Mitsuyasu Hasebe

List of Publications by Year
in descending order

#	Article	IF	Citations
1	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	12.6	1,712
2	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	12.6	794
3	The ASYMMETRIC LEAVES2 Gene of Arabidopsis thaliana, Required for Formation of a Symmetric Flat Leaf Lamina, Encodes a Member of a Novel Family of Proteins Characterized by Cysteine Repeats and a Leucine Zipper. Plant and Cell Physiology, 2002, 43, 467-478.	3.1	356
4	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: Implication for land plant evolution. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8007-8012.	7.1	341
5	Microtubule-dependent microtubule nucleation based on recruitment of Î³-tubulin in higher plants. Nature Cell Biology, 2005, 7, 961-968.	10.3	325
6	rbcL gene sequences provide evidence for the evolutionary lineages of leptosporangiate ferns.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 5730-5734.	7.1	269
7	Fern Phylogeny Based on rbcL Nucleotide Sequences. American Fern Journal, 1995, 85, 134.	0.3	265
8	ANXUR1 and 2, Sister Genes to FERONIA/SIRENE, Are Male Factors for Coordinated Fertilization. Current Biology, 2009, 19, 1327-1331.	3.9	254
9	Contribution of NAC Transcription Factors to Plant Adaptation to Land. Science, 2014, 343, 1505-1508.	12.6	222
10	Two Ancient Classes of MIKC-type MADS-box Genes are Present in the Moss Physcomitrella patens. Molecular Biology and Evolution, 2002, 19, 801-814.	8.9	216
11	The Floral Regulator LEAFY Evolves by Substitutions in the DNA Binding Domain. Science, 2005, 308, 260-263.	12.6	195
12	The GID1-Mediated Gibberellin Perception Mechanism Is Conserved in the Lycophyte <i>Selaginella moellendorffii</i> but Not in the Bryophyte <i>Physcomitrella patens</i>. Plant Cell, 2007, 19, 3058-3079.	6.6	188
13	Molecular evolution of the AP2 subfamily. Gene, 2006, 366, 256-265.	2.2	172
14	Reannotation and extended community resources for the genome of the non-seed plant Physcomitrella patens provide insights into the evolution of plant gene structures and functions. BMC Genomics, 2013, 14, 498.	2.8	170
15	Cryptochrome Light Signals Control Development to Suppress Auxin Sensitivity in the Moss Physcomitrella patens. Plant Cell, 2002, 14, 373-386.	6.6	161
16	Class 1 KNOX genes are not involved in shoot development in the moss <i>Physcomitrella patens</i> but do function in sporophyte development. Evolution & Development, 2008, 10, 555-566.	2.0	157
17	Plant Cytokinesis: Terminology for Structures and Processes. Trends in Cell Biology, 2017, 27, 885-894.	7.9	155
18	FlgB, FlgC, FlgF and FlgG. Journal of Molecular Biology, 1990, 211, 465-477.	4.2	148

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19	Diversification of gene function: homologs of the floral regulator FLO/LFY control the first zygotic cell division in the moss Physcomitrella patens. Development (Cambridge), 2005, 132, 1727-1736.	2.5	138
20	A polycomb repressive complex 2 gene regulates apogamy and gives evolutionary insights into early land plant evolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16321-16326.	7.1	138
21	<i>WOX13</i>-<i>like</i> genes are required for reprogramming of leaf and protoplast cells into stem cells in the moss <i>Physcomitrella patens</i>. Development (Cambridge), 2014, 141, 1660-1670.	2.5	136
22	KNOX2 Genes Regulate the Haploid-to-Diploid Morphological Transition in Land Plants. Science, 2013, 339, 1067-1070.	12.6	132
23	High levels of RNA editing in a vascular plant chloroplast genome: analysis of transcripts from the fern Adiantum capillus-veneris. Gene, 2004, 339, 89-97.	2.2	130
24	Characterization of MADS-box genes in charophycean green algae and its implication for the evolution of MADS-box genes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2436-2441.	7.1	128
25	AP2-type transcription factors determine stem cell identity in the moss <i>Physcomitrella patens</i>. Development (Cambridge), 2012, 139, 3120-3129.	2.5	124
26	Involvement of auxin and a homeodomain-leucine zipper I gene in rhizoid development of the moss Physcomitrella patens. Development (Cambridge), 2003, 130, 4835-4846.	2.5	121
27	Eight types of stem cells in the life cycle of the moss Physcomitrella patens. Current Opinion in Plant Biology, 2014, 17, 13-21.	7.1	121
28	Evolution and Divergence of the MADS-Box Gene Family Based on Genome-Wide Expression Analyses. Molecular Biology and Evolution, 2003, 20, 1963-1977.	8.9	119
29	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. Nature Communications, 2014, 5, 4784.	12.8	118
30	Chloroplast Phylogeny Indicates that Bryophytes Are Monophyletic. Molecular Biology and Evolution, 2004, 21, 1813-1819.	8.9	116
31	Phylogeny of the sundews, <i>Drosera</i> (Droseraceae), based on chloroplast <i>rbc</i><i>L</i> and nuclear 18S ribosomal DNA Sequences. American Journal of Botany, 2003, 90, 123-130.	1.7	106
32	Complete Nucleotide Sequence of the Chloroplast Genome from a Leptosporangiate Fern, Adiantum capillus-veneris L.. DNA Research, 2003, 10, 59-65.	3.4	104
33	Characterization of MADS homeotic genes in the fern Ceratopteris richardii. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6222-6227.	7.1	103
34	KNOX homeobox genes potentially have similar function in both diploid unicellular and multicellular meristems, but not in haploid meristems. Evolution & Development, 2005, 7, 69-78.	2.0	102
35	Convergent evolution of shoots in land plants: lack of auxin polar transport in moss shoots. Evolution & Development, 2008, 10, 176-186.	2.0	102
36	Mechanism of microtubule array expansion in the cytokinetic phragmoplast. Nature Communications, 2013, 4, 1967.	12.8	102

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37	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	7.8	99
38	<i>Physcomitrella</i>Cyclin-Dependent Kinase A Links Cell Cycle Reactivation to Other Cellular Changes during Reprogramming of Leaf Cells Â Â. Plant Cell, 2011, 23, 2924-2938.	6.6	98
39	Endogenous Diterpenes Derived from <i>ent</i>-Kaurene, a Common Gibberellin Precursor, Regulate Protonema Differentiation of the Moss <i>Physcomitrella patens</i> Â Â Â. Plant Physiology, 2010, 153, 1085-1097.	4.8	96
40	The role of dynamic instability in microtubule organization. Frontiers in Plant Science, 2014, 5, 511.	3.6	95
41	Sex Chromosome Turnover Contributes to Genomic Divergence between Incipient Stickleback Species. PLoS Genetics, 2014, 10, e1004223.	3.5	93
42	Genes for the peptidoglycan synthesis pathway are essential for chloroplast division in moss. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6753-6758.	7.1	92
43	Methylome Diversification through Changes in DNA Methyltransferase Sequence Specificity. PLoS Genetics, 2014, 10, e1004272.	3.5	92
44	Heterotrimeric G proteins control stem cell proliferation through <scp>CLAVATA</scp> signaling in <i>Arabidopsis</i>. EMBO Reports, 2014, 15, 1202-1209.	4.5	92
45	Kinesins Are Indispensable for Interdigitation of Phragmoplast Microtubules in the Moss<i>Physcomitrella patens</i>. Plant Cell, 2008, 20, 3094-3106.	6.6	89
46	The Gibberellin perception system evolved to regulate a pre-existing GAMYB-mediated system during land plant evolution. Nature Communications, 2011, 2, 544.	12.8	79
47	Isolation of Homeodomainâ€"Leucine Zipper Genes from the Moss Physcomitrella patens and the Evolution of Homeodomainâ€"Leucine Zipper Genes in Land Plants. Molecular Biology and Evolution, 2001, 18, 491-502.	8.9	76
48	Molecular Phylogeny of Coriaria, with Special Emphasis on the Disjunct Distribution. Molecular Phylogenetics and Evolution, 2000, 14, 11-19.	2.7	72
49	System for Stable Î²-Estradiol-Inducible Gene Expression in the Moss Physcomitrella patens. PLoS ONE, 2013, 8, e77356.	2.5	71
50	The chloroplast genome from a lycophyte (microphyllophyte), Selaginella uncinata, has a unique inversion, transpositions and many gene losses. Journal of Plant Research, 2007, 120, 281-290.	2.4	70
51	Between Two Fern Genomes. GigaScience, 2014, 3, 15.	6.4	69
52	Calcium dynamics during trap closure visualized in transgenic Venus flytrap. Nature Plants, 2020, 6, 1219-1224.	9.3	67
53	Characterization of MADS genes in the gymnosperm Gnetum parvifolium and its implication on the evolution of reproductive organs in seed plants. Evolution & Development, 1999, 1, 180-190.	2.0	66
54	The modified ABC model explains the development of the petaloid perianth of Agapanthus praecox ssp. orientalis (Agapanthaceae) flowers. Plant Molecular Biology, 2005, 58, 435-445.	3.9	65

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55	BAM 1 and RECEPTOR â€•LIKE PROTEIN KINASE 2 constitute a signaling pathway and modulate CLE peptideâ€triggered growth inhibition in A rabidopsis root. New Phytologist, 2015, 208, 1104-1113.	7.3	64
56	Adiantum capillus-veneris Chloroplast DNA Clone Bank: As Useful Heterologous Probes in the Systematics of the Leptosporangiate Ferns. American Fern Journal, 1990, 80, 20.	0.3	63
57	ppdb: plant promoter database version 3.0. Nucleic Acids Research, 2014, 42, D1188-D1192.	14.5	61
58	A plant U-box protein, PUB4, regulates asymmetric cell division and cell proliferation in the root meristem. Development (Cambridge), 2015, 142, 444-453.	2.5	61
59	Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory. Current Biology, 2020, 30, 2312-2320.e5.	3.9	60
60	Adaxialâ€"abaxial polarity: The developmental basis of leaf shape diversity. Genesis, 2014, 52, 1-18.	1.6	59
61	Phylogeny of the Lady Fern Group, Tribe Physematieae (Dryopteridaceae), Based on Chloroplast rbcL Gene Sequences. Molecular Phylogenetics and Evolution, 2000, 15, 403-413.	2.7	56
62	Phylogeny and divergence of basal angiosperms inferred from APETALA3- and PISTILLATA-like MADS-box genes. Journal of Plant Research, 2004, 117, 229-44.	2.4	55
63	Biological implications of the occurrence of 32 members of the XTH (xyloglucan) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 427 T Journal, 2010, 64, 645-656.	5.7	53
64	Phylogeny of gymnosperms inferred fromrbcL gene sequences. Botanical Magazine, 1992, 105, 673-679.	0.6	52
65	Common-path multimodal three-dimensional fluorescence and phase imaging system. Journal of Biomedical Optics, 2020, 25, 1.	2.6	52
66	Identification of New Chalcone Synthase Genes for Flower Pigmentation in the Japanese and Common Morning Glories. Plant and Cell Physiology, 1997, 38, 754-758.	3.1	51
67	A systemic gene silencing method suitable for high throughput, reverse genetic analyses of gene function in fern gametophytes. BMC Plant Biology, 2004, 4, 6.	3.6	51
68	Physcomitrella MADS-box genes regulate water supply and sperm movement for fertilization. Nature Plants, 2018, 4, 36-45.	9.3	51
69	Oriented cell division shapes carnivorous pitcher leaves of Sarracenia purpurea. Nature Communications, 2015, 6, 6450.	12.8	50
70	Evolution of MADS-Box Gene Induction by FLO/LFY Genes. Journal of Molecular Evolution, 2001, 53, 387-393.	1.8	49
71	A draft genome assembly of the solar-powered sea slug Elysia chlorotica. Scientific Data, 2019, 6, 190022.	5.3	48
72	Early evolution of the vascular plant body plan â€" the missing mechanisms. Current Opinion in Plant Biology, 2014, 17, 126-136.	7.1	45

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73	The KAC Family of Kinesin-Like Proteins is Essential for the Association of Chloroplasts with the Plasma Membrane in Land Plants. Plant and Cell Physiology, 2012, 53, 1854-1865.	3.1	44
74	Ancient trans-Acting siRNAs Confer Robustness and Sensitivity onto the Auxin Response. Developmental Cell, 2016, 36, 276-289.	7.0	44
75	Cytoplasmic MTOCs control spindle orientation for asymmetric cell division in plants. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8847-E8854.	7.1	44
76	Establishment of gene-trap and enhancer-trap systems in the moss Physcomitrella patens. Plant Journal, 2001, 28, 105-116.	5.7	43
77	A Novel Katanin-Tethering Machinery Accelerates Cytokinesis. Current Biology, 2019, 29, 4060-4070.e3.	3.9	42
78	NIMAâ€related kinases 6, 4, and 5 interact with each other to regulate microtubule organization during epidermal cell expansion in <i>Arabidopsis thaliana</i>. Plant Journal, 2011, 67, 993-1005.	5.7	41
79	Characterization of aFLORICAULA/LEAFYHomologue ofGnetum parvifoliumand Its Implications for the Evolution of Reproductive Organs in Seed Plants. International Journal of Plant Sciences, 2001, 162, 1199-1209.	1.3	40
80	Microtubule-dependent microtubule nucleation in plant cells. Journal of Plant Research, 2007, 120, 73-78.	2.4	39
81	Single-cell transcriptome analysis of Physcomitrella leaf cells during reprogramming using microcapillary manipulation. Nucleic Acids Research, 2019, 47, 4539-4553.	14.5	39
82	Intrageneric relationships of maple trees based on the chloroplast DNA restriction fragment length polymorphisms. Journal of Plant Research, 1998, 111, 441-451.	2.4	37
83	Complete Genome Sequence of <i>Burkholderia</i> sp. Strain RPE64, Bacterial Symbiont of the Bean Bug <i>Riptortus pedestris</i>. Genome Announcements, 2013, 1, .	0.8	37
84	A Lin28 homologue reprograms differentiated cells to stem cells in the moss Physcomitrella patens. Nature Communications, 2017, 8, 14242.	12.8	37
85	Ethylene signaling mediates host invasion by parasitic plants. Science Advances, 2020, 6, .	10.3	37
86	Phylogenetic relationships of ferns deduced from rbcL gene sequence. Journal of Molecular Evolution, 1993, 37, 476-482.	1.8	35
87	Evolution of Reproductive Organs in Land Plants. Journal of Plant Research, 1999, 112, 463-474.	2.4	34
88	Identification of IAA Transport Inhibitors Including Compounds Affecting Cellular PIN Trafficking by Two Chemical Screening Approaches Using Maize Coleoptile Systems. Plant and Cell Physiology, 2012, 53, 1671-1682.	3.1	34
89	Chloroplast DNA from Adiantum capillus-veneris L., a fern species (Adiantaceae); clone bank, physical map and unusual gene localization in comparison with angiosperm chloroplast DNA. Current Genetics, 1990, 17, 359-364.	1.7	32
90	Ecogenomics of cleistogamous and chasmogamous flowering: genomeâ€wide gene expression patterns from crossâ€species microarray analysis in <i>Cardamine kokaiensis</i> (Brassicaceae). Journal of Ecology, 2008, 96, 1086-1097.	4.0	32

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91	Identification of an EMS-induced causal mutation in a gene required for boron-mediated root development by low-coverage genome re-sequencing inArabidopsis. Plant Signaling and Behavior, 2013, 8, e22534.	2.4	32
92	Physcomitrella STEMIN transcription factor induces stem cell formation with epigenetic reprogramming. Nature Plants, 2019, 5, 681-690.	9.3	32
93	Multi-point Scanning Two-photon Excitation Microscopy by Utilizing a High-peak-power 1042-nm Laser. Analytical Sciences, 2015, 31, 307-313.	1.6	31
94	Î³-Tubulin distribution during cortical microtubule reorganization at the M/G1 interface in tobacco BY-2 cells. European Journal of Cell Biology, 2003, 82, 43-51.	3.6	29
95	Microtubules Regulate Dynamic Organization of Vacuoles in Physcomitrella patens. Plant and Cell Physiology, 2009, 50, 855-868.	3.1	29
96	Chloroplast acquisition without the gene transfer in kleptoplastic sea slugs, Plakobranchus ocellatus. ELife, 2021, 10, .	6.0	29
97	Involvement of mitochondrial-targeted RecA in the repair of mitochondrial DNA in the moss, Physcomitrella patens. Genes and Genetic Systems, 2007, 82, 43-51.	0.7	28
98	Expression of Exogenous Genes Under the Control of Endogenous HSP70 and CAB Promoters in the Closterium peracerosumâ€“strigosumâ€“littorale complex. Plant and Cell Physiology, 2008, 49, 625-632.	3.1	28
99	Digital Gene Expression Profiling by 5â€²-End Sequencing of cDNAs during Reprogramming in the Moss Physcomitrella patens. PLoS ONE, 2012, 7, e36471.	2.5	27
100	BEACH-Domain Proteins Act Together in a Cascade to Mediate Vacuolar Protein Trafficking and Disease Resistance in Arabidopsis. Molecular Plant, 2015, 8, 389-398.	8.3	27
101	Polyamine Resistance Is Increased by Mutations in a Nitrate Transporter Gene NRT1.3 (AtNPF6.4) in Arabidopsis thaliana. Frontiers in Plant Science, 2016, 7, 834.	3.6	26
102	Phylogenetic relationships in gnetophyta deduced fromrbcL gene sequences. Botanical Magazine, 1992, 105, 385-391.	0.6	25
103	A SABATH Methyltransferase from the moss Physcomitrella patens catalyzes S-methylation of thiols and has a role in detoxification. Phytochemistry, 2012, 81, 31-41.	2.9	25
104	Optical Property Analyses of Plant Cells for Adaptive Optics Microscopy. International Journal of Optomechatronics, 2014, 8, 89-99.	6.6	24
105	Phylogenetic Studies of Extant Pteridophytes. , 1998, , 541-556.		24
106	Expression and Complementation Analyses of a Chloroplast-Localized Homolog of Bacterial RecA in the Moss<i>Physcomitrella patens</i>. Bioscience, Biotechnology and Biochemistry, 2008, 72, 1340-1347.	1.3	23
107	DNA damage triggers reprogramming of differentiated cells into stem cells in Physcomitrella. Nature Plants, 2020, 6, 1098-1105.	9.3	22
108	Variations on theme: spindle assembly in diverse cells. Protoplasma, 2011, 248, 439-446.	2.1	21

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109	Identification and characterization of cDNAs encoding pentatricopeptide repeat proteins in the basal land plant, the moss Physcomitrella patens. Gene, 2004, 343, 305-311.	2.2	20
110	Tandem Repeat rDNA Sequences Derived from Parents Were Stably Maintained in Hexaploids of Drosera spathulata Complex (Droseraceae). Cytologia, 2008, 73, 313-325.	0.6	20
111	Characterization of the Selaginella remotifolia MADS-box gene. Journal of Plant Research, 2003, 116, 69-73.	2.4	19
112	Biosystematic Studies on the Family Tofieldiaceae I. Phylogeny and Circumscription of the Family Inferred from DNA Sequences ofmatK andrbcL. Plant Biology, 2004, 6, 562-567.	3.8	19
113	How do Plants Organize Microtubules Without a Centrosome?. Journal of Integrative Plant Biology, 2007, 49, 1154-1163.	8.5	19
114	Physcomitrella PpORS, Basal to Plant Type III Polyketide Synthases in Phylogenetic Trees, Is a Very Long Chain 2â€²-Oxoalkylresorcinol Synthase. Journal of Biological Chemistry, 2013, 288, 2767-2777.	3.4	19
115	Antheridial development in the moss <i>Physcomitrella patens</i> : implications for understanding stem cells in mosses. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20160494.	4.0	19
116	Cells reprogramming to stem cells inhibit the reprogramming of adjacent cells in the moss Physcomitrella patens. Scientific Reports, 2017, 7, 1909.	3.3	18
117	Diplazium subsinuatum and Di. tomitaroanum should be Moved to Deparia According to Molecular, Morphological, and Cytological Characters. Journal of Plant Research, 2000, 113, 157-163.	2.4	17
118	Isolation and Identification of Antheridiogens in the Ferns, Lygodium microphyllum and Lygodium reticulatum. Bioscience, Biotechnology and Biochemistry, 2001, 65, 2311-2314.	1.3	17
119	Convergences and divergences in polar auxin transport and shoot development in land plant evolution. Plant Signaling and Behavior, 2009, 4, 313-315.	2.4	17
120	The Polycomb group protein CLF emerges as a specific tri-methylase of H3K27 regulating gene expression and development in Physcomitrella patens. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 860-870.	1.9	17
121	Rapid movements in plants. Journal of Plant Research, 2021, 134, 3-17.	2.4	17
122	Gene localization on the chloroplast DNA of the maiden hair fern;Adiantum capillus-veneris. Botanical Magazine, 1992, 105, 413-419.	0.6	16
123	Isolation of Mutant Lines with Decreased Numbers of Chloroplasts per Cell from a Tagged Mutant Library of the Moss Physcomitrella patens. Plant Biology, 2005, 7, 300-306.	3.8	16
124	A chloroplast-DNA phylogeny ofKalimeris andAster, with reference to the generic circumscription. Journal of Plant Research, 1995, 108, 93-96.	2.4	14
125	Evolution of MADS Gene Family in Plants. , 1997, , 179-197.		14
126	A Dibasic Amino Acid Pair Conserved in the Activation Loop Directs Plasma Membrane Localization and Is Necessary for Activity of Plant Type I/II Phosphatidylinositol Phosphate Kinase Â. Plant Physiology, 2010, 153, 1004-1015.	4.8	13

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127	Two ANGUSTIFOLIA genes regulate gametophore and sporophyte development in Physcomitrella patens. Plant Journal, 2020, 101, 1318-1330.	5.7	13
128	Identification of crystalline material found in the thallus of the lichen, Myelochroa leucotyliza. Journal of Structural Biology, 2004, 146, 393-400.	2.8	12
129	Whole-Genome Sequence of <i>Burkholderia</i> sp. Strain RPE67, a Bacterial Gut Symbiont of the Bean Bug <i>Riptortus pedestris</i>. Genome Announcements, 2014, 2, .	0.8	12
130	Isolation and Characterization of a cDNA for Phenylalanine Ammonia-Lyase(PAL) from Dianthus caryophyllus (carnation).. Plant Biotechnology, 2000, 17, 325-329.	1.0	12
131	Unveiling the nature of a miniature world: a horizon scan of fundamental questions in bryology. Journal of Bryology, 2022, 44, 1-34.	1.2	12
132	Crystal structure of the liganded anti-gibberellin A4 antibody 4-B8(8)/E9 Fab fragment. Biochemical and Biophysical Research Communications, 2002, 293, 489-496.	2.1	11
133	Development of an Agrobacterium-Mediated Stable Transformation Method for the Sensitive Plant Mimosa pudica. PLoS ONE, 2014, 9, e88611.	2.5	11
134	Evolutionary origin of a periodical massâ€flowering plant. Ecology and Evolution, 2019, 9, 4373-4381.	1.9	10
135	Networking and Specificity-Changing DNA Methyltransferases in Helicobacter pylori. Frontiers in Microbiology, 2020, 11, 1628.	3.5	9
136	Cell cycle reentry from the late S phase: implications from stem cell formation in the moss Physcomitrella patens. Journal of Plant Research, 2015, 128, 399-405.	2.4	8
137	Phylogeny ofTyphonium (Araceae) inferred from restriction fragment analysis of chloroplast DNA. Journal of Plant Research, 1993, 106, 11-14.	2.4	7
138	An extraction method for tobacco mosaic virus movement protein localizing in plasmodesmata. Protoplasma, 2005, 225, 85-92.	2.1	7
139	Nucleotide sequence variation was unexpectedly low in an endangered species, Aldrovanda vesiculosa L. (Droseraceae). Chromosome Botany, 2006, 1, 27-32.	0.2	7
140	A discordance of seasonally covarying cues uncovers misregulated phenotypes in the heterophyllous pitcher plant<i>Cephalotus follicularis</i>. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20202568.	2.6	7
141	Gene Tagging, Gene- and Enhancer-Trapping, and Full-Length cDNA Overexpression in Physcomitrella Patens. , 2004, , 111-132.		7
142	Carnivorous plant genomes. , 2018, , .		7
143	Overexpression of <i>ATG8/LC3</i> enhances wound-induced somatic reprogramming in <i>Physcomitrium patens</i>. Autophagy, 2022, 18, 1463-1466.	9.1	7
144	Localization of tobacco germin-like protein 1 in leaf intercellular space. Plant Physiology and Biochemistry, 2014, 85, 1-8.	5.8	6

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145	Low-invasive 5D visualization of mitotic progression by two-photon excitation spinning-disk confocal microscopy. Scientific Reports, 2022, 12, 809.	3.3	6
146	Imaging the Mitotic Spindle by Spinning Disk Microscopy in Tobacco Suspension Cultured Cells. Methods in Molecular Biology, 2014, 1136, 47-55.	0.9	5
147	Artificial testing targets with controllable blur for adaptive optics microscopes. Optical Engineering, 2017, 56, 1.	1.0	4
148	Molecular mechanisms of reprogramming of differentiated cells into stem cells in the moss Physcomitrium patens. Current Opinion in Plant Biology, 2022, 65, 102123.	7.1	4
149	Gametangia Development in the MossPhyscomitrella patens. , 0, , 167-181.		3
150	Topoisomerase 1Î± is required for synchronous spermatogenesis in <i>Physcomitrium patens</i>. New Phytologist, 2022, 234, 137-148.	7.3	2
151	A PSTAIRE-type cyclin-dependent kinase controls light responses in land plants. Science Advances, 2022, 8, eabk2116.	10.3	2
152	Moss development: Starting BELL for embryos. Nature Plants, 2016, 2, 16004.	9.3	0
153	Adaptive optical imaging through complex living plant cells. , 2017, , .		0
154	Formation of a Symmetric Flat Leaf Lamina in Arabidopsis. , 2003, , 177-187.		0
155	Mechanism of phragmoplast expansion. Plant Morphology, 2014, 26, 53-58.	0.1	0