

# 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  | The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.   | 27.8 | 70        |
| 2  | The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.   | 27.8 | 314       |
| 3  | Proteomic and transcriptomic profiling of aerial organ development in <i>Arabidopsis</i> . <i>Scientific Data</i> , 2020, 7, 334.   | 5.3  | 20        |
| 4  | Mass-spectrometry-based draft of the <i>Arabidopsis</i> proteome. <i>Nature</i> , 2020, 579, 409-414.   | 27.8 | 328       |
| 5  | Detecting Large Chromosomal Modifications Using Short Read Data From Genotyping-by-Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 1133.                                      | 3.6  | 22        |
| 6  | Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.  | 21.4 | 230       |
| 7  | 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        |
| 8  | Evolutionary approaches to explorative design methods in architecture. , 2019, , 134-141.   |      | 0         |
| 9  | The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , 2018, 95, 168-182.   | 5.7  | 115       |
| 10 | 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        |
| 11 | 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       |
| 12 | Analysis of Stress Resistance Using Next Generation Techniques. <i>Agronomy</i> , 2018, 8, 130.   | 3.0  | 12        |
| 13 | 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        |
| 14 | The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.   | 28.9 | 420       |
| 15 | Genome mapping of seed-borne allergens and immunoresponsive proteins in wheat. <i>Science Advances</i> , 2018, 4, eaar8602.   | 10.3 | 130       |
| 16 | The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .   | 12.6 | 768       |
| 17 | Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .  | 12.6 | 2,424     |
| 18 | Hidden variation in polyploid wheat drives local adaptation. <i>Genome Research</i> , 2018, 28, 1319-1332.  | 5.5  | 41        |

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|----|---|------|-----------|
| 19 | Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017, 90, 447-465.   | 5.7  | 97        |
| 20 | 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       |
| 21 | 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        |
| 22 | Spatio-temporal patterning of arginyl-tRNA protein transferase (<sc>ATE</sc>) contributes to gametophytic development in a moss. <i>New Phytologist</i> , 2016, 209, 1014-1027.   | 7.3  | 35        |
| 23 | 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        |
| 24 | 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        |
| 25 | Origin and function of stomata in the moss <i>Physcomitrella patens</i> . <i>Nature Plants</i> , 2016, 2, 16179.  | 9.3  | 138       |
| 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. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.            | 6.6  | 98        |
| 27 | The Genome of the Model Moss <i>Physcomitrella patens</i> . <i>Advances in Botanical Research</i> , 2016, 78, 97-140.   | 1.1  | 9         |
| 28 | Evolutionary Processes as Models for Exploratory Design. <i>Biologically-inspired Systems</i> , 2016, , 295-318.  | 0.2  | 3         |
| 29 | 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        |
| 30 | 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       |
| 31 | 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. <i>New Phytologist</i> , 2015, 205, 869-881. | 7.3  | 84        |
| 32 | 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        |
| 33 | ppdb: plant promoter database version 3.0. <i>Nucleic Acids Research</i> , 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. <i>Plant Physiology</i> , 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. <i>Journal of Experimental Botany</i> , 2014, 65, 2533-2543.               | 4.8  | 57        |
| 36 | Large-scale gene expression profiling data for the model moss <i>Physcomitrella patens</i> aid understanding of developmental progression, culture and stress conditions. <i>Plant Journal</i> , 2014, 79, 530-539.                                       | 5.7  | 82        |

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|----|---|------|-----------|
| 37 | 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       |
| 38 | Evolutionary Importance of Generative Polyploidy for Genome Evolution of Haploid-Dominant Land Plants. , 2013, , 295-305.   |      | 14        |
| 39 | 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       |
| 40 | 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         |
| 41 | The Ectocarpus Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.  | 1.1  | 18        |
| 42 | 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         |
| 43 | Generation-Biased Gene Expression in a Bryophyte Model System. <i>Molecular Biology and Evolution</i> , 2011, 28, 803-812.  | 8.9  | 49        |
| 44 | 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       |
| 45 | Microarray analysis of the moss <i>Physcomitrella patens</i> reveals evolutionarily conserved transcriptional regulation of salt stress and abscisic acid signalling. <i>Plant Molecular Biology</i> , 2010, 72, 27-45.   | 3.9  | 110       |
| 46 | 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        |
| 47 | The Ectocarpus genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.   | 27.8 | 774       |
| 48 | Emerging functions for plant MAP kinase phosphatases. <i>Trends in Plant Science</i> , 2010, 15, 322-329.   | 8.8  | 101       |
| 49 | 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        |
| 50 | The evolution of nuclear auxin signalling. <i>BMC Evolutionary Biology</i> , 2009, 9, 126.  | 3.2  | 115       |
| 51 | 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        |
| 52 | A uniquely high number of <i>fts</i>Z genes in the moss <i>Physcomitrella patens</i>. <i>Plant Biology</i> , 2009, 11, 744-750.   | 3.8  | 20        |
| 53 | Exploring plant biodiversity: the <i>Physcomitrella</i> genome and beyond. <i>Trends in Plant Science</i> , 2008, 13, 542-549.  | 8.8  | 132       |
| 54 | 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     |

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|----|--|-----|-----------|
| 55 | A sequence-anchored genetic linkage map for the moss, <i>Physcomitrella patens</i> . Plant Journal, 2008, 56, 855-866.   | 5.7 | 42        |
| 56 | A P-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       |
| 57 | PlantAPDB, a Phylogeny-Based Resource of Plant Transcription-Associated Proteins. Plant Physiology, 2007, 143, 1452-1466.  | 4.8 | 79        |
| 58 | An ancient genome duplication contributed to the abundance of metabolic genes in the moss <i>Physcomitrella patens</i> . BMC Evolutionary Biology, 2007, 7, 130.   | 3.2 | 171       |
| 59 | Dating the early evolution of plants: detection and molecular clock analyses of orthologs. Molecular Genetics and Genomics, 2007, 278, 393-402.  | 2.1 | 103       |
| 60 | 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        |
| 61 | Large-scale Analysis of 73 329 <i>Physcomitrella</i> Plants Transformed with Different Gene Disruption Libraries: Production Parameters and Mutant Phenotypes. Plant Biology, 2005, 7, 228-237.  | 3.8 | 45        |
| 62 | 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        |
| 63 | EST Sequencing from Embryogenic <i>Cyclamen persicum</i> 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        |
| 64 | 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       |
| 65 | Comparative Genomics. , 0, , 42-75.  |     | 4         |