

# Nicholas J Provart

## List of Publications by Citations

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96  
papers

10,345  
citations

38  
h-index

101  
g-index

112  
ext. papers

12,792  
ext. citations

9.2  
avg. IF

5.67  
L-index

#	Paper	IF	Citations
96	An "Electronic Fluorescent Pictograph" browser for exploring and analyzing large-scale biological data sets. <i>PLoS ONE</i> , <b>2007</b> , 2, e718	3.7	1796
95	Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. <i>Science</i> , <b>2009</b> , 324, 1068-71	33.3	1782
94	Expression profile matrix of Arabidopsis transcription factor genes suggests their putative functions in response to environmental stresses. <i>Plant Cell</i> , <b>2002</b> , 14, 559-74	11.6	732
93	The Botany Array Resource: e-Northern, Expression Angling, and promoter analyses. <i>Plant Journal</i> , <b>2005</b> , 43, 153-63	6.9	587
92	The developmental dynamics of the maize leaf transcriptome. <i>Nature Genetics</i> , <b>2010</b> , 42, 1060-7	36.3	550
91	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , <b>2009</b> , 32, 1633-51	8.4	373
90	The transcriptional landscape of polyploid wheat. <i>Science</i> , <b>2018</b> , 361,	33.3	368
89	Expansion and diversification of the Populus R2R3-MYB family of transcription factors. <i>Plant Physiology</i> , <b>2009</b> , 149, 981-93	6.6	346
88	A predicted interactome for Arabidopsis. <i>Plant Physiology</i> , <b>2007</b> , 145, 317-29	6.6	233
87	Next-generation mapping of Arabidopsis genes. <i>Plant Journal</i> , <b>2011</b> , 67, 715-25	6.9	228
86	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> , <b>2011</b> , 108, 9709-14	11.5	177
85	Comparative analyses of C <sub>3</sub> and C <sub>4</sub> photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 1158-65	44.5	160
84	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , <b>2017</b> , 29, 1806-1821	11.6	150
83	AtMetExpress development: a phytochemical atlas of Arabidopsis development. <i>Plant Physiology</i> , <b>2010</b> , 152, 566-78	6.6	149
82	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. <i>Nature</i> , <b>2018</b> , 553, 342-346	50.4	137
81	50 years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , <b>2016</b> , 209, 921-44	9.8	128
80	Gene expression phenotypes of Arabidopsis associated with sensitivity to low temperatures. <i>Plant Physiology</i> , <b>2003</b> , 132, 893-906	6.6	120

79	Transcriptional control of nutrient partitioning during rice grain filling. <i>Plant Biotechnology Journal</i> , <b>2003</b> , 1, 59-70	11.6	120
78	Genotype and time of day shape the Populus drought response. <i>Plant Journal</i> , <b>2009</b> , 60, 703-15	6.9	109
77	Cloning and sequence comparison of the mouse, human, and chicken engrailed genes reveal potential functional domains and regulatory regions. <i>Genesis</i> , <b>1992</b> , 13, 345-58		105
76	Web-queryable large-scale data sets for hypothesis generation in plant biology. <i>Plant Cell</i> , <b>2009</b> , 21, 1034-51	11.6	98
75	Elucidating the germination transcriptional program using small molecules. <i>Plant Physiology</i> , <b>2008</b> , 147, 143-55	6.6	89
74	A mesoscale abscisic acid hormone interactome reveals a dynamic signaling landscape in Arabidopsis. <i>Developmental Cell</i> , <b>2014</b> , 29, 360-72	10.2	83
73	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> , <b>2015</b> , 27, 2692-708	11.6	80
72	The re-establishment of desiccation tolerance in germinated Arabidopsis thaliana seeds and its associated transcriptome. <i>PLoS ONE</i> , <b>2011</b> , 6, e29123	3.7	79
71	BAR expressolog identification: expression profile similarity ranking of homologous genes in plant species. <i>Plant Journal</i> , <b>2012</b> , 71, 1038-50	6.9	78
70	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> , <b>1997</b> , 11, 871-82	6.9	78
69	Analysis of gene expression patterns during seed coat development in Arabidopsis. <i>Molecular Plant</i> , <b>2011</b> , 4, 1074-91	14.4	66
68	Incipient stem cell niche conversion in tissue culture: using a systems approach to probe early events in WUSCHEL-dependent conversion of lateral root primordia into shoot meristems. <i>Plant Journal</i> , <b>2013</b> , 73, 798-813	6.9	65
67	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in Brachypodium distachyon. <i>New Phytologist</i> , <b>2017</b> , 215, 1009-1029	9.8	60
66	Embryogenesis: pattern formation from a single cell. <i>The Arabidopsis Book</i> , <b>2009</b> , 7, e0126	3	59
65	A gene expression map of shoot domains reveals regulatory mechanisms. <i>Nature Communications</i> , <b>2019</b> , 10, 141	17.4	58
64	High Temporal-Resolution Transcriptome Landscape of Early Maize Seed Development. <i>Plant Cell</i> , <b>2019</b> , 31, 974-992	11.6	55
63	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , <b>2019</b> , 97, 1154-1167	6.9	54
62	Changes in stomatal function and water use efficiency in potato plants with altered sucrolytic activity. <i>Plant, Cell and Environment</i> , <b>2012</b> , 35, 747-59	8.4	51

61	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> , <b>2004</b> , 45, 1875-81	4.9	47
60	ccNET: Database of co-expression networks with functional modules for diploid and polyploid <i>Gossypium</i> . <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D1090-D1099	20.1	42
59	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . <i>Plant Journal</i> , <b>2016</b> , 88, 879-894	6.9	42
58	Forward and reverse genetics to identify genes involved in the age-related resistance response in <i>Arabidopsis thaliana</i> . <i>Molecular Plant Pathology</i> , <b>2009</b> , 10, 621-34	5.7	38
57	New BAR tools for mining expression data and exploring Cis-elements in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , <b>2016</b> , 88, 490-504	6.9	36
56	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> , <b>2013</b> , 14, 578	4.5	35
55	Characterization of pea chloroplastic carbonic anhydrase. Expression in <i>Escherichia coli</i> and site-directed mutagenesis. <i>Plant Molecular Biology</i> , <b>1993</b> , 22, 937-43	4.6	33
54	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D1250-4	20.1	31
53	ePlant and the 3D data display initiative: integrative systems biology on the world wide web. <i>PLoS ONE</i> , <b>2011</b> , 6, e15237	3.7	31
52	Multiple horizontal gene transfer events and domain fusions have created novel regulatory and metabolic networks in the oomycete genome. <i>PLoS ONE</i> , <b>2009</b> , 4, e6133	3.7	30
51	Nod factors potentiate auxin signaling for transcriptional regulation and lateral root formation in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , <b>2017</b> , 68, 569-583	7	29
50	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , <b>2020</b> , 32, 833-852	11.6	28
49	The Bio-Analytic Resource for Plant Biology. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1533, 119-148	1.4	27
48	Functional annotation of the Arabidopsis P450 superfamily based on large-scale co-expression analysis. <i>Biochemical Society Transactions</i> , <b>2006</b> , 34, 1192-8	5.1	27
47	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. <i>Plant Cell</i> , <b>2019</b> , 31, 2888-2911	11.6	25
46	Systems approaches to understanding cell signaling and gene regulation. <i>Current Opinion in Plant Biology</i> , <b>2004</b> , 7, 605-9	9.9	25
45	Polymerization of glucans by enzymatically active membranes. <i>Biotechnology Progress</i> , <b>2002</b> , 18, 964-8	2.8	22
44	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , <b>2019</b> , 179, 1893-1907	6.6	21

43	BlastDigester--a web-based program for efficient CAPS marker design. <i>Trends in Genetics</i> , <b>2004</b> , 20, 280-8.5	20
42	Developmental transcriptional profiling reveals key insights into Triticeae reproductive development. <i>Plant Journal</i> , <b>2013</b> , 74, 971-88	6.9 19
41	Transcriptional responses to low temperature and their regulation in Arabidopsis. <i>Canadian Journal of Botany</i> , <b>2003</b> , 81, 1168-1174	19
40	Tung Tree ( <i>Vernicia fordii</i> ) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2019</b> , 17, 558-575	6.5 19
39	Regulation of Cell Type-Specific Immunity Networks in Arabidopsis Roots. <i>Plant Cell</i> , <b>2020</b> , 32, 2742-2762	11.6 18
38	Expression Atlas of Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. <i>Plant Cell</i> , <b>2020</b> , 32, 853-870	11.6 17
37	An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. <i>Communications Biology</i> , <b>2020</b> , 3, 145	6.7 16
36	An TFP-Seq Browser for visualizing and exploring RNA sequencing data. <i>Plant Journal</i> , <b>2019</b> , 100, 641-654	16
35	Extreme breeding: Leveraging genomics for crop improvement. <i>Journal of the Science of Food and Agriculture</i> , <b>2007</b> , 87, 925-929	4.3 14
34	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , <b>2019</b> , 3, e00109	3.3 13
33	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> , <b>2014</b> , 9, e94808	3.7 13
32	Complexity and specificity of the maize ( <i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , <b>2017</b> , 68, 2175-2185	7 12
31	Correlation networks visualization. <i>Frontiers in Plant Science</i> , <b>2012</b> , 3, 240	6.2 12
30	A comparative genomic analysis of ESTs from <i>Ustilago maydis</i> . <i>Functional and Integrative Genomics</i> , <b>2004</b> , 4, 207-18	3.8 12
29	The Bio-Analytic Resource: Data visualization and analytic tools for multiple levels of plant biology. <i>Current Plant Biology</i> , <b>2016</b> , 7-8, 2-5	3.3 11
28	Regulation of Root Angle and Gravitropism. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 3841-3855	3.2 11
27	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , <b>2017</b> , 175, 1499-1509	6.6 10
26	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , <b>2021</b> , 7,	14.3 10

25	Sequence analysis and regulation of expression of a gene coding for carbonic anhydrase in <i>Chlamydomonas reinhardtii</i> . <i>Canadian Journal of Botany</i> , <b>1991</b> , 69, 1097-1102		9
24	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. <i>Plant Journal</i> , <b>2021</b> , 107, 287-302	6.9	9
23	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , <b>2021</b> , 184, 3333-3348.e19	56.2	9
22	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , <b>2021</b> , 10,	8.9	8
21	Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. <i>Plant Cell</i> , <b>2020</b> , 32, 2683-2686	11.6	6
20	Anno genominis XX: 20 years of Arabidopsis genomics. <i>Plant Cell</i> , <b>2021</b> , 33, 832-845	11.6	5
19	A Human "eFP" Browser for Generating Gene Expression Anatograms. <i>PLoS ONE</i> , <b>2016</b> , 11, e0150982	3.7	5
18	Analyses of Protein Interaction Networks Using Computational Tools. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1794, 97-117	1.4	5
17	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> , <b>2020</b> , 9,	7.6	4
16	Bioinformatic tools in Arabidopsis research. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1062, 97-136	1.4	4
15	Gene expression analyses for elucidating mechanisms of hormonal action in plants. <i>Methods in Molecular Biology</i> , <b>2009</b> , 495, 21-37	1.4	4
14	Topo-phylogeny: Visualizing evolutionary relationships on a topographic landscape. <i>PLoS ONE</i> , <b>2017</b> , 12, e0175895	3.7	4
13	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , <b>2020</b> , 4, e00248	3.3	4
12	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> , <b>2021</b> , 21, 124	5.3	4
11	Gene Slider: sequence logo interactive data-visualization for education and research. <i>Bioinformatics</i> , <b>2016</b> , 32, 3670-3672	7.2	3
10	Elevated tyrosine results in the cytosolic retention of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , <b>2021</b> ,	6.9	3
9	Innovation, conservation and repurposing of gene function in plant root cell type development		2
8	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2200, 25-89	1.4	2

7	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. <i>Scientific Data</i> , <b>2019</b> , 6, 190025	8.2	2
6	A gene expression atlas for kiwifruit ( <i>Actinidia chinensis</i> ) and network analysis of transcription factors. <i>BMC Plant Biology</i> , <b>2021</b> , 21, 121	5.3	2
5	Arabidopsis bioinformatics: tools and strategies. <i>Plant Journal</i> , <b>2021</b> ,	6.9	1
4	Seed bioinformatics. <i>Methods in Molecular Biology</i> , <b>2011</b> , 773, 403-19	1.4	1
3	Evolutionary divergence in embryo and seed coat development of U $\bar{E}$ Triangle Brassica species illustrated by a spatiotemporal transcriptome atlas. <i>New Phytologist</i> , <b>2022</b> , 233, 30-51	9.8	0
2	Bioinformatics Tools to Discover Co-Expressed Genes in Plants307-335		
1	Developments in plant and animal genome research. <i>Journal of the Science of Food and Agriculture</i> , <b>2004</b> , 84, 743-744	4.3	