
all docs

192  
docs citations

192  
times ranked

4206  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Identification of QTLs conferring resistance to begomovirus isolate of PepYLCIV in <i>Capsicum chinense</i> . <i>Euphytica</i> , 2022, 218, 1.	1.2	6
3	Phylogeography of a canopy-forming kelp, <i>Eisenia bicyclis</i> (Laminariales, Phaeophyceae), based on a genome-wide sequencing analysis. <i>Journal of Phycology</i> , 2022, , .	2.3	1
4	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
5	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
6	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
7	The basic leucine zipper transcription factor <i>OsZIP83</i> and the glutaredoxins <i>OsGRX6</i> and <i>OsGRX9</i> facilitate rice iron utilization under the control of <i>OsHRZ</i> ubiquitin ligases. <i>Plant Journal</i> , 2022, , .	5.7	5
8	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
9	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
10	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
11	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
12	Genetic diversity of loquat ( <i>Eriobotrya japonica</i> ) revealed using RAD-Seq SNP markers. <i>Scientific Reports</i> , 2022, 12, .	3.3	10
13	An efficient early pooling protocol for environmental DNA metabarcoding. <i>Environmental DNA</i> , 2022, 4, 1212-1228.	5.8	9
14	Back Cover Image. <i>Plant, Cell and Environment</i> , 2022, 45, .	5.7	0
15	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
16	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
17	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
18	Neighbor GWAS: incorporating neighbor genotypic identity into genome-wide association studies of field herbivory. <i>Heredity</i> , 2021, 126, 597-614.	2.6	10

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19	Mapping of QTLs controlling epicotyl length in adzuki bean (<i>Vigna angularis</i>). <i>Breeding Science</i> , 2021, 71, 208-216.	1.9	5
20	Characterization of citrus leaf blotch virus from <i>Nandina domestica</i> "Otafukunanten". <i>Journal of General Plant Pathology</i> , 2021, 87, 113-116.	1.0	1
21	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
22	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
23	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
24	Mating system evolution and genetic structure of diploid sexual populations of <i>Cyrtomium falcatum</i> in Japan. <i>Scientific Reports</i> , 2021, 11, 3124.	3.3	0
25	Genome editing reveals fitness effects of a gene for sexual dichromatism in Sulawesian fishes. <i>Nature Communications</i> , 2021, 12, 1350.	12.8	36
26	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
27	Elucidation of Japanese pepper ( <i>Zanthoxylum piperitum</i> De Candolle) domestication using RAD-Seq. <i>Scientific Reports</i> , 2021, 11, 6464.	3.3	7
28	Genetic basis for variation in the number of cephalic pores in a hybrid zone between closely related species of goby, <i>Gymnogobius breunigii</i> and <i>Gymnogobius castaneus</i>. <i>Biological Journal of the Linnean Society</i> , 2021, 133, 143-154.	1.6	0
29	Maintaining higher leaf photosynthesis after heading stage could promote biomass accumulation in rice. <i>Scientific Reports</i> , 2021, 11, 7579.	3.3	21
30	Analysis of Genetic Diversity and Population Structure of <i>Orobanche foetida</i> Populations From Tunisia Using RADseq. <i>Frontiers in Plant Science</i> , 2021, 12, 618245.	3.6	10
31	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
32	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
33	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
34	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
35	Genomic Basis of Transcriptome Dynamics in Rice under Field Conditions. <i>Plant and Cell Physiology</i> , 2021, 62, 1436-1445.	3.1	9
36	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

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37	Relationship between gene regulation network structure and prediction accuracy in high dimensional regression. <i>Scientific Reports</i> , 2021, 11, 11483.	3.3	0
38	A recessive gene <i>pepy-1</i> encoding <i>Pelota</i> confers resistance to begomovirus isolates of <i>PepYLCIV</i> and <i>PepYLCAV</i> in <i>Capsicum annuum</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 2947-2964.	3.6	27
39	Mitochondrial introgression by ancient admixture between two distant lacustrine fishes in Sulawesi Island. <i>PLoS ONE</i> , 2021, 16, e0245316.	2.5	17
40	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
41	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
42	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
43	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
44	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
45	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
46	Mapping of quantitative trait loci underlying a magic trait in ongoing ecological speciation. <i>BMC Genomics</i> , 2021, 22, 615.	2.8	3
47	Species divergence and repeated ancient hybridization in a Sulawesian lake system. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1767-1780.	1.7	13
48	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
49	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
50	Phylogeographic and demographic modeling analyses of the multiple origins of the rheophytic goldenrod <i>Solidago yokusaiana</i> Makino. <i>Heredity</i> , 2021, 126, 831-845.	2.6	2
51	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
52	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
53	Stacksbinder: online tool for visualizing and summarizing Stacks output to aid filtering of SNPs identified using RAD sequencing. <i>Conservation Genetics Resources</i> , 2020, 12, 1-3.	0.8	1
54	Genetic isolation by distance in the yellowfin goby populations revealed by RAD sequencing. <i>Ichthyological Research</i> , 2020, 67, 98-104.	0.8	13

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55	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
56	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
57	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
58	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
59	Diurnal metabolic regulation of isoflavones and soyasaponins in soybean roots. <i>Plant Direct</i> , 2020, 4, e00286.	1.9	19
60	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
61	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
62	Seasonal plasticity and diel stability of H3K27me3 in natural fluctuating environments. <i>Nature Plants</i> , 2020, 6, 1091-1097.	9.3	21
63	Genetic Architecture of Innate Fear Behavior in Chickens. <i>Behavior Genetics</i> , 2020, 50, 411-422.	2.1	7
64	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
65	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
66	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
67	Genetic analysis of body weight in wild populations of medaka fish from different latitudes. <i>PLoS ONE</i> , 2020, 15, e0234803.	2.5	4
68	Relationship between plant reproduction and environmental stress. <i>Ikushugaku Kenkyu</i> , 2020, 22, 62-67.	0.3	0
69	Endoplasmic reticulum-derived bodies enable a single-cell chemical defense in Brassicaceae plants. <i>Communications Biology</i> , 2020, 3, 21.	4.4	26
70	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
71	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
72	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

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73	Radiation history of Asian <i>Asarum</i> (sect. <i>Heterotropa</i> , <i>Aristolochiaceae</i> ) resolved using a phylogenomic approach based on double-digested RAD-seq data. <i>Annals of Botany</i> , 2020, 126, 245-260.	2.9	13
74	Low-cost and Multiplexable Whole mRNA-Seq Library Preparation Method with Oligo-dT Magnetic Beads for Illumina Sequencing Platforms. <i>Bio-protocol</i> , 2020, 10, e3496.	0.4	2
75	Genetic analysis of body weight in wild populations of medaka fish from different latitudes. , 2020, 15, e0234803.		0
76	Genetic analysis of body weight in wild populations of medaka fish from different latitudes. , 2020, 15, e0234803.		0
77	Genetic analysis of body weight in wild populations of medaka fish from different latitudes. , 2020, 15, e0234803.		0
78	Genetic analysis of body weight in wild populations of medaka fish from different latitudes. , 2020, 15, e0234803.		0
79	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
80	Evidence for sympatric speciation in a Wallacean ancient lake. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1898-1915.	2.3	23
81	Frequent chloroplast capture among <i>Isodon</i> ( <i>Lamiaceae</i> ) 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
82	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
83	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
84	Simplification of circadian rhythm measurement using species-independent time-indicated genes. <i>Current Plant Biology</i> , 2019, 19, 100118.	4.7	2
85	Genetic analysis of Taishu horses on and off Tsushima Island: Implications for conservation. <i>Journal of Equine Science</i> , 2019, 30, 33-40.	0.8	2
86	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
87	A key metabolic gene for recurrent freshwater colonization and radiation in fishes. <i>Science</i> , 2019, 364, 886-889.	12.6	109
88	Plant trichomes and a single gene <i>GLABRA1</i> contribute to insect community composition on field-grown <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2019, 19, 163.	3.6	28
89	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
90	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

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91	Genetic Properties Responsible for the Transgressive Segregation of Days to Heading in Rice. G3: Genes, Genomes, Genetics, 2019, 9, 1655-1662.	1.8	20
92	Construction of a high-density linkage map for bronze loquat using RAD-Seq. Scientia Horticulturae, 2019, 251, 59-64.	3.6	11
93	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> . G3: Genes, Genomes, Genetics, 2019, 9, 3537-3545.	1.8	14
94	Identification of quantitative trait loci for increased $\gamma$ -tocopherol biosynthesis in wild soybean using a high-density genetic map. BMC Plant Biology, 2019, 19, 510.	3.6	18
95	Characterization and quantitative trait locus mapping of late-flowering from a Thai soybean cultivar introduced into a photoperiod-insensitive genetic background. PLoS ONE, 2019, 14, e0226116.	2.5	20
96	Profiling SNP and Nucleotide Diversity to Characterize Mekong Delta Rice Landraces in Southeast Asian Populations. Plant Genome, 2019, 12, 190042.	2.8	6
97	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. Genetic Resources and Crop Evolution, 2019, 66, 441-451.	1.6	8
98	Annual transcriptome dynamics in natural environments reveals plant seasonal adaptation. Nature Plants, 2019, 5, 74-83.	9.3	109
99	Quantitative trait loci mapping for the shear force value in breast muscle of F2chickens. Poultry Science, 2019, 98, 1096-1101.	3.4	5
100	A Survey on Plant Viruses in Natural Brassicaceae Communities Using RNA-Seq. Microbial Ecology, 2019, 78, 113-121.	2.8	13
101	Mutation in the putative ketoacyl-ACP reductase CaKR1 induces loss of pungency in Capsicum. Theoretical and Applied Genetics, 2019, 132, 65-80.	3.6	43
102	New taxa of <i>Rhododendron tschonoskii</i> alliance (Ericaceae) from East Asia. PhytoKeys, 2019, 134, 97-114.	1.0	6
103	Title is missing!. , 2019, 14, e0226116.		0
104	Title is missing!. , 2019, 14, e0226116.		0
105	Title is missing!. , 2019, 14, e0226116.		0
106	Title is missing!. , 2019, 14, e0226116.		0
107	Does genomic variation in a foundation species predict arthropod community structure in a riparian forest?. Molecular Ecology, 2018, 27, 1284-1295.	3.9	15
108	Functional divergence of duplicate genes several million years after gene duplication in Arabidopsis. DNA Research, 2018, 25, 327-339.	3.4	9

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109	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
110	Phylogenetic relationships of Aurantioideae (Rutaceae) based on RAD-Seq. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	24
111	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
112	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
113	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
114	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
115	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
116	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
117	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
118	Auxin Contributes to the Intraorgan Regulation of Gene Expression in Response to Shade. <i>Plant Physiology</i> , 2018, 177, 847-862.	4.8	12
119	Growth and Environmental Change-Independent Genes Associated with Clock Gene <i>TOC1</i> in Green <i>Perilla</i> . <i>Environmental Control in Biology</i> , 2018, 56, 137-142.	0.7	0
120	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
121	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
122	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
123	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
124	First report of <i>Pelargonium zonate</i> spot virus from wild Brassicaceae plants in Japan. <i>Journal of General Plant Pathology</i> , 2017, 83, 329-332.	1.0	5
125	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
126	Oxidative rearrangement of (+)-sesamin by CYP92B14 co-generates twin dietary lignans in sesame. <i>Nature Communications</i> , 2017, 8, 2155.	12.8	45



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127	FIT: statistical modeling tool for transcriptome dynamics under fluctuating field conditions. <i>Bioinformatics</i> , 2017, 33, 1672-1680.	4.1	6
128	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
129	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
130	RAD-Seq analysis of typical and minor <i>Citrus</i> accessions, including Bhutanese varieties. <i>Breeding Science</i> , 2016, 66, 797-807.	1.9	27
131	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
132	Circadian Oscillation of the Lettuce Transcriptome under Constant Light and Lightâ€“Dark Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1114.	3.6	23
133	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
134	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
135	Genetic distance of inbred lines of Chinese cabbage and its relationship to heterosis. <i>Plant Gene</i> , 2016, 5, 1-7.	2.3	48
136	RNA-Seq reveals virusâ€“virus and virusâ€“plant interactions in nature. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw176.	2.7	96
137	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
138	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	12.8	138
139	Microbial communities on flower surfaces act as signatures of pollinator visitation. <i>Scientific Reports</i> , 2015, 5, 8695.	3.3	80
140	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
141	Noiseâ€“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
142	Detection of Plant Viruses in Natural Environments by Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2015, 1236, 89-98.	0.9	48
143	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
144	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

#	ARTICLE	IF	CITATIONS
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