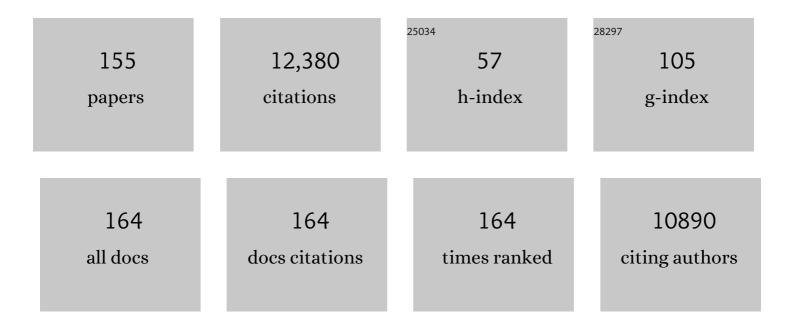
Mitsuyasu Hasebe

List of Publications by Year in descending order

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MITSHVASH HASERE

#	Article	IF	CITATIONS
1	Overexpression of <i>ATG8/LC3</i> enhances wound-induced somatic reprogramming in <i>Physcomitrium patens</i> . Autophagy, 2022, 18, 1463-1466.	9.1	7
2	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
3	Low-invasive 5D visualization of mitotic progression by two-photon excitation spinning-disk confocal microscopy. Scientific Reports, 2022, 12, 809.	3.3	6
4	Topoisomerase 1α is required for synchronous spermatogenesis in <i>Physcomitrium patens</i> . New Phytologist, 2022, 234, 137-148.	7.3	2
5	A PSTAIRE-type cyclin-dependent kinase controls light responses in land plants. Science Advances, 2022, 8, eabk2116.	10.3	2
6	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
7	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
8	Rapid movements in plants. Journal of Plant Research, 2021, 134, 3-17.	2.4	17
9	Chloroplast acquisition without the gene transfer in kleptoplastic sea slugs, Plakobranchus ocellatus. ELife, 2021, 10, .	6.0	29
10	Two ANGUSTIFOLIA genes regulate gametophore and sporophyte development in Physcomitrella patens. Plant Journal, 2020, 101, 1318-1330.	5.7	13
11	Calcium dynamics during trap closure visualized in transgenic Venus flytrap. Nature Plants, 2020, 6, 1219-1224.	9.3	67
12	Networking and Specificity-Changing DNA Methyltransferases in Helicobacter pylori. Frontiers in Microbiology, 2020, 11, 1628.	3.5	9
13	Ethylene signaling mediates host invasion by parasitic plants. Science Advances, 2020, 6, .	10.3	37
14	DNA damage triggers reprogramming of differentiated cells into stem cells in Physcomitrella. Nature Plants, 2020, 6, 1098-1105.	9.3	22
15	Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory. Current Biology, 2020, 30, 2312-2320.e5.	3.9	60
16	Common-path multimodal three-dimensional fluorescence and phase imaging system. Journal of Biomedical Optics, 2020, 25, 1.	2.6	52
17	Physcomitrella STEMIN transcription factor induces stem cell formation with epigenetic reprogramming. Nature Plants, 2019, 5, 681-690.	9.3	32
18	A draft genome assembly of the solar-powered sea slug Elysia chlorotica. Scientific Data, 2019, 6, 190022.	5.3	48

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19	Single-cell transcriptome analysis of Physcomitrella leaf cells during reprogramming using microcapillary manipulation. Nucleic Acids Research, 2019, 47, 4539-4553.	14.5	39
20	Evolutionary origin of a periodical massâ€flowering plant. Ecology and Evolution, 2019, 9, 4373-4381.	1.9	10
21	A Novel Katanin-Tethering Machinery Accelerates Cytokinesis. Current Biology, 2019, 29, 4060-4070.e3.	3.9	42
22	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
23	Physcomitrella MADS-box genes regulate water supply and sperm movement for fertilization. Nature Plants, 2018, 4, 36-45.	9.3	51
24	Carnivorous plant genomes. , 2018, , .		7
25	A Lin28 homologue reprograms differentiated cells to stem cells in the moss Physcomitrella patens. Nature Communications, 2017, 8, 14242.	12.8	37
26	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	7.8	99
27	Adaptive optical imaging through complex living plant cells. , 2017, , .		Ο
28	Cells reprogramming to stem cells inhibit the reprogramming of adjacent cells in the moss Physcomitrella patens. Scientific Reports, 2017, 7, 1909.	3.3	18
29	Plant Cytokinesis: Terminology for Structures and Processes. Trends in Cell Biology, 2017, 27, 885-894.	7.9	155
30	Cytoplasmic MTOCs control spindle orientation for asymmetric cell division in plants. Proceedings of the United States of America, 2017, 114, E8847-E8854.	7.1	44
31	Artificial testing targets with controllable blur for adaptive optics microscopes. Optical Engineering, 2017, 56, 1.	1.0	4
32	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
33	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
34	Moss development: Starting BELL for embryos. Nature Plants, 2016, 2, 16004.	9.3	0
35	Ancient trans-Acting siRNAs Confer Robustness and Sensitivity onto the Auxin Response. Developmental Cell, 2016, 36, 276-289.	7.0	44
36	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

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37	BAM 1 and RECEPTOR ―LIKE PROTEIN KINASE 2 constitute a signaling pathway and modulate CLE peptideâ€ŧriggered growth inhibition in A rabidopsis root. New Phytologist, 2015, 208, 1104-1113.	7.3	64
38	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
39	Oriented cell division shapes carnivorous pitcher leaves of Sarracenia purpurea. Nature Communications, 2015, 6, 6450.	12.8	50
40	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
41	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
42	Development of an Agrobacterium-Mediated Stable Transformation Method for the Sensitive Plant Mimosa pudica. PLoS ONE, 2014, 9, e88611.	2.5	11
43	ppdb: plant promoter database version 3.0. Nucleic Acids Research, 2014, 42, D1188-D1192.	14.5	61
44	Methylome Diversification through Changes in DNA Methyltransferase Sequence Specificity. PLoS Genetics, 2014, 10, e1004272.	3.5	92
45	The role of dynamic instability in microtubule organization. Frontiers in Plant Science, 2014, 5, 511.	3.6	95
46	Sex Chromosome Turnover Contributes to Genomic Divergence between Incipient Stickleback Species. PLoS Genetics, 2014, 10, e1004223.	3.5	93
47	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
48	Optical Property Analyses of Plant Cells for Adaptive Optics Microscopy. International Journal of Optomechatronics, 2014, 8, 89-99.	6.6	24
49	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
50	Adaxial–abaxial polarity: The developmental basis of leaf shape diversity. Genesis, 2014, 52, 1-18.	1.6	59
51	Between Two Fern Genomes. GigaScience, 2014, 3, 15.	6.4	69
52	<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
53	Contribution of NAC Transcription Factors to Plant Adaptation to Land. Science, 2014, 343, 1505-1508.	12.6	222
54	Early evolution of the vascular plant body plan — the missing mechanisms. Current Opinion in Plant Biology, 2014, 17, 126-136.	7.1	45

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55	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
56	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. Nature Communications, 2014, 5, 4784.	12.8	118
57	Localization of tobacco germin-like protein 1 in leaf intercellular space. Plant Physiology and Biochemistry, 2014, 85, 1-8.	5.8	6
58	Imaging the Mitotic Spindle by Spinning Disk Microscopy in Tobacco Suspension Cultured Cells. Methods in Molecular Biology, 2014, 1136, 47-55.	0.9	5
59	Mechanism of phragmoplast expansion. Plant Morphology, 2014, 26, 53-58.	0.1	0
60	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
61	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
62	Mechanism of microtubule array expansion in the cytokinetic phragmoplast. Nature Communications, 2013, 4, 1967.	12.8	102
63	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
64	Physcomitrella PpORS, Basal to Plant Type III Polyketide Synthases in Phylogenetic Trees, Is a Very Long Chain 2′-Oxoalkylresorcinol Synthase. Journal of Biological Chemistry, 2013, 288, 2767-2777.	3.4	19
65	KNOX2 Genes Regulate the Haploid-to-Diploid Morphological Transition in Land Plants. Science, 2013, 339, 1067-1070.	12.6	132
66	System for Stable Î ² -Estradiol-Inducible Gene Expression in the Moss Physcomitrella patens. PLoS ONE, 2013, 8, e77356.	2.5	71
67	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
68	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
69	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
70	Digital Gene Expression Profiling by 5′-End Sequencing of cDNAs during Reprogramming in the Moss Physcomitrella patens. PLoS ONE, 2012, 7, e36471.	2.5	27
71	AP2-type transcription factors determine stem cell identity in the moss <i>Physcomitrella patens</i> . Development (Cambridge), 2012, 139, 3120-3129.	2.5	124
72	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

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73	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	12.6	794
74	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
75	Variations on theme: spindle assembly in diverse cells. Protoplasma, 2011, 248, 439-446.	2.1	21
76	<i>Physcomitrella</i> Cyclin-Dependent Kinase A Links Cell Cycle Reactivation to Other Cellular Changes during Reprogramming of Leaf Cells Â. Plant Cell, 2011, 23, 2924-2938.	6.6	98
77	Biological implications of the occurrence of 32 members of the XTH (xyloglucan) Tj ETQq1 1 0.784314 rgBT /Ov Journal, 2010, 64, 645-656.	verlock 10 5.7	Tf 50 587 Td 53
78	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
79	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
80	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
81	Microtubules Regulate Dynamic Organization of Vacuoles in Physcomitrella patens. Plant and Cell Physiology, 2009, 50, 855-868.	3.1	29
82	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
83	ANXUR1 and 2, Sister Genes to FERONIA/SIRENE, Are Male Factors for Coordinated Fertilization. Current Biology, 2009, 19, 1327-1331.	3.9	254
84	Convergent evolution of shoots in land plants: lack of auxin polar transport in moss shoots. Evolution & Development, 2008, 10, 176-186.	2.0	102
85	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
86	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
87	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	12.6	1,712
88	Expression of Exogenous Genes Under the Control of Endogenous HSP70 and CAB Promoters in the Closterium peracerosum–strigosum–littorale complex. Plant and Cell Physiology, 2008, 49, 625-632.	3.1	28
89	Kinesins Are Indispensable for Interdigitation of Phragmoplast Microtubules in the Moss <i>Physcomitrella patens</i> . Plant Cell, 2008, 20, 3094-3106.	6.6	89
90	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

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91	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
92	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
93	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
94	How do Plants Organize Microtubules Without a Centrosome?. Journal of Integrative Plant Biology, 2007, 49, 1154-1163.	8.5	19
95	Microtubule-dependent microtubule nucleation in plant cells. Journal of Plant Research, 2007, 120, 73-78.	2.4	39
96	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
97	Molecular evolution of the AP2 subfamily. Gene, 2006, 366, 256-265.	2.2	172
98	Nucleotide sequence variation was unexpectedly low in an endangered species, Aldrovanda vesiculosa L. (Droseraceae). Chromosome Botany, 2006, 1, 27-32.	0.2	7
99	Cenes 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
100	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
101	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
102	An extraction method for tobacco mosaic virus movement protein localizing in plasmodesmata. Protoplasma, 2005, 225, 85-92.	2.1	7
103	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
104	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
105	The Floral Regulator LEAFY Evolves by Substitutions in the DNA Binding Domain. Science, 2005, 308, 260-263.	12.6	195
106	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
107	Microtubule-dependent microtubule nucleation based on recruitment of Î ³ -tubulin in higher plants. Nature Cell Biology, 2005, 7, 961-968.	10.3	325
108	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

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109	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
110	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
111	Chloroplast Phylogeny Indicates that Bryophytes Are Monophyletic. Molecular Biology and Evolution, 2004, 21, 1813-1819.	8.9	116
112	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
113	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
114	Identification of crystalline material found in the thallus of the lichen, Myelochroa leucotyliza. Journal of Structural Biology, 2004, 146, 393-400.	2.8	12
115	Gene Tagging, Gene- and Enhancer-Trapping, and Full-Length cDNA Overexpression in Physcomitrella Patens. , 2004, , 111-132.		7
116	Characterization of the Selaginella remotifolia MADS-box gene. Journal of Plant Research, 2003, 116, 69-73.	2.4	19
117	Î ³ -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
118	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
119	Phylogeny of the sundews, <i>Drosera</i> (Droseraceae), based on chloroplast <i>rbcL</i> and nuclear 18S ribosomal DNA Sequences. American Journal of Botany, 2003, 90, 123-130.	1.7	106
120	Complete Nucleotide Sequence of the Chloroplast Genome from a Leptosporangiate Fern, Adiantum capillus-veneris L DNA Research, 2003, 10, 59-65.	3.4	104
121	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
122	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
123	Formation of a Symmetric Flat Leaf Lamina in Arabidopsis. , 2003, , 177-187.		0
124	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
125	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
126	Cryptochrome Light Signals Control Development to Suppress Auxin Sensitivity in the Moss Physcomitrella patens. Plant Cell, 2002, 14, 373-386.	6.6	161

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127	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
128	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
129	Isolation of Homeodomain–Leucine Zipper Genes from the Moss Physcomitrella patens and the Evolution of Homeodomain–Leucine Zipper Genes in Land Plants. Molecular Biology and Evolution, 2001, 18, 491-502.	8.9	76
130	Evolution of MADS-Box Gene Induction by FLO/LFY Genes. Journal of Molecular Evolution, 2001, 53, 387-393.	1.8	49
131	Establishment of gene-trap and enhancer-trap systems in the moss Physcomitrella patens. Plant Journal, 2001, 28, 105-116.	5.7	43
132	Isolation and Identification of Antheridiogens in the Ferns, Lygodium microphyllum and Lygodium reticulatum. Bioscience, Biotechnology and Biochemistry, 2001, 65, 2311-2314.	1.3	17
133	Molecular Phylogeny of Coriaria, with Special Emphasis on the Disjunct Distribution. Molecular Phylogenetics and Evolution, 2000, 14, 11-19.	2.7	72
134	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
135	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
136	Isolation and Characterization of a cDNA for Phenylalanine Ammonia-Lyase(PAL) from Dianthus caryophyllus (carnation) Plant Biotechnology, 2000, 17, 325-329.	1.0	12
137	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
138	Evolution of Reproductive Organs in Land Plants. Journal of Plant Research, 1999, 112, 463-474.	2.4	34
139	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
140	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
141	Phylogenetic Studies of Extant Pteridophytes. , 1998, , 541-556.		24
142	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
143	Evolution of MADS Gene Family in Plants. , 1997, , 179-197.		14
144	A chloroplast-DNA phylogeny ofKalimeris andAster, with reference to the generic circumscription. Journal of Plant Research, 1995, 108, 93-96.	2.4	14

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145	Fern Phylogeny Based on rbcL Nucleotide Sequences. American Fern Journal, 1995, 85, 134.	0.3	265
146	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
147	Phylogenetic relationships of ferns deduced from rbcL gene sequence. Journal of Molecular Evolution, 1993, 37, 476-482.	1.8	35
148	Phylogeny ofTyphonium (Araceae) inferred from restriction fragment analysis of chloroplast DNA. Journal of Plant Research, 1993, 106, 11-14.	2.4	7
149	Phylogeny of gymnosperms inferred fromrbcL gene sequences. Botanical Magazine, 1992, 105, 673-679.	0.6	52
150	Phylogenetic relationships in gnetophyta deduced fromrbcL gene sequences. Botanical Magazine, 1992, 105, 385-391.	0.6	25
151	Gene localization on the chloroplast DNA of the maiden hair fern;Adiantum capillus-veneris. Botanical Magazine, 1992, 105, 413-419.	0.6	16
152	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
153	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
154	FlgB, FlgC, FlgF and FlgG. Journal of Molecular Biology, 1990, 211, 465-477.	4.2	148
155	Gametangia Development in the MossPhyscomitrella patens. , 0, , 167-181.		3