

# Daniel Lang

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

10,993  
citations

81900

39  
h-index

118850

62  
g-index

70  
all docs

70  
docs citations

70  
times ranked

11902  
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
2	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	12.6	1,712
3	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
4	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
5	The <i>Chara</i> Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
6	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	406
7	Mass-spectrometry-based draft of the <i>Arabidopsis</i> proteome. <i>Nature</i> , 2020, 579, 409-414.	27.8	328
8	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
9	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	21.4	230
10	Genome-Wide Phylogenetic Comparative Analysis of Plant Transcriptional Regulation: A Timeline of Loss, Gain, Expansion, and Correlation with Complexity. <i>Genome Biology and Evolution</i> , 2010, 2, 488-503.	2.5	174
11	An ancient genome duplication contributed to the abundance of metabolic genes in the moss <i>Physcomitrella patens</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 130.	3.2	171
12	Reannotation and extended community resources for the genome of the non-seed plant <i>Physcomitrella patens</i> provide insights into the evolution of plant gene structures and functions. <i>BMC Genomics</i> , 2013, 14, 498.	2.8	170
13	A high-quality genome assembly of quinoa provides insights into the molecular basis of salt bladder-based salinity tolerance and the exceptional nutritional value. <i>Cell Research</i> , 2017, 27, 1327-1340.	12.0	170
14	Stomatal Guard Cells Co-opted an Ancient ABA-Dependent Desiccation Survival System to Regulate Stomatal Closure. <i>Current Biology</i> , 2015, 25, 928-935.	3.9	154
15	Origin and function of stomata in the moss <i>Physcomitrella patens</i> . <i>Nature Plants</i> , 2016, 2, 16179.	9.3	138
16	Exploring plant biodiversity: the <i>Physcomitrella</i> genome and beyond. <i>Trends in Plant Science</i> , 2008, 13, 542-549.	8.8	132
17	The Plant Ontology as a Tool for Comparative Plant Anatomy and Genomic Analyses. <i>Plant and Cell Physiology</i> , 2013, 54, e1-e1.	3.1	131
18	Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. <i>Science Advances</i> , 2018, 4, eaar8602.	10.3	130

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19	A P <sup>11B</sup> -type Ca <sup>2+</sup> -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
20	The evolution of nuclear auxin signalling. BMC Evolutionary Biology, 2009, 9, 126.	3.2	115
21	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. Plant Journal, 2018, 95, 168-182.	5.7	115
22	Microarray analysis of the moss <i>Physcomitrella patens</i> reveals evolutionarily conserved transcriptional regulation of salt stress and abscisic acid signalling. Plant Molecular Biology, 2010, 72, 27-45.	3.9	110
23	Day Length and Temperature Strongly Influence Sexual Reproduction and Expression of a Novel MADS-Box Gene in the Moss <i>Physcomitrella patens</i> . Plant Biology, 2002, 4, 595-602.	3.8	105
24	Dating the early evolution of plants: detection and molecular clock analyses of orthologs. Molecular Genetics and Genomics, 2007, 278, 393-402.	2.1	103
25	Emerging functions for plant MAP kinase phosphatases. Trends in Plant Science, 2010, 15, 322-329.	8.8	101
26	Genetic analysis of <i>Physcomitrella patens</i> 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
27	Phylogenomic analysis of gene expression networks reveals the evolution of functional modules. Plant Journal, 2017, 90, 447-465.	5.7	97
28	Representation and High-Quality Annotation of the <i>Physcomitrella patens</i> Transcriptome Demonstrates a High Proportion of Proteins Involved in Metabolism in Mosses. Plant Biology, 2005, 7, 238-250.	3.8	96
29	Insights from the cold transcriptome of <i>Physcomitrella 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
30	Large-scale gene expression profiling data for the model moss <i>Physcomitrella patens</i> aid understanding of developmental progression, culture and stress conditions. Plant Journal, 2014, 79, 530-539.	5.7	82
31	PlanTAPDB, a Phylogeny-Based Resource of Plant Transcription-Associated Proteins. Plant Physiology, 2007, 143, 1452-1466.	4.8	79
32	The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119.	27.8	70
33	ppdb: plant promoter database version 3.0. Nucleic Acids Research, 2014, 42, D1188-D1192.	14.5	61
34	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
35	Isopentenyltransferase-1 (IPT1) knockout in <i>Physcomitrella</i> 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
36	Protein encoding genes in an ancient plant: analysis of codon usage, retained genes and splice sites in a moss, <i>Physcomitrella patens</i> . BMC Genomics, 2005, 6, 43.	2.8	56

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37	Generation-Biased Gene Expression in a Bryophyte Model System. <i>Molecular Biology and Evolution</i> , 2011, 28, 803-812.	8.9	49
38	Large-scale Analysis of 73 329 <i>Physcomitrella</i> Plants Transformed with Different Gene Disruption Libraries: Production Parameters and Mutant Phenotypes. <i>Plant Biology</i> , 2005, 7, 228-237.	3.8	45
39	Targeted Gene Knockouts Reveal Overlapping Functions of the Five <i>Physcomitrella patens</i> FtsZ Isoforms in Chloroplast Division, Chloroplast Shaping, Cell Patterning, Plant Development, and Gravity Sensing. <i>Molecular Plant</i> , 2009, 2, 1359-1372.	8.3	44
40	A sequence-anchored genetic linkage map for the moss, <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2008, 56, 855-866.	5.7	42
41	Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.	5.5	41
42	Single-cell transcriptome analysis of <i>Physcomitrella</i> leaf cells during reprogramming using microcapillary manipulation. <i>Nucleic Acids Research</i> , 2019, 47, 4539-4553.	14.5	39
43	EST Sequencing from Embryogenic <i>Cyclamen persicum</i> Cell Cultures Identifies a High Proportion of Transcripts Homologous to Plant Genes Involved in Somatic Embryogenesis. <i>Journal of Plant Growth Regulation</i> , 2005, 24, 102-115.	5.1	37
44	Spatio-temporal patterning of arginyl-tRNA protein transferase ( <i>ATE</i> ) contributes to gametophytic development in a moss. <i>New Phytologist</i> , 2016, 209, 1014-1027.	7.3	35
45	Identification of Targets and Interaction Partners of Arginyl-tRNA Protein Transferase in the Moss <i>Physcomitrella patens</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1808-1822.	3.8	25
46	The loss of SMG1 causes defects in quality control pathways in <i>Physcomitrella patens</i> . <i>Nucleic Acids Research</i> , 2018, 46, 5822-5836.	14.5	24
47	The Evolution of Transcriptional Regulation in the Viridiplantae and its Correlation with Morphological Complexity. <i>Advances in Marine Genomics</i> , 2015, , 301-333.	1.2	23
48	Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.	3.6	22
49	Selfing in Haploid Plants and Efficacy of Selection: Codon Usage Bias in the Model Moss <i>Physcomitrella patens</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1528-1546.	2.5	21
50	A uniquely high number of <i>ftsZ</i> genes in the moss <i>Physcomitrella patens</i> . <i>Plant Biology</i> , 2009, 11, 744-750.	3.8	20
51	Proteomic and transcriptomic profiling of aerial organ development in <i>Arabidopsis</i> . <i>Scientific Data</i> , 2020, 7, 334.	5.3	20
52	Predicted protein-protein interactions in the moss <i>Physcomitrella patens</i> : a new bioinformatic resource. <i>BMC Bioinformatics</i> , 2015, 16, 89.	2.6	19
53	Host Cell Proteome of <i>Physcomitrella patens</i> Harbors Proteases and Protease Inhibitors under Bioproduction Conditions. <i>Journal of Proteome Research</i> , 2018, 17, 3749-3760.	3.7	19
54	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18

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55	The Polycomb group protein CLF emerges as a specific tri-methylase of H3K27 regulating gene expression and development in <i>Physcomitrella patens</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 860-870.	1.9	17
56	Auxin-binding proteins without KDEL sequence in the moss <i>Funaria hygrometrica</i> . <i>Plant Cell Reports</i> , 2009, 28, 1747-1758.	5.6	14
57	Evolutionary Importance of Generative Polyploidy for Genome Evolution of Haploid-Dominant Land Plants. , 2013, , 295-305.		14
58	Identification and characterization of NAGNAG alternative splicing in the moss <i>Physcomitrella patens</i> . <i>BMC Plant Biology</i> , 2010, 10, 76.	3.6	13
59	Analysis of Stress Resistance Using Next Generation Techniques. <i>Agronomy</i> , 2018, 8, 130.	3.0	12
60	The Genome of the Model Moss <i>Physcomitrella patens</i> . <i>Advances in Botanical Research</i> , 2016, 78, 97-140.	1.1	9
61	Comparative Genomics. , 0, , 42-75.		4
62	Evolutionary Processes as Models for Exploratory Design. <i>Biologically-inspired Systems</i> , 2016, , 295-318.	0.2	3
63	TSSi€”an R package for transcription start site identification from 5â€² mRNA tag data. <i>Bioinformatics</i> , 2012, 28, 1641-1642.	4.1	2
64	Correction for Qudeimat et al., A P<sub>II</sub>-type Ca<sup>2+</sup>-ATPase is essential for stress adaptation in <i>Physcomitrella patens</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18566-18566.	7.1	1
65	Evolutionary approaches to explorative design methods in architecture. , 2019, , 134-141.		0