Ralf Reski

List of Publications by Year
in descending order

210 papers	13,329 citations	16451 64 h-index	30922 102 g-index
231 all docs	231 docs citations	231 times ranked	10960 citing authors

#	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	Transcriptional Control of Gene Expression by MicroRNAs. Cell, 2010, 140, 111-122.	28.9	431
3	The <i>Physcomitrella patens</i> chromosomeâ€scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
4	Targeted knockouts of Physcomitrella lacking plant-specific immunogenic N-glycans. Plant Biotechnology Journal, 2004, 2, 517-523.	8.3	221
5	Physcomitrella patens is highly tolerant against drought, salt and osmotic stress. Planta, 2005, 220, 384-394.	3.2	205
6	Identification of a novel D6-acyl-group desaturase by targeted gene disruption in Physcomitrella patens. Plant Journal, 1998, 15, 39-48.	5.7	193
7	Genome-Wide Phylogenetic Comparative Analysis of Plant Transcriptional Regulation: A Timeline of Loss, Gain, Expansion, and Correlation with Complexity. Genome Biology and Evolution, 2010, 2, 488-503.	2.5	174
8	An ancient genome duplication contributed to the abundance of metabolic genes in the moss Physcomitrella patens. BMC Evolutionary Biology, 2007, 7, 130.	3.2	171
9	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
10	A phenol-enriched cuticle is ancestral to lignin evolution in land plants. Nature Communications, 2017, 8, 14713.	12.8	157
11	Stomatal Guard Cells Co-opted an Ancient ABA-Dependent Desiccation Survival System to Regulate Stomatal Closure. Current Biology, 2015, 25, 928-935.	3.9	154
12	Gene clusters involved in anaerobic benzoate degradation of <i>Geobacter metallireducens</i>. Molecular Microbiology, 2005, 58, 1238-1252.	2.5	147
13	Origin and function of stomata in the moss Physcomitrella patens. Nature Plants, 2016, 2, 16179.	9.3	138
14	Moss Systems Biology en Route: Phytohormones in Physcomitrella Development. Plant Biology, 2006, 8, 397-406.	3.8	135
15	Regulation of stem cell maintenance by the Polycomb protein FIE has been conserved during land plant evolution. Development (Cambridge), 2009, 136, 2433-2444.	2.5	133
16	Plasma Membrane-Targeted PIN Proteins Drive Shoot Development in a Moss. Current Biology, 2014, 24, 2776-2785.	3.9	133
17	Exploring plant biodiversity: the Physcomitrella genome and beyond. Trends in Plant Science, 2008, 13, 542-549.	8.8	132
18	The Plant Ontology as a Tool for Comparative Plant Anatomy and Genomic Analyses. Plant and Cell Physiology, 2013, 54, e1-e1.	3.1	131

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19	Moss (<i>Physcomitrella patens</i>) GH3 proteins act in auxin homeostasis. New Phytologist, 2009, 181, 323-338.	7.3	129
20	The mechanism of gene targeting in Physcomitrella patens: homologous recombination, concatenation and multiple integration. Nucleic Acids Research, 2006, 34, 6205-6214.	14.5	126
21	The moss <i>Physcomitrella patens</i> contains cyclopentenones but no jasmonates: mutations in allene oxide cyclase lead to reduced fertility and altered sporophyte morphology. New Phytologist, 2010, 188, 740-749.	7.3	125
22	Strigolactone biosynthesis is evolutionarily conserved, regulated by phosphate starvation and contributes to resistance against phytopathogenic fungi in a moss, <i>Physcomitrella patens</i>. New Phytologist, 2017, 216, 455-468.	7.3	121
23	A P _{IIB} -type Ca ²⁺ -ATPase is essential for stress adaptation in <i>Physcomitrella patens</i>. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19555-19560.	7.1	116
24	A single homeobox gene triggers phase transition, embryogenesis and asexual reproduction. Nature Plants, 2016, 2, 15209.	9.3	116
25	The evolution of nuclear auxin signalling. BMC Evolutionary Biology, 2009, 9, 126.	3.2	115
26	The <i>Physcomitrella patens</i> gene atlas project: largeâ€scale <scp>RNA</scp>â€seq based expression data. Plant Journal, 2018, 95, 168-182.	5.7	115
27	Plant functional genomics. Die Naturwissenschaften, 2002, 89, 235-249.	1.6	114
28	Microarray analysis of the moss Physcomitrella patens reveals evolutionarily conserved transcriptional regulation of salt stress and abscisic acid signalling. Plant Molecular Biology, 2010, 72, 27-45.	3.9	110
29	An improved and highly standardised transformation procedure allows efficient production of single and multiple targeted gene-knockouts in a moss, Physcomitrella patens. Current Genetics, 2004, 44, 339-347.	1.7	109
30	Specific Gene Silencing by Artificial MicroRNAs in <i>Physcomitrella patens</i>: An Alternative to Targeted Gene Knockouts Â Â. Plant Physiology, 2008, 148, 684-693.	4.8	109
31	Evidence for the rapid expansion of microRNA-mediated regulation in early land plant evolution. BMC Plant Biology, 2007, 7, 13.	3.6	108
32	Dating the early evolution of plants: detection and molecular clock analyses of orthologs. Molecular Genetics and Genomics, 2007, 278, 393-402.	2.1	103
33	Visualization of a Cytoskeleton-like Ftsz Network in Chloroplasts. Journal of Cell Biology, 2000, 151, 945-950.	5.2	102
34	Moss transcriptome and beyond. Trends in Plant Science, 2002, 7, 535-538.	8.8	102
35	The moss bioreactor. Current Opinion in Plant Biology, 2004, 7, 166-170.	7.1	102
36	Physcomitrella and Arabidopsis: the David and Goliath of reverse genetics. Trends in Plant Science, 1998, 3, 209-210.	8.8	99

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37	Genetic analysis of Physcomitrella patens identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. Plant Cell, 2016, 28, tpc.00091.2016.	6.6	98
38	Cloning and functional characterisation of an enzyme involved in the elongation of Î”6-polyunsaturated fatty acids from the moss Physcomitrella patens. Plant Journal, 2002, 31, 255-268.	5.7	97
39	Unique Tissue-Specific Cell Cycle in Physcomitrella. Plant Biology, 2003, 5, 50-58.	3.8	97
40	Mossâ€made pharmaceuticals: from bench to bedside. Plant Biotechnology Journal, 2015, 13, 1191-1198.	8.3	95
41	Evolutionary conservation of plant gibberellin signalling pathway components. BMC Plant Biology, 2007, 7, 65.	3.6	93
42	A Novel Calcium Binding Site in the Slow Vacuolar Cation Channel TPC1 Senses Luminal Calcium Levels. Plant Cell, 2011, 23, 2696-2707.	6.6	93
43	Two RpoT genes of Physcomitrella patens encode phage-type RNA polymerases with dual targeting to mitochondria and plastids. Gene, 2002, 290, 95-105.	2.2	91
44	Current achievements in the production of complex biopharmaceuticals with moss bioreactors. Bioprocess and Biosystems Engineering, 2008, 31, 3-9.	3.4	89
45	A red light-controlled synthetic gene expression switch for plant systems. Molecular BioSystems, 2014, 10, 1679-1688.	2.9	89
46	Genome analysis of the moss Physcomitrella patens (Hedw.) B.S.G.. Molecular Genetics and Genomics, 1994, 244, 352-359.	2.4	87
47	Quantitative promoter analysis in Physcomitrella patens: a set of plant vectors activating gene expression within three orders of magnitude. BMC Biotechnology, 2004, 4, 13.	3.3	87
48	Production of biologically active recombinant human factor H in <i>Physcomitrella</i>. Plant Biotechnology Journal, 2011, 9, 373-383.	8.3	86
49	Insights from the cold transcriptome of <i><scp>P</scp>hyscomitrella patens</i>: global specialization pattern of conserved transcriptional regulators and identification of orphan genes involved in cold acclimation. New Phytologist, 2015, 205, 869-881.	7.3	84
50	Molecular genetics of Physcomitrella. Planta, 1999, 208, 301-309.	3.2	83
51	A mitochondrial protein homologous to the mammalian peripheralâ€type benzodiazepine receptor is essential for stress adaptation in plants. Plant Journal, 2007, 51, 1004-1018.	5.7	83
52	Balanced activity of microRNA166/165 and its target transcripts from the class III homeodomain-leucine zipper family regulates root growth in Arabidopsis thaliana. Plant Cell Reports, 2014, 33, 945-953.	5.6	83
53	Largeâ€scale gene expression profiling data for the model moss <i><scp>P</scp>hyscomitrella patens</i> aid understanding of developmental progression, culture and stress conditions. Plant Journal, 2014, 79, 530-539.	5.7	82
54	Optimisation of a bioreactor culture of the moss Physcomitrella patens for mass production of protoplasts. Plant Science, 2002, 163, 69-74.	3.6	79

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55	PlanTAPDB, a Phylogeny-Based Resource of Plant Transcription-Associated Proteins. Plant Physiology, 2007, 143, 1452-1466.	4.8	79
56	Identification of genic moss SSR markers and a comparative analysis of twenty-four algal and plant gene indices reveal species-specific rather than group-specific characteristics of microsatellites. BMC Plant Biology, 2006, 6, 9.	3.6	78
57	Metabolite profiling of the moss Physcomitrella patens reveals evolutionary conservation of osmoprotective substances. Plant Cell Reports, 2012, 31, 427-436.	5.6	78
58	High frequency of phenotypic deviations in Physcomitrella patens plants transformed with a gene-disruption library. BMC Plant Biology, 2002, 2, 6.	3.6	75
59	Mossâ€based production of asialoâ€erythropoietin devoid of Lewis A and other plantâ€typical carbohydrate determinants. Plant Biotechnology Journal, 2012, 10, 851-861.	8.3	74
60	Functional Knockout of the Adenosine 5â€²-Phosphosulfate Reductase Gene in Physcomitrella patens Revives an Old Route of Sulfate Assimilation. Journal of Biological Chemistry, 2002, 277, 32195-32201.	3.4	73
61	Moss bioreactors producing improved biopharmaceuticals. Current Opinion in Biotechnology, 2007, 18, 393-398.	6.6	73
62	Prediction of dual protein targeting to plant organelles. New Phytologist, 2009, 183, 224-236.	7.3	73
63	Cloning and characterization of an adenosine kinase fromPhyscomitrellainvolved in cytokinin metabolism. Plant Journal, 1998, 13, 249-257.	5.7	72
64	System for Stable Î²-Estradiol-Inducible Gene Expression in the Moss Physcomitrella patens. PLoS ONE, 2013, 8, e77356.	2.5	71
65	The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119.	27.8	70
66	Enhanced recovery of a secreted recombinant human growth factor using stabilizing additives and by co-expression of human serum albumin in the moss Physcomitrella patens. Plant Biotechnology Journal, 2005, 3, 331-340.	8.3	68
67	Involvement of a Class III Peroxidase and the Mitochondrial Protein TSPO in Oxidative Burst Upon Treatment of Moss Plants with a Fungal Elicitor. Molecular Plant-Microbe Interactions, 2012, 25, 363-371.	2.6	66
68	Expansins in the bryophyte Physcomitrella patens. Plant Molecular Biology, 2002, 50, 789-802.	3.9	65
69	ppdb: plant promoter database version 3.0. Nucleic Acids Research, 2014, 42, D1188-D1192.	14.5	61
70	Quantitative Analysis of the Mitochondrial and Plastid Proteomes of the Moss <i>Physcomitrella patens</i> Reveals Protein Macrocompartmentation and Microcompartmentation. Plant Physiology, 2014, 164, 2081-2095.	4.8	61
71	Best options for the exposure of traditional and innovative moss bags: A systematic evaluation in three European countries. Environmental Pollution, 2016, 214, 362-373.	7.5	61
72	Effects of nutrients, cell density and culture techniques on protoplast regeneration and early protonema development in a moss,Physcomitrella patens. Journal of Plant Physiology, 2003, 160, 209-212.	3.5	60

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73	Chloroplast FBPase and SBPase are thioredoxin-linked enzymes with similar architecture but different evolutionary histories. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6779-6784.	7.1	60
74	Expression of the bacterial ipt gene in Physcomitrella rescues mutations in budding and in plastid division. Planta, 1998, 206, 196-203.	3.2	59
75	THE SPECIATION HISTORY OF THE<i>PHYSCOMITRIUM-PHYSCOMITRELLA</i>SPECIES COMPLEX. Evolution; International Journal of Organic Evolution, 2010, 64, 217-231.	2.3	59
76	Glycoprotein production in moss bioreactors. Plant Cell Reports, 2012, 31, 453-460.	5.6	57
77	Isopentenyltransferase-1 (IPT1) knockout in Physcomitrella together with phylogenetic analyses of IPTs provide insights into evolution of plant cytokinin biosynthesis. Journal of Experimental Botany, 2014, 65, 2533-2543.	4.8	57
78	Dual targeting of plastid division protein FtsZ to chloroplasts and the cytoplasm. EMBO Reports, 2004, 5, 889-894.	4.5	56
79	Protein encoding genes in an ancient plant: analysis of codon usage, retained genes and splice sites in a moss, Physcomitrella patens. BMC Genomics, 2005, 6, 43.	2.8	56
80	Biosynthesis of C9-aldehydes in the moss Physcomitrella patensâ˜†. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2006, 1761, 301-312.	2.4	54
81	Simultaneous isolation of pure and intact chloroplasts and mitochondria from moss as the basis for sub-cellular proteomics. Plant Cell Reports, 2011, 30, 205-215.	5.6	53
82	A gene responsible for prolyl-hydroxylation of moss-produced recombinant human erythropoietin. Scientific Reports, 2013, 3, 3019.	3.3	50
83	Physcomitrella patens, a versatile synthetic biology chassis. Plant Cell Reports, 2018, 37, 1409-1417.	5.6	50
84	Loss of GH3 function does not affect phytochrome-mediated development in a moss, Physcomitrella patens. Journal of Plant Physiology, 2004, 161, 823-835.	3.5	49
85	Mitochondrial Dynamics and the ER: The Plant Perspective. Frontiers in Cell and Developmental Biology, 2015, 3, 78.	3.7	49
86	An efficient protocol for the identification of protein phosphorylation in a seedless plant, sensitive enough to detect members of signalling cascades. Electrophoresis, 2004, 25, 1149-1159.	2.4	48
87	PpASCL, a moss ortholog of antherâ€specific chalcone synthaseâ€like enzymes, is a hydroxyalkylpyrone synthase involved in an evolutionarily conserved sporopollenin biosynthesis pathway. New Phytologist, 2011, 192, 855-868.	7.3	48
88	Molecular evidence for convergent evolution and allopolyploid speciation within the Physcomitrium-Physcomitrellaspecies complex. BMC Evolutionary Biology, 2014, 14, 158.	3.2	48
89	High contents of very long-chain polyunsaturated fatty acids in different moss species. Plant Cell Reports, 2014, 33, 245-254.	5.6	48
90	Cloning and expression of the tobacco CHLM sequence encoding Mg protoporphyrin IX methyltransferase and its interaction with Mg chelatase. Plant Molecular Biology, 2005, 57, 679-691.	3.9	47

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91	Chloroplasts require glutathione reductase to balance reactive oxygen species and maintain efficient photosynthesis. Plant Journal, 2020, 103, 1140-1154.	5.7	47
92	DICER-LIKE3 Activity in Physcomitrella patens DICER-LIKE4 Mutants Causes Severe Developmental Dysfunction and Sterility. Molecular Plant, 2012, 5, 1281-1294.	8.3	45
93	DNA METHYLTRANSFERASE 1 is involved in mCG and mCCG DNA methylation and is essential for sporophyte development in Physcomitrella patens. Plant Molecular Biology, 2015, 88, 387-400.	3.9	45
94	Function of the HYDROXYCINNAMOYL-CoA:SHIKIMATE HYDROXYCINNAMOYL TRANSFERASE is evolutionarily conserved in embryophytes. Plant Cell, 2021, 33, 1472-1491.	6.6	45
95	Cytokinin affects nuclear- and plastome-encoded energy-converting plastid enzymes. Planta, 1997, 201, 261-272.	3.2	44
96	Rings and networks: the amazing complexity of FtsZ in chloroplasts. Trends in Plant Science, 2002, 7, 103-105.	8.8	44
97	Targeted Gene Knockouts Reveal Overlapping Functions of the Five Physcomitrella patens FtsZ Isoforms in Chloroplast Division, Chloroplast Shaping, Cell Patterning, Plant Development, and Gravity Sensing. Molecular Plant, 2009, 2, 1359-1372.	8.3	44
98	RecQ Helicases Function in Development, DNA Repair, and Gene Targeting in <i>Physcomitrella patens</i>. Plant Cell, 2018, 30, 717-736.	6.6	44
99	Moss-Produced, Glycosylation-Optimized Human Factor H for Therapeutic Application in Complement Disorders. Journal of the American Society of Nephrology: JASN, 2017, 28, 1462-1474.	6.1	43
100	A sequenceâ€anchored genetic linkage map for the moss, <i>Physcomitrella patens</i>. Plant Journal, 2008, 56, 855-866.	5.7	42
101	Clonal in vitro propagation of peat mosses (Sphagnum L.) as novel green resources for basic and applied research. Plant Cell, Tissue and Organ Culture, 2015, 120, 1037-1049.	2.3	42
102	Functional crossâ€kingdom conservation of mammalian and moss (<i>Physcomitrella patens</i>) transcription, translation and secretion machineries. Plant Biotechnology Journal, 2009, 7, 73-86.	8.3	41
103	Use of endogenous signal sequences for transient production and efficient secretion by moss (Physcomitrella patens) cells. BMC Biotechnology, 2005, 5, 30.	3.3	39
104	Biosynthesis of allene oxides in Physcomitrella patens. BMC Plant Biology, 2012, 12, 228.	3.6	39
105	Glyco-engineering for biopharmaceutical production in moss bioreactors. Frontiers in Plant Science, 2014, 5, 346.	3.6	39
106	Single-cell transcriptome analysis of Physcomitrella leaf cells during reprogramming using microcapillary manipulation. Nucleic Acids Research, 2019, 47, 4539-4553.	14.5	39
107	Mosses in biotechnology. Current Opinion in Biotechnology, 2020, 61, 21-27.	6.6	39
108	Dithiol disulphide exchange in redox regulation of chloroplast enzymes in response to evolutionary and structural constraints. Plant Science, 2017, 255, 1-11.	3.6	38

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109	Mapping of the Physcomitrella patens proteome. Phytochemistry, 2004, 65, 1589-1607.	2.9	37
110	EST Sequencing from Embryogenic Cyclamen persicum Cell Cultures Identifies a High Proportion of Transcripts Homologous to Plant Genes Involved in Somatic Embryogenesis. Journal of Plant Growth Regulation, 2005, 24, 102-115.	5.1	37
111	The Putative Moss 3â€²-Phosphoadenosine-5â€²-phosphosulfate Reductase Is a Novel Form of Adenosine-5â€²-phosphosulfate Reductase without an Iron-Sulfur Cluster. Journal of Biological Chemistry, 2007, 282, 22930-22938.	3.4	37
112	Cyclin D-knockout uncouples developmental progression from sugar availability. Plant Molecular Biology, 2003, 53, 227-236.	3.9	36
113	From axenic spore germination to molecular farming. Plant Cell Reports, 2005, 23, 513-521.	5.6	36
114	High-throughput-PCR screen of 15,000 transgenicPhyscomitrella plants. Plant Molecular Biology Reporter, 2002, 20, 43-47.	1.8	35
115	Spatioâ€temporal patterning of arginylâ€<scp>tRNA</scp> protein transferase (<scp>ATE</scp>) contributes to gametophytic development in a moss. New Phytologist, 2016, 209, 1014-1027.	7.3	35
116	Recombinant Spider Silk: Promises and Bottlenecks. Frontiers in Bioengineering and Biotechnology, 2022, 10, 835637.	4.1	35
117	A novel aspartic proteinase is targeted to the secretory pathway and to the vacuole in the moss Physcomitrella patens. European Journal of Cell Biology, 2004, 83, 145-152.	3.6	34
118	Metal and proton adsorption capacities of natural and cloned Sphagnum mosses. Journal of Colloid and Interface Science, 2016, 461, 326-334.	9.4	34
119	Diversification of fts Z During Early Land Plant Evolution. Journal of Molecular Evolution, 2004, 58, 154-162.	1.8	33
120	Isolation and characterisation of three moss-derived beta-tubulin promoters suitable for recombinant expression. Current Genetics, 2005, 47, 111-120.	1.7	33
121	Natural Products from Bryophytes: From Basic Biology to Biotechnological Applications. Critical Reviews in Plant Sciences, 2021, 40, 191-217.	5.7	33
122	Rapid Alteration of the Phosphoproteome in the MossPhyscomitrellapatensafter Cytokinin Treatment. Journal of Proteome Research, 2006, 5, 2283-2293.	3.7	32
123	A fast and flexible PEG-mediated transient expression system in plants for high level expression of secreted recombinant proteins. Journal of Biotechnology, 2005, 119, 332-342.	3.8	31
124	An Env-derived multi-epitope HIV chimeric protein produced in the moss Physcomitrella patens is immunogenic in mice. Plant Cell Reports, 2015, 34, 425-433.	5.6	31
125	Enabling the water-to-land transition. Nature Plants, 2018, 4, 67-68.	9.3	31
126	Convergence of sphingolipid desaturation across over 500 million years of plant evolution. Nature Plants, 2021, 7, 219-232.	9.3	31

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127	Filamentous temperatureâ€sensitive Z (FtsZ) isoforms specifically interact in the chloroplasts and in the cytosol of <i>Physcomitrella patens</i>. New Phytologist, 2007, 176, 299-310.	7.3	30
128	ABA-Induced Vegetative Diaspore Formation in Physcomitrella patens. Frontiers in Plant Science, 2019, 10, 315.	3.6	30
129	Effect of Ploidy Level on Growth, Differentiation, and Morphology in Physcomitrella patens. Bryologist, 2005, 108, 27-35.	0.6	29
130	<i>MicroRNA534a</i> control of <i>BLADEâ€ONâ€PETIOLE 1</i> and <i>2</i> mediates juvenileâ€toâ€adult gametophyte transition in <i>Physcomitrella patens</i>. Plant Journal, 2011, 65, 661-674.	5.7	29
131	Molecular and chemical characterization of a Sphagnum palustre clone: Key steps towards a standardized and sustainable moss bag technique. Ecological Indicators, 2016, 71, 388-397.	6.3	29
132	Sphagnum palustre clone vs native Pseudoscleropodium purum : A first trial in the field to validate the future of the moss bag technique. Environmental Pollution, 2017, 225, 323-328.	7.5	29
133	The MFHR1 Fusion Protein Is a Novel Synthetic Multitarget Complement Inhibitor with Therapeutic Potential. Journal of the American Society of Nephrology: JASN, 2018, 29, 1141-1153.	6.1	28
134	Axenic <i>in vitro</i> cultivation of 19 peat moss (<i>Sphagnum</i> L.) species as a resource for basic biology, biotechnology, and paludiculture. New Phytologist, 2021, 229, 861-876.	7.3	28
135	A large plant beta-tubulin family with minimal C-terminal variation but differences in expression. Gene, 2004, 340, 151-160.	2.2	27
136	Implications of plant glycans in the development of innovative vaccines. Expert Review of Vaccines, 2016, 15, 915-925.	4.4	26
137	Identification of Targets and Interaction Partners of Arginyl-tRNA Protein Transferase in the Moss Physcomitrella patens. Molecular and Cellular Proteomics, 2016, 15, 1808-1822.	3.8	25
138	Physcomitrella patens. Current Biology, 2004, 14, R261-R262.	3.9	24
139	The loss of SMG1 causes defects in quality control pathways in Physcomitrella patens. Nucleic Acids Research, 2018, 46, 5822-5836.	14.5	24
140	Recombinant Production of MFHR1, A Novel Synthetic Multitarget Complement Inhibitor, in Moss Bioreactors. Frontiers in Plant Science, 2019, 10, 260.	3.6	24
141	Dead end for auxin conjugates in Physcomitrella?. Plant Signaling and Behavior, 2009, 4, 116-118.	2.4	23
142	Moss (Physcomitrella patens) functional genomics -- Gene discovery and tool development, with implications for crop plants and human health. Briefings in Functional Genomics & Proteomics, 2005, 4, 48-57.	3.8	22
143	Challenges to our current view on chloroplasts. Biological Chemistry, 2009, 390, 731-738.	2.5	22
144	Overexpression of the Arabidopsis Gene <i>UPRIGHT ROSETTE</i> Reveals a Homeostatic Control for Indole-3-Acetic Acid Â Â. Plant Physiology, 2010, 153, 1311-1320.	4.8	22

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145	The relevance of compartmentation for cysteine synthesis in phototrophic organisms. Protoplasma, 2012, 249, 147-155.	2.1	22
146	Selfing in Haploid Plants and Efficacy of Selection: Codon Usage Bias in the Model Moss Physcomitrella patens. Genome Biology and Evolution, 2017, 9, 1528-1546.	2.5	21
147	Stable Protein Sialylation in Physcomitrella. Frontiers in Plant Science, 2020, 11, 610032.	3.6	21
148	The plastome-encoded zfpA gene of a moss contains procaryotic as well as eucaryotic promoter consensus sequences and its RNA abundance is modulated by cytokinin. Current Genetics, 1992, 22, 327-333.	1.7	20
149	Matrix solid phase dispersion method for determination of polycyclic aromatic hydrocarbons in moss. Journal of Chromatography A, 2015, 1406, 19-26.	3.7	20
150	Chemical and structural characterization of copper adsorbed on mosses (Bryophyta). Journal of Hazardous Materials, 2016, 308, 343-354.	12.4	20
151	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
152	Alternation of generations â€" unravelling the underlying molecular mechanism of a 165â€yearâ€old botanical observation. Plant Biology, 2016, 18, 549-551.	3.8	19
153	Host Cell Proteome of<i>Physcomitrella patens</i>Harbors Proteases and Protease Inhibitors under Bioproduction Conditions. Journal of Proteome Research, 2018, 17, 3749-3760.	3.7	19
154	Gene Targeting for Precision Glyco-Engineering: Production of Biopharmaceuticals Devoid of Plant-Typical Glycosylation in Moss Bioreactors. Methods in Molecular Biology, 2015, 1321, 213-224.	0.9	19
155	Targeted knockâ€out of a gene encoding sulfite reductase in the moss <i>Physcomitrella patens</i> affects gametophytic and sporophytic development. FEBS Letters, 2010, 584, 2271-2278.	2.8	18
156	The first analysed archegoniate mitochondrial gene (COX3) exhibits extraordinary features. Current Genetics, 1991, 20, 319-329.	1.7	17
157	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
158	The single berberine bridge enzyme homolog of <i>PhyscomitrellaÂpatens</i> is a cellobiose oxidase. FEBS Journal, 2018, 285, 1923-1943.	4.7	17
159	Quantitative moss cell biology. Current Opinion in Plant Biology, 2018, 46, 39-47.	7.1	17
160	Testing a novel biotechnological passive sampler for monitoring atmospheric PAH pollution. Journal of Hazardous Materials, 2020, 381, 120949.	12.4	17
161	Isolation of nuclear, chloroplast and mitochondrial DNA from the moss Physcomitrella patens. Plant Science, 1989, 61, 235-244.	3.6	16
162	Automated and semi-automated enhancement, segmentation and tracing of cytoskeletal networks in microscopic images: A review. Computational and Structural Biotechnology Journal, 2021, 19, 2106-2120.	4.1	16

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163	The role of the novel adenosine 5â€²-phosphosulfate reductase in regulation of sulfate assimilation of Physcomitrella patens. Plant Molecular Biology, 2007, 65, 667-676.	3.9	15
164	The potential ofPhyscomitrella patensas a platform for the production of plant-based vaccines. Expert Review of Vaccines, 2014, 13, 203-212.	4.4	15
165	Biosurface properties and lead adsorption in a clone of Sphagnum palustre (Mosses): Towards a unified protocol of biomonitoring of airborne heavy metal pollution. Chemosphere, 2019, 236, 124375.	8.2	15
166	Auxin-binding proteins without KDEL sequence in the moss Funaria hygrometrica. Plant Cell Reports, 2009, 28, 1747-1758.	5.6	14
167	Computational 3D imaging to quantify structural components and assembly of protein networks. Acta Biomaterialia, 2018, 69, 206-217.	8.3	14
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