

Nicholas J Provart

List of Publications by Year in descending order

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99
papers

14,100
citations

66234

42
h-index

34900

98
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112
all docs

112
docs citations

112
times ranked

16949
citing authors

#	ARTICLE	IF	CITATIONS
1	Abscisic Acid Inhibits Type 2C Protein Phosphatases via the PYR/PYL Family of START Proteins. <i>Science</i> , 2009, 324, 1068-1071.	6.0	2,385
2	An "Electronic Fluorescent Pictograph" Browser for Exploring and Analyzing Large-Scale Biological Data Sets. <i>PLoS ONE</i> , 2007, 2, e718.	1.1	2,236
3	Expression Profile Matrix of Arabidopsis Transcription Factor Genes Suggests Their Putative Functions in Response to Environmental Stresses[W]. <i>Plant Cell</i> , 2002, 14, 559-574.	3.1	849
4	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
5	The Botany Array Resource: e-Northern, Expression Angling, and promoter analyses. <i>Plant Journal</i> , 2005, 43, 153-163.	2.8	707
6	The developmental dynamics of the maize leaf transcriptome. <i>Nature Genetics</i> , 2010, 42, 1060-1067.	9.4	660
7	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , 2009, 32, 1633-1651.	2.8	480
8	Expansion and Diversification of the <i>Populus</i> R2R3-MYB Family of Transcription Factors. <i>Plant Physiology</i> , 2009, 149, 981-993.	2.3	450
9	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , 2017, 29, 1806-1821.	3.1	316
10	A Predicted Interactome for Arabidopsis. <i>Plant Physiology</i> , 2007, 145, 317-329.	2.3	285
11	Next-generation mapping of Arabidopsis genes. <i>Plant Journal</i> , 2011, 67, 715-725.	2.8	284
12	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. <i>Nature</i> , 2018, 553, 342-346.	13.7	241
13	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014, 32, 1158-1165.	9.4	228
14	Genome-wide network model capturing seed germination reveals coordinated regulation of plant cellular phase transitions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9709-9714.	3.3	210
15	50 years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016, 209, 921-944.	3.5	186
16	AtMetExpress Development: A Phytochemical Atlas of Arabidopsis Development. <i>Plant Physiology</i> , 2010, 152, 566-578.	2.3	161
17	High Temporal-Resolution Transcriptome Landscape of Early Maize Seed Development. <i>Plant Cell</i> , 2019, 31, 974-992.	3.1	141
18	Gene Expression Phenotypes of Arabidopsis Associated with Sensitivity to Low Temperatures. <i>Plant Physiology</i> , 2003, 132, 893-906.	2.3	135

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19	Transcriptional control of nutrient partitioning during rice grain filling. <i>Plant Biotechnology Journal</i> , 2002, 1, 59-70.	4.1	131
20	Cloning and sequence comparison of the mouse, human, and chicken engrailed genes reveal potential functional domains and regulatory regions. <i>Genesis</i> , 1992, 13, 345-358.	3.1	124
21	Genotype and time of day shape the <i>Populus</i> drought response. <i>Plant Journal</i> , 2009, 60, 703-715.	2.8	123
22	Inference of Longevity-Related Genes from a Robust Coexpression Network of Seed Maturation Identifies Regulators Linking Seed Storability to Biotic Defense-Related Pathways. <i>Plant Cell</i> , 2015, 27, tpc.15.00632.	3.1	116
23	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , 2019, 97, 1154-1167.	2.8	114
24	A Mesoscale Abscisic Acid Hormone Interactome Reveals a Dynamic Signaling Landscape in Arabidopsis. <i>Developmental Cell</i> , 2014, 29, 360-372.	3.1	109
25	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in <i>Brachypodium distachyon</i> . <i>New Phytologist</i> , 2017, 215, 1009-1025.	3.5	108
26	Elucidating the Germination Transcriptional Program Using Small Molecules. <i>Plant Physiology</i> , 2008, 147, 143-155.	2.3	104
27	BAR expressolog identification: expression profile similarity ranking of homologous genes in plant species. <i>Plant Journal</i> , 2012, 71, 1038-1050.	2.8	102
28	Web-Queryable Large-Scale Data Sets for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , 2009, 21, 1034-1051.	3.1	101
29	The Re-Establishment of Desiccation Tolerance in Germinated Arabidopsis thaliana Seeds and Its Associated Transcriptome. <i>PLoS ONE</i> , 2011, 6, e29123.	1.1	100
30	A gene expression map of shoot domains reveals regulatory mechanisms. <i>Nature Communications</i> , 2019, 10, 141.	5.8	96
31	ccNET: Database of co-expression networks with functional modules for diploid and polyploid <i>Gossypium</i> . <i>Nucleic Acids Research</i> , 2017, 45, D1090-D1099.	6.5	89
32	Embryogenesis: Pattern Formation from a Single Cell. <i>The Arabidopsis Book</i> , 2009, 7, e0126.	0.5	85
33	Potato guard cells respond to drying soil by a complex change in the expression of genes related to carbon metabolism and turgor regulation. <i>Plant Journal</i> , 1997, 11, 871-882.	2.8	83
34	Analysis of Gene Expression Patterns during Seed Coat Development in Arabidopsis. <i>Molecular Plant</i> , 2011, 4, 1074-1091.	3.9	83
35	Incipient stem cell niche conversion in tissue culture: using a systems approach to probe early events in <i>WUSCHEL</i> -dependent conversion of lateral root primordia into shoot meristems. <i>Plant Journal</i> , 2013, 73, 798-813.	2.8	80
36	New BAR tools for mining expression data and exploring Cis-elements in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 490-504.	2.8	75

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37	Changes in stomatal function and water use efficiency in potato plants with altered sucrolytic activity. <i>Plant, Cell and Environment</i> , 2012, 35, 747-759.	2.8	65
38	A Comprehensive Expression Analysis of the Arabidopsis Proline-rich Extensin-like Receptor Kinase Gene Family using Bioinformatic and Experimental Approaches. <i>Plant and Cell Physiology</i> , 2004, 45, 1875-1881.	1.5	63
39	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . <i>Plant Journal</i> , 2016, 88, 879-894.	2.8	60
40	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , 2020, 32, 833-852.	3.1	60
41	Regulation of Cell Type-Specific Immunity Networks in Arabidopsis Roots. <i>Plant Cell</i> , 2020, 32, 2742-2762.	3.1	59
42	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. <i>Plant Cell</i> , 2019, 31, 2888-2911.	3.1	57
43	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , 2021, 184, 3333-3348.e19.	13.5	48
44	Forward and reverse genetics to identify genes involved in the age-related resistance response in <i>Arabidopsis thaliana</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 621-634.	2.0	46
45	Tung Tree (<i>Vernicia fordii</i>) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 558-575.	3.0	43
46	ePlant and the 3D Data Display Initiative: Integrative Systems Biology on the World Wide Web. <i>PLoS ONE</i> , 2011, 6, e15237.	1.1	43
47	An <i>eFP</i> Browser™ for visualizing and exploring <i>RNA</i> sequencing data. <i>Plant Journal</i> , 2019, 100, 641-654.	2.8	41
48	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012, 40, D1250-D1254.	6.5	40
49	RNA-Seq effectively monitors gene expression in <i>Eutrema salsugineum</i> plants growing in an extreme natural habitat and in controlled growth cabinet conditions. <i>BMC Genomics</i> , 2013, 14, 578.	1.2	40
50	Nod factors potentiate auxin signaling for transcriptional regulation and lateral root formation in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2017, 68, erw474.	2.4	40
51	Expression Atlas of <i>Selaginella moellendorffii</i> Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. <i>Plant Cell</i> , 2020, 32, 853-870.	3.1	39
52	Characterization of pea chloroplastic carbonic anhydrase. Expression in <i>Escherichia coli</i> and site-directed mutagenesis. <i>Plant Molecular Biology</i> , 1993, 22, 937-943.	2.0	37
53	The Bio-Analytic Resource for Plant Biology. <i>Methods in Molecular Biology</i> , 2017, 1533, 119-148.	0.4	36
54	An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. <i>Communications Biology</i> , 2020, 3, 145.	2.0	36

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55	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019, 179, 1893-1907.	2.3	34
56	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
57	Multiple Horizontal Gene Transfer Events and Domain Fusions Have Created Novel Regulatory and Metabolic Networks in the Oomycete Genome. <i>PLoS ONE</i> , 2009, 4, e6133.	1.1	32
58	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	2.8	31
59	Functional annotation of the Arabidopsis P450 superfamily based on large-scale co-expression analysis. <i>Biochemical Society Transactions</i> , 2006, 34, 1192-1198.	1.6	30
60	Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. <i>Plant Cell</i> , 2020, 32, 2683-2686.	3.1	28
61	Systems approaches to understanding cell signaling and gene regulation. <i>Current Opinion in Plant Biology</i> , 2004, 7, 605-609.	3.5	27
62	Polymerization of Glucans by Enzymatically Active Membranes. <i>Biotechnology Progress</i> , 2002, 18, 964-968.	1.3	24
63	Correlation networks visualization. <i>Frontiers in Plant Science</i> , 2012, 3, 240.	1.7	24
64	Regulation of Root Angle and Gravitropism. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3841-3855.	0.8	24
65	Transcriptional responses to low temperature and their regulation in Arabidopsis. <i>Canadian Journal of Botany</i> , 2003, 81, 1168-1174.	1.2	22
66	Developmental transcriptional profiling reveals key insights into <i>Triticaceae</i> reproductive development. <i>Plant Journal</i> , 2013, 74, 971-988.	2.8	22
67	BlastDigester – a web-based program for efficient CAPS marker design. <i>Trends in Genetics</i> , 2004, 20, 280-283.	2.9	20
68	Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , 2017, 68, 2175-2185.	2.4	19
69	A gene expression atlas for kiwifruit (<i>Actinidia chinensis</i>) and network analysis of transcription factors. <i>BMC Plant Biology</i> , 2021, 21, 121.	1.6	18
70	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. <i>Plant Journal</i> , 2021, 107, 287-302.	2.8	18
71	The Bio-Analytic Resource: Data visualization and analytic tools for multiple levels of plant biology. <i>Current Plant Biology</i> , 2016, 7-8, 2-5.	2.3	17
72	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. <i>Scientific Data</i> , 2019, 6, 190025.	2.4	17

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73	Evolutionary divergence in embryo and seed coat development of U TM s Triangle <i>Brassica</i> species illustrated by a spatiotemporal transcriptome atlas. <i>New Phytologist</i> , 2022, 233, 30-51.	3.5	16
74	Gene co-expression analysis of tomato seed maturation reveals tissue-specific regulatory networks and hubs associated with the acquisition of desiccation tolerance and seed vigour. <i>BMC Plant Biology</i> , 2021, 21, 124.	1.6	15
75	Extreme breeding: Leveraging genomics for crop improvement. <i>Journal of the Science of Food and Agriculture</i> , 2007, 87, 925-929.	1.7	14
76	New Insights into <i>Dehalococcoides mccartyi</i> Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of <i>D. mccartyi</i> Transcriptomes. <i>PLoS ONE</i> , 2014, 9, e94808.	1.1	14
77	<i>Arabidopsis</i> bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	0.8	14
78	A comparative genomic analysis of ESTs from <i>Ustilago maydis</i> . <i>Functional and Integrative Genomics</i> , 2004, 4, 207-18.	1.4	13
79	Current status of the multinational <i>Arabidopsis</i> community. <i>Plant Direct</i> , 2020, 4, e00248.	0.8	13
80	The red flower wintersweet genome provides insights into the evolution of magnoliids and the molecular mechanism for tepal color development. <i>Plant Journal</i> , 2021, 108, 1662-1678.	2.8	12
81	The Next Generation of Training for <i>Arabidopsis</i> Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	2.3	11
82	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	3.3	11
83	Anno genominis XX: 20 years of <i>Arabidopsis</i> genomics. <i>Plant Cell</i> , 2021, 33, 832-845.	3.1	11
84	Sequence analysis and regulation of expression of a gene coding for carbonic anhydrase in <i>Chlamydomonas reinhardtii</i> . <i>Canadian Journal of Botany</i> , 1991, 69, 1097-1102.	1.2	10
85	A Human "eFP" Browser for Generating Gene Expression Anatograms. <i>PLoS ONE</i> , 2016, 11, e0150982.	1.1	10
86	<i>Arabidopsis</i> bioinformatics: tools and strategies. <i>Plant Journal</i> , 2021, 108, 1585-1596.	2.8	9
87	Gene Slider: sequence logo interactive data-visualization for education and research. <i>Bioinformatics</i> , 2016, 32, 3670-3672.	1.8	8
88	Elevated tyrosine results in the cytosolic retention of 3 ^{deoxy} carabinoheptulosonate 7 ^{phosphate} synthase in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2022, 109, 789-803.	2.8	7
89	Bioinformatic Tools in <i>Arabidopsis</i> Research. <i>Methods in Molecular Biology</i> , 2014, 1062, 97-136.	0.4	6
90	Analyses of Protein Interaction Networks Using Computational Tools. <i>Methods in Molecular Biology</i> , 2018, 1794, 97-117.	0.4	6

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91	Editorial: Resistance to Salinity and Water Scarcity in Higher Plants. Insights From Extremophiles and Stress-Adapted Plants: Tools, Discoveries and Future Prospects. <i>Frontiers in Plant Science</i> , 2019, 10, 373.	1.7	6
92	Gene Expression Analyses for Elucidating Mechanisms of Hormonal Action in Plants. <i>Methods in Molecular Biology</i> , 2009, 495, 21-37.	0.4	4
93	Topo-phylogeny: Visualizing evolutionary relationships on a topographic landscape. <i>PLoS ONE</i> , 2017, 12, e0175895.	1.1	4
94	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , 2021, 2200, 25-89.	0.4	4
95	Bioinformatics Tools to Discover Co-Expressed Genes in Plants. , 0, , 307-335.		1
96	Seed Bioinformatics. <i>Methods in Molecular Biology</i> , 2011, 773, 403-419.	0.4	1
97	First Plant Cell Atlas symposium report. <i>Plant Direct</i> , 2022, 6, .	0.8	1
98	Developments in plant and animal genome research. <i>Journal of the Science of Food and Agriculture</i> , 2004, 84, 743-744.	1.7	0
99	An Evaluation of Interaction Methods for Controlling RSVP Displays in Visual Search Tasks. , 2016, , .		0