

Nicholas J Provart

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Evolutionary divergence in embryo and seed coat development of U ^T Triangle Brassica species illustrated by a spatiotemporal transcriptome atlas. <i>New Phytologist</i> , 2022 , 233, 30-51	9.8	0
95	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , 2021 , 2200, 25-89	1.4	2
94	Elevated tyrosine results in the cytosolic retention of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase in Arabidopsis thaliana. <i>Plant Journal</i> , 2021 ,	6.9	3
93	Arabidopsis bioinformatics: tools and strategies. <i>Plant Journal</i> , 2021 ,	6.9	1
92	Anno genominis XX: 20 years of Arabidopsis genomics. <i>Plant Cell</i> , 2021 , 33, 832-845	11.6	5
91	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	5.3	4
90	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021 , 7,	14.3	10
89	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. <i>Plant Journal</i> , 2021 , 107, 287-302	6.9	9
88	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , 2021 , 184, 3333-3348.e19	56.2	9
87	A gene expression atlas for kiwifruit (<i>Actinidia chinensis</i>) and network analysis of transcription factors. <i>BMC Plant Biology</i> , 2021 , 21, 121	5.3	2
86	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021 , 10,	8.9	8
85	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoe fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020 , 9,	7.6	4
84	An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. <i>Communications Biology</i> , 2020 , 3, 145	6.7	16
83	Expression Atlas of Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. <i>Plant Cell</i> , 2020 , 32, 853-870	11.6	17
82	Regulation of Cell Type-Specific Immunity Networks in Arabidopsis Roots. <i>Plant Cell</i> , 2020 , 32, 2742-2762	11.6	18
81	Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. <i>Plant Cell</i> , 2020 , 32, 2683-2686	11.6	6
80	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020 , 4, e00248	3.3	4

79	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	11.6	28
78	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019 , 179, 1893-1907	6.6	21
77	High Temporal-Resolution Transcriptome Landscape of Early Maize Seed Development. <i>Plant Cell</i> , 2019 , 31, 974-992	11.6	55
76	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019 , 3, e00109	3.3	13
75	An TFP-Seq Browser for visualizing and exploring RNA sequencing data. <i>Plant Journal</i> , 2019 , 100, 641-654		16
74	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. <i>Plant Cell</i> , 2019 , 31, 2888-2911	11.6	25
73	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. <i>Scientific Data</i> , 2019 , 6, 190025	8.2	2
72	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	6.5	19
71	A gene expression map of shoot domains reveals regulatory mechanisms. <i>Nature Communications</i> , 2019 , 10, 141	17.4	58
70	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , 2019 , 97, 1154-1167	6.9	54
69	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. <i>Nature</i> , 2018 , 553, 342-346	50.4	137
68	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018 , 361,	33.3	368
67	Regulation of Root Angle and Gravitropism. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3841-3855	3.2	11
66	Analyses of Protein Interaction Networks Using Computational Tools. <i>Methods in Molecular Biology</i> , 2018 , 1794, 97-117	1.4	5
65	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	9.8	60
64	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, 569-583	7	29
63	The Bio-Analytic Resource for Plant Biology. <i>Methods in Molecular Biology</i> , 2017 , 1533, 119-148	1.4	27
62	Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , 2017 , 68, 2175-2185	7	12

61	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , 2017 , 29, 1806-1821	11.6	150
60	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017 , 175, 1499-1509	6.6	10
59	ccNET: Database of co-expression networks with functional modules for diploid and polyploid Gossypium. <i>Nucleic Acids Research</i> , 2017 , 45, D1090-D1099	20.1	42
58	Topo-phylogeny: Visualizing evolutionary relationships on a topographic landscape. <i>PLoS ONE</i> , 2017 , 12, e0175895	3.7	4
57	Gene Slider: sequence logo interactive data-visualization for education and research. <i>Bioinformatics</i> , 2016 , 32, 3670-3672	7.2	3
56	New BAR tools for mining expression data and exploring Cis-elements in Arabidopsis thaliana. <i>Plant Journal</i> , 2016 , 88, 490-504	6.9	36
55	A Human "eFP" Browser for Generating Gene Expression Anatograms. <i>PLoS ONE</i> , 2016 , 11, e0150982	3.7	5
54	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	3.3	11
53	50 years of Arabidopsis research: highlights and future directions. <i>New Phytologist</i> , 2016 , 209, 921-44	9.8	128
52	The developmental transcriptome atlas of the biofuel crop Camelina sativa. <i>Plant Journal</i> , 2016 , 88, 879-894	6.9	42
51	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, 2692-708	11.6	80
50	Comparative analyses of C ₃ and C ₄ photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014 , 32, 1158-65	44.5	160
49	New insights into Dehalococcoides mccartyi metabolism from a reconstructed metabolic network-based systems-level analysis of D. mccartyi transcriptomes. <i>PLoS ONE</i> , 2014 , 9, e94808	3.7	13
48	Bioinformatic tools in Arabidopsis research. <i>Methods in Molecular Biology</i> , 2014 , 1062, 97-136	1.4	4
47	A mesoscale abscisic acid hormone interactome reveals a dynamic signaling landscape in Arabidopsis. <i>Developmental Cell</i> , 2014 , 29, 360-72	10.2	83
46	Developmental transcriptional profiling reveals key insights into Triticeae reproductive development. <i>Plant Journal</i> , 2013 , 74, 971-88	6.9	19
45	RNA-Seq effectively monitors gene expression in Eutrema salsugineum plants growing in an extreme natural habitat and in controlled growth cabinet conditions. <i>BMC Genomics</i> , 2013 , 14, 578	4.5	35
44	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> , 2013 , 73, 798-813	6.9	65

43	BAR expressolog identification: expression profile similarity ranking of homologous genes in plant species. <i>Plant Journal</i> , 2012 , 71, 1038-50	6.9	78
42	Changes in stomatal function and water use efficiency in potato plants with altered sucrolytic activity. <i>Plant, Cell and Environment</i> , 2012 , 35, 747-59	8.4	51
41	Correlation networks visualization. <i>Frontiers in Plant Science</i> , 2012 , 3, 240	6.2	12
40	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012 , 40, D1250-4	20.1	31
39	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, 9709-14	11.5	177
38	The re-establishment of desiccation tolerance in germinated <i>Arabidopsis thaliana</i> seeds and its associated transcriptome. <i>PLoS ONE</i> , 2011 , 6, e29123	3.7	79
37	Analysis of gene expression patterns during seed coat development in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2011 , 4, 1074-91	14.4	66
36	Next-generation mapping of <i>Arabidopsis</i> genes. <i>Plant Journal</i> , 2011 , 67, 715-25	6.9	228
35	ePlant and the 3D data display initiative: integrative systems biology on the world wide web. <i>PLoS ONE</i> , 2011 , 6, e15237	3.7	31
34	Seed bioinformatics. <i>Methods in Molecular Biology</i> , 2011 , 773, 403-19	1.4	1
33	The developmental dynamics of the maize leaf transcriptome. <i>Nature Genetics</i> , 2010 , 42, 1060-7	36.3	550
32	AtMetExpress development: a phytochemical atlas of <i>Arabidopsis</i> development. <i>Plant Physiology</i> , 2010 , 152, 566-78	6.6	149
31	Expansion and diversification of the <i>Populus</i> R2R3-MYB family of transcription factors. <i>Plant Physiology</i> , 2009 , 149, 981-93	6.6	346
30	Embryogenesis: pattern formation from a single cell. <i>The Arabidopsis Book</i> , 2009 , 7, e0126	3	59
29	Web-queryable large-scale data sets for hypothesis generation in plant biology. <i>Plant Cell</i> , 2009 , 21, 1034-51	4.5	98
28	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , 2009 , 32, 1633-51	8.4	373
27	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, 621-34	5.7	38
26	Genotype and time of day shape the <i>Populus</i> drought response. <i>Plant Journal</i> , 2009 , 60, 703-15	6.9	109

25	Gene expression analyses for elucidating mechanisms of hormonal action in plants. <i>Methods in Molecular Biology</i> , 2009 , 495, 21-37	1.4	4
24	Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. <i>Science</i> , 2009 , 324, 1068-71	33.3	1782
23	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	3.7	30
22	Elucidating the germination transcriptional program using small molecules. <i>Plant Physiology</i> , 2008 , 147, 143-55	6.6	89
21	An "Electronic Fluorescent Pictograph" browser for exploring and analyzing large-scale biological data sets. <i>PLoS ONE</i> , 2007 , 2, e718	3.7	1796
20	Extreme breeding: Leveraging genomics for crop improvement. <i>Journal of the Science of Food and Agriculture</i> , 2007 , 87, 925-929	4.3	14
19	A predicted interactome for Arabidopsis. <i>Plant Physiology</i> , 2007 , 145, 317-29	6.6	233
18	Functional annotation of the Arabidopsis P450 superfamily based on large-scale co-expression analysis. <i>Biochemical Society Transactions</i> , 2006 , 34, 1192-8	5.1	27
17	The Botany Array Resource: e-Northern, Expression Angling, and promoter analyses. <i>Plant Journal</i> , 2005 , 43, 153-63	6.9	587
16	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, 1875-81	4.9	47
15	BlastDigester--a web-based program for efficient CAPS marker design. <i>Trends in Genetics</i> , 2004 , 20, 280-8.5	8.5	20
14	Systems approaches to understanding cell signaling and gene regulation. <i>Current Opinion in Plant Biology</i> , 2004 , 7, 605-9	9.9	25
13	A comparative genomic analysis of ESTs from <i>Ustilago maydis</i> . <i>Functional and Integrative Genomics</i> , 2004 , 4, 207-18	3.8	12
12	Developments in plant and animal genome research. <i>Journal of the Science of Food and Agriculture</i> , 2004 , 84, 743-744	4.3	
11	Gene expression phenotypes of Arabidopsis associated with sensitivity to low temperatures. <i>Plant Physiology</i> , 2003 , 132, 893-906	6.6	120
10	Transcriptional control of nutrient partitioning during rice grain filling. <i>Plant Biotechnology Journal</i> , 2003 , 1, 59-70	11.6	120
9	Transcriptional responses to low temperature and their regulation in Arabidopsis. <i>Canadian Journal of Botany</i> , 2003 , 81, 1168-1174		19
8	Polymerization of glucans by enzymatically active membranes. <i>Biotechnology Progress</i> , 2002 , 18, 964-8	2.8	22

7	Expression profile matrix of Arabidopsis transcription factor genes suggests their putative functions in response to environmental stresses. <i>Plant Cell</i> , 2002 , 14, 559-74	11.6	732
6	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, 871-82	6.9	78
5	Characterization of pea chloroplastic carbonic anhydrase. Expression in Escherichia coli and site-directed mutagenesis. <i>Plant Molecular Biology</i> , 1993 , 22, 937-43	4.6	33
4	Cloning and sequence comparison of the mouse, human, and chicken engrailed genes reveal potential functional domains and regulatory regions. <i>Genesis</i> , 1992 , 13, 345-58		105
3	Sequence analysis and regulation of expression of a gene coding for carbonic anhydrase in Chlamydomonas reinhardtii. <i>Canadian Journal of Botany</i> , 1991 , 69, 1097-1102		9
2	Bioinformatics Tools to Discover Co-Expressed Genes in Plants307-335		
1	Innovation, conservation and repurposing of gene function in plant root cell type development		2