Paul J Rushton

List of Publications by Year
in descending order

43 papers	10,260 citations	29 h-index	42 g-index
44 all docs	44 docs citations	44 times ranked	10125 citing authors

172457

265206

#	Article	IF	Citations
1	Dynamic differential evolution schemes of WRKY transcription factors in domesticated and wild rice. Scientific Reports, 2021, 11, 14887.	3.3	4
2	Metabolomic Profiling of Soybeans (Glycine max L.) Reveals the Importance of Sugar and Nitrogen Metabolism under Drought and Heat Stress. Plants, 2017, 6, 21.	3.5	154
3	Comparative Metabolome Profile between Tobacco and Soybean Grown under Water-Stressed Conditions. BioMed Research International, 2017, 2017, 1-12.	1.9	53
4	Proteomic Responses of Switchgrass and Prairie Cordgrass to Senescence. Frontiers in Plant Science, 2016, 7, 293.	3.6	8
5	Characterization of 40 soybean (Glycine max) promoters, isolated from across 5 thematic gene groups. Plant Cell, Tissue and Organ Culture, 2016, 127, 145-160.	2.3	14
6	What Have We Learned About Synthetic Promoter Construction?. Methods in Molecular Biology, 2016, 1482, 1-13.	0.9	20
7	A toolbox of genes, proteins, metabolites and promoters for improving drought tolerance in soybean includes the metabolite coumestrol and stomatal development genes. BMC Genomics, 2016, 17, 102.	2.8	88
8	Transcript structure and domain display: a customizable transcript visualization tool. Bioinformatics, 2016, 32, 2024-2025.	4.1	3
9	Structure and Evolution of WRKY Transcription Factors. , 2016, , 163-181.		4
10	The WRKY transcription factor family and senescence in switchgrass. BMC Genomics, 2015, 16, 912.	2.8	62
11	Understanding Water-Stress Responses in Soybean Using Hydroponics Systemâ€"A Systems Biology Perspective. Frontiers in Plant Science, 2015, 6, 1145.	3.6	26
12	Tobacco drought stress responses reveal new targets for Solanaceae crop improvement. BMC Genomics, 2015, 16, 484.	2.8	78
13	Transcriptome profiling of tobacco under water deficit conditions. Genomics Data, 2015, 5, 61-63.	1.3	3
14	Transcriptomics analyses of soybean leaf and root samples during water-deficit. Genomics Data, 2015, 5, 164-166.	1.3	15
15	The interactome of soybean GmWRKY53 using yeast 2-hybrid library screening to saturation. Plant Signaling and Behavior, 2015, 10, e1028705.	2.4	11
16	Three WRKY transcription factors additively repress abscisic acid and gibberellin signaling in aleurone cells. Plant Science, 2015, 236, 214-222.	3.6	65
17	The evolution of WRKY transcription factors. BMC Plant Biology, 2015, 15, 66.	3.6	204
18	NtERF32: a non-NIC2 locus AP2/ERF transcription factor required in jasmonate-inducible nicotine biosynthesis in tobacco. Plant Molecular Biology, 2014, 84, 49-66.	3.9	75

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19	A systems biology perspective on the role of WRKY transcription factors in drought responses in plants. Planta, 2014, 239, 255-266.	3.2	190
20	The Potential of Transcription Factor-Based Genetic Engineering in Improving Crop Tolerance to Drought. OMICS A Journal of Integrative Biology, 2014, 18, 601-614.	2.0	79
21	Dehydration-induced WRKY genes from tobacco and soybean respond to jasmonic acid treatments in BY-2 cell culture. Biochemical and Biophysical Research Communications, 2013, 431, 409-414.	2.1	32
22	<i>GmWRKY53</i>, a water- and salt-inducible soybean gene for rapid dissection of regulatory elements in BY-2 cell culture. Plant Signaling and Behavior, 2013, 8, e24097.	2.4	5
23	Extending MapMan Ontology to Tobacco for Visualization of Gene Expression. Dataset Papers in Biology, 2013, 2013, 1-7.	0.5	4
24	Tobacco Transcription Factors NtMYC2a and NtMYC2b Form Nuclear Complexes with the NtJAZ1 Repressor and Regulate Multiple Jasmonate-Inducible Steps in Nicotine Biosynthesis. Molecular Plant, 2012, 5, 73-84.	8.3	181
25	The WRKY transcription factor family in Brachypodium distachyon. BMC Genomics, 2012, 13, 270.	2.8	85
26	WRKY transcription factors: key components in abscisic acid signalling. Plant Biotechnology Journal, 2012, 10, 2-11.	8.3	485
27	The Potential of Proteomics Technologies for Crop Improvement under Drought Conditions. Critical Reviews in Plant Sciences, 2011, 30, 471-490.	5.7	29
28	High level transgenic expression of soybean (Glycine max) GmERF and Gmubi gene promoters isolated by a novel promoter analysis pipeline. BMC Plant Biology, 2010, 10, 237.	3.6	67
29	WRKY transcription factors. Trends in Plant Science, 2010, 15, 247-258.	8.8	2,080
30	TOBFAC: the database of tobacco transcription factors. BMC Bioinformatics, 2008, 9, 53.	2.6	76
31	Sequencing and analysis of the gene-rich space of cowpea. BMC Genomics, 2008, 9, 103.	2.8	98
32	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science, 2008, 319, 64-69.	12.6	1,712
33	Tobacco Transcription Factors: Novel Insights into Transcriptional Regulation in the Solanaceae Â Â Â. Plant Physiology, 2008, 147, 280-295.	4.8	237
34	CGKB: an annotation knowledge base for cowpea (Vigna unguiculata L.) methylation filtered genomic genespace sequences. BMC Bioinformatics, 2007, 8, 129.	2.6	54
35	Engineering plants with increased disease resistance: what are we going to express?. Trends in Biotechnology, 2005, 23, 275-282.	9.3	156
36	Engineering plants with increased disease resistance: how are we going to express it?. Trends in Biotechnology, 2005, 23, 283-290.	9.3	197

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37	Synthetic Plant Promoters Containing Defined Regulatory Elements Provide Novel Insights into Pathogen- and Wound-Induced Signaling. Plant Cell, 2002, 14, 749-762.	6.6	375
38	Leucine zipper-containing WRKY proteins widen the spectrum of immediate early elicitor-induced WRKY transcription factors in parsley. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1576, 92-100.	2.4	96
39	The WRKY superfamily of plant transcription factors. Trends in Plant Science, 2000, 5, 199-206.	8.8	2,462
40	DNase1 footprints suggest the involvement of at least three types of transcription factors in the regulation of alpha-Amy2/A by gibberellin. Plant Molecular Biology, 1998, 38, 817-825.	3.9	23
41	Transcriptional control of plant genes responsive to pathogens. Current Opinion in Plant Biology, 1998, 1, 311-315.	7.1	358
42	Members of a new family of DNA-binding proteins bind to a conserved cis-element in the promoters of ?-Amy2 genes. Plant Molecular Biology, 1995, 29, 691-702.	3.9	248
43	Aleurone nuclear proteins bind to similar elements in the promoter regions of two gibberellin-regulated ?-amylase genes. Plant Molecular Biology, 1992, 19, 891-901.	3.9	39