Julia Bailey-Serres

List of Publications by Citations

130 papers	13,888 citations	62 h-index	117 g-index
144 ext. papers	16,667 ext. citations	11 avg, IF	6.83 L-index

#	Paper	IF	Citations
130	Sub1A is an ethylene-response-factor-like gene that confers submergence tolerance to rice. *Nature*, **2006**, 442, 705-8	50.4	1084
129	Genetic mechanisms of abiotic stress tolerance that translate to crop yield stability. *Nature Reviews Genetics*, **2015**, 16, 237-51	30.1	547
128	A variable cluster of ethylene response factor-like genes regulates metabolic and developmental acclimation responses to submergence in rice. *Plant Cell*, **2006**, 18, 2021-34	11.6	489
127	Profiling translatomes of discrete cell populations resolves altered cellular priorities during hypoxia in Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 18843-8	11.5	442
126	Homeostatic response to hypoxia is regulated by the N-end rule pathway in plants. *Nature*, **2011**, 479, 415-8	50.4	438
125	Making sense of low oxygen sensing. *Trends in Plant Science*, **2012**, 17, 129-38	13.1	365
124	Flood adaptive traits and processes: an overview. *New Phytologist*, **2015**, 206, 57-73	9.8	363
123	The submergence tolerance regulator SUB1A mediates crosstalk between submergence and drought tolerance in rice. *Plant Cell*, **2011**, 23, 412-27	11.6	353
122	Genetic strategies for improving crop yields. *Nature*, **2019**, 575, 109-118	50.4	318
121	RopGAP4-dependent Rop GTPase rheostat control of Arabidopsis oxygen deprivation tolerance. *Science*, **2002**, 296, 2026-8	33.3	304
120	Submergence tolerance conferred by Sub1A is mediated by SLR1 and SLRL1 restriction of gibberellin responses in rice. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 16814-9	11.5	302
119	Plant responses to hypoxia--is survival a balancing act?. *Trends in Plant Science*, **2004**, 9, 449-56	13.1	299
118	Selective mRNA translation coordinates energetic and metabolic adjustments to cellular oxygen deprivation and reoxygenation in Arabidopsis thaliana. *Plant Journal*, **2008**, 56, 743-55	6.9	268
117	Differential mRNA translation contributes to gene regulation under non-stress and dehydration stress conditions in Arabidopsis thaliana. *Plant Journal*, **2004**, 38, 823-39	6.9	254
116	Cross-kingdom comparison of transcriptomic adjustments to low-oxygen stress highlights conserved and plant-specific responses. *Plant Physiology*, **2010**, 152, 1484-500	6.6	248
115	Translational dynamics revealed by genome-wide profiling of ribosome footprints in Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E203-12	11.5	245
114	Waterproofing crops: effective flooding survival strategies. *Plant Physiology*, **2012**, 160, 1698-709	6.6	243

113	Genome-wide analysis of transcript abundance and translation in Arabidopsis seedlings subjected to oxygen deprivation. *Annals of Botany*, **2005**, 96, 647-60	4.1	238
112	The Organization of Cytoplasmic Ribosomal Protein Genes in the Arabidopsis Genome. *Plant Physiology*, **2001**, 127, 398-415	6.6	230
111	Hairy root transformation using Agrobacterium rhizogenes as a tool for exploring cell type-specific gene expression and function using tomato as a model. *Plant Physiology*, **2014**, 166, 455-69	6.6	219
110	Submergence Tolerant Rice: SUB1's Journey from Landrace to Modern Cultivar. *Rice*, **2010**, 3, 138-147	5.8	216
109	Sensing and signalling in response to oxygen deprivation in plants and other organisms. *Annals of Botany*, **2005**, 96, 507-18	4.1	193
108	Immunopurification of polyribosomal complexes of Arabidopsis for global analysis of gene expression. *Plant Physiology*, **2005**, 138, 624-35	6.6	189
107	A trehalose-6-phosphate phosphatase enhances anaerobic germination tolerance in rice. *Nature Plants*, **2015**, 1, 15124	11.5	178
106	Unraveling the tapestry of networks involving reactive oxygen species in plants. *Plant Physiology*, **2008**, 147, 978-84	6.6	177
105	Life in the balance: a signaling network controlling survival of flooding. *Current Opinion in Plant Biology*, **2010**, 13, 489-94	9.9	163
104	mRNA sequence features that contribute to translational regulation in Arabidopsis. *Nucleic Acids Research*, **2005**, 33, 955-65	20.1	148
103	Molecular characterization of the submergence response of the Arabidopsis thaliana ecotype Columbia. *New Phytologist*, **2011**, 190, 457-71	9.8	144
102	Regulation of translational initiation in plants. *Current Opinion in Plant Biology*, **2002**, 5, 460-5	9.9	142
101	Redundant ERF-VII Transcription Factors Bind to an Evolutionarily Conserved cis-Motif to Regulate Hypoxia-Responsive Gene Expression in Arabidopsis. *Plant Cell*, **2016**, 28, 160-80	11.6	139
100	The submergence tolerance regulator Sub1A mediates stress-responsive expression of AP2/ERF transcription factors. *Plant Physiology*, **2010**, 152, 1674-92	6.6	138
99	Annotating genes of known and unknown function by large-scale coexpression analysis. *Plant Physiology*, **2008**, 147, 41-57	6.6	137
98	Proteomic characterization of evolutionarily conserved and variable proteins of Arabidopsis cytosolic ribosomes. *Plant Physiology*, **2005**, 137, 848-62	6.6	127
97	Selective translation of cytoplasmic mRNAs in plants. *Trends in Plant Science*, **1999**, 4, 142-148	13.1	123
96	Flooding tolerance: O2 sensing and survival strategies. *Current Opinion in Plant Biology*, **2013**, 16, 647-53	9.9	122

95	Mechanism of cytoplasmic mRNA translation. *The Arabidopsis Book*, **2015**, 13, e0176	3	118
94	Profiling of Accessible Chromatin Regions across Multiple Plant Species and Cell Types Reveals Common Gene Regulatory Principles and New Control Modules. *Plant Cell*, **2018**, 30, 15-36	11.6	116
93	Mitochondrial genome rearrangement leads to extension and relocation of the cytochrome c oxidase subunit I gene in sorghum. *Cell*, **1986**, 47, 567-76	56.2	113
92	Hypoxic stress-induced changes in ribosomes of maize seedling roots. *Plant Physiology*, **1990**, 94, 1237-42	6.6	109
91	Selective mRNA sequestration by OLIGOURIDYLATE-BINDING PROTEIN 1 contributes to translational control during hypoxia in Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 2373-8	11.5	106
90	Ethylene: A key regulator of submergence responses in rice. *Plant Science*, **2008**, 175, 43-51	5.3	104
89	Regulated phosphorylation of 40S ribosomal protein S6 in root tips of maize. *Plant Physiology*, **2003**, 132, 2086-97	6.6	102
88	Two Rumex species from contrasting hydrological niches regulate flooding tolerance through distinct mechanisms. *Plant Cell*, **2013**, 25, 4691-707	11.6	101
87	Global analysis of ribosome-associated noncoding RNAs unveils new modes of translational regulation. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E10018-E10027	11.5	100
86	Getting the message across: cytoplasmic ribonucleoprotein complexes. *Trends in Plant Science*, **2009**, 14, 443-53	13.1	97
85	Transient MPK6 activation in response to oxygen deprivation and reoxygenation is mediated by mitochondria and aids seedling survival in Arabidopsis. *Plant Molecular Biology*, **2012**, 78, 109-22	4.6	96
84	Isolation of plant polysomal mRNA by differential centrifugation and ribosome immunopurification methods. *Methods in Molecular Biology*, **2009**, 553, 109-26	1.4	95
83	The submergence tolerance gene SUB1A delays leaf senescence under prolonged darkness through hormonal regulation in rice. *Plant Physiology*, **2012**, 160, 1795-807	6.6	93
82	Ethylene-mediated nitric oxide depletion pre-adapts plants to hypoxia stress. *Nature Communications*, **2019**, 10, 4020	17.4	89
81	Comparison of GC-MS and NMR for metabolite profiling of rice subjected to submergence stress. *Journal of Proteome Research*, **2013**, 12, 898-909	5.6	88
80	Natural variation of submergence tolerance among Arabidopsis thaliana accessions. *New Phytologist*, **2011**, 190, 299-310	9.8	87
79	Dynamic Light Regulation of Translation Status in Arabidopsis thaliana. *Frontiers in Plant Science*, **2012**, 3, 66	6.2	85
78	Polysomes, Stress Granules, and Processing Bodies: A Dynamic Triumvirate Controlling Cytoplasmic mRNA Fate and Function. *Plant Physiology*, **2018**, 176, 254-269	6.6	85

77	Community recommendations on terminology and procedures used in flooding and low oxygen stress research. *New Phytologist*, **2017**, 214, 1403-1407	9.8	84
76	Synonymous codon usage in Zea mays L. nuclear genes is varied by levels of C and G-ending codons. *Nucleic Acids Research*, **1993**, 21, 5294-300	20.1	80
75	A stress recovery signaling network for enhanced flooding tolerance in. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E6085-E6094	11.5	78
74	Post-transcriptional regulation of gene expression in oxygen-deprived roots of maize. *Plant Journal* , **1995**, 7, 287-295	6.9	75
73	Linking genes of unknown function with abiotic stress responses by high-throughput phenotype screening. *Physiologia Plantarum*, **2013**, 148, 322-33	4.6	66
72	Molecular and biochemical characterization of cytosolic phosphoglucomutase in maize. Expression during development and in response to oxygen deprivation. *Plant Physiology*, **1998**, 117, 997-1006	6.6	65
71	Selective recruitment of mRNAs and miRNAs to polyribosomes in response to rhizobia infection in Medicago truncatula. *Plant Journal*, **2013**, 73, 289-301	6.9	64
70	A trihelix DNA binding protein counterbalances hypoxia-responsive transcriptional activation in Arabidopsis. *PLoS Biology*, **2014**, 12, e1001950	9.7	62
69	Transcriptional and post-transcriptional processes regulate gene expression in oxygen-deprived roots of maize. *Plant Journal*, **1998**, 15, 727-735	6.9	62
68	Evolutionary analysis of the Sub1 gene cluster that confers submergence tolerance to domesticated rice. *Annals of Botany*, **2009**, 103, 143-50	4.1	59
67	Transcriptomes of Eight Arabidopsis thaliana Accessions Reveal Core Conserved, Genotype- and Organ-Specific Responses to Flooding Stress. *Plant Physiology*, **2016**, 172, 668-689	6.6	58
66	Characterization of distinct root and shoot responses to low-oxygen stress in Arabidopsis with a focus on primary C- and N-metabolism. *Plant, Cell and Environment*, **2014**, 37, 2366-80	8.4	54
65	Posttranscriptional control of photosynthetic mRNA decay under stress conditions requires 3' and 5' untranslated regions and correlates with differential polysome association in rice. *Plant Physiology*, **2012**, 159, 1111-24	6.6	54
64	What makes species unique? The contribution of proteins with obscure features. *Genome Biology*, **2006**, 7, R57	18.3	54
63	Evolutionary analyses of the 12-kDa acidic ribosomal P-proteins reveal a distinct protein of higher plant ribosomes. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 2378-83	11.5	54
62	Differential metabolic regulation governed by the rice SUB1A gene during submergence stress and identification of alanylglycine by 1H NMR spectroscopy. *Journal of Proteome Research*, **2012**, 11, 320-30	5.6	52
61	Expression of rice SUB1A and SUB1C transcription factors in Arabidopsis uncovers flowering inhibition as a submergence tolerance mechanism. *Plant Journal*, **2011**, 67, 434-46	6.9	51
60	Profiling of translatomes of in vivo-grown pollen tubes reveals genes with roles in micropylar guidance during pollination in Arabidopsis. *Plant Cell*, **2014**, 26, 602-18	11.6	50

59	Water-deficit-induced translational control in Nicotiana tabacum. *Plant, Cell and Environment*, **2003**, 26, 221-229	8.4	50
58	Gene and enhancer trap transposable elements reveal oxygen deprivation-regulated genes and their complex patterns of expression in Arabidopsis. *Annals of Botany*, **2003**, 91 Spec No, 129-41	4.1	49
57	Noncanonical Alternative Polyadenylation Contributes to Gene Regulation in Response to Hypoxia. *Plant Cell*, **2017**, 29, 1262-1277	11.6	48
56	Translating Ribosome Affinity Purification (TRAP) followed by RNA sequencing technology (TRAP-SEQ) for quantitative assessment of plant translatomes. *Methods in Molecular Biology*, **2015**, 1284, 185-207	1.4	48
55	Oxygen deprivation stimulates Ca2+-mediated phosphorylation of mRNA cap-binding protein eIF4E in maize roots. *Plant Journal*, **1999**, 19, 21-30	6.9	47
54	Nuclear-mitochondrial interactions in cytoplasmic male-sterile sorghum. *Theoretical and Applied Genetics*, **1986**, 73, 252-60	6	42
53	Cold shock protein□1 chaperones mRNAs during translation in Arabidopsis thaliana. *Plant Journal*, **2013**, 74, 1016-28	6.9	41
52	Evolutionary flexibility in flooding response circuitry in angiosperms. *Science*, **2019**, 365, 1291-1295	33.3	40
51	Rice SUB1A constrains remodelling of the transcriptome and metabolome during submergence to facilitate post-submergence recovery. *Plant, Cell and Environment*, **2018**, 41, 721-736	8.4	40
50	After The Deluge: Plant Revival Post-Flooding. *Trends in Plant Science*, **2019**, 24, 443-454	13.1	36
49	Applying Genomics Tools for Breeding Submergence Tolerance in Rice **2013**, 9-30		35
48	Proteomic LC-MS analysis of Arabidopsis cytosolic ribosomes: Identification of ribosomal protein paralogs and re-annotation of the ribosomal protein genes. *Journal of Proteomics*, **2015**, 128, 436-49	3.9	33
47	Regulated heterogeneity in 12-kDa P-protein phosphorylation and composition of ribosomes in maize (Zea mays L.). *Journal of Biological Chemistry*, **2001**, 276, 10921-8	5.4	33
46	Co-operation between cytosolic and plastidic oxidative pentose phosphate pathways revealed by 6-phosphogluconate dehydrogenase-deficient genotypes of maize. *Plant Journal*, **1998**, 14, 449-457	6.9	32
45	Genome cluster database. A sequence family analysis platform for Arabidopsis and rice. *Plant Physiology*, **2005**, 138, 47-54	6.6	30
44	Size distributions of circular molecules in plant mitochondrial DNAs. *Current Genetics*, **1987**, 12, 49-53	2.9	30
43	Bioorthogonal Noncanonical Amino Acid Tagging (BONCAT) Enables Time-Resolved Analysis of Protein Synthesis in Native Plant Tissue. *Plant Physiology*, **2017**, 173, 1543-1553	6.6	29
42	Nuclear Transcriptomes at High Resolution Using Retooled INTACT. *Plant Physiology*, **2018**, 176, 270-281	6.6	29

41	Integrative Analysis from the Epigenome to Translatome Uncovers Patterns of Dominant Nuclear Regulation during Transient Stress. *Plant Cell*, **2019**, 31, 2573-2595	11.6	28
40	Emerging roles of long non-coding RNA in root developmental plasticity and regulation of phosphate homeostasis. *Frontiers in Plant Science*, **2015**, 6, 400	6.2	28
39	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. *G3: Genes, Genomes, Genetics*, **2017**, 7, 203-219	3.2	27
38	Ribosome profiling: a tool for quantitative evaluation of dynamics in mRNA translation. *Methods in Molecular Biology*, **2015**, 1284, 139-73	1.4	20
37	The Arabidopsis translatome cell-specific mRNA atlas: Mining suberin and cutin lipid monomer biosynthesis genes as an example for data application. *Plant Signaling and Behavior*, **2010**, 5, 320-4	2.5	20
36	Purification and characterization of cytosolic 6-phosphogluconate dehydrogenase isozymes from maize. *Plant Physiology*, **1992**, 100, 1580-3	6.6	20
35	Characteristics and significance of intergenic polyadenylated RNA transcription in Arabidopsis. *Plant Physiology*, **2013**, 161, 210-24	6.6	18
34	Expression and distribution of cytosolic 6-phosphogluconate dehydrogenase isozymes in maize. *Biochemical Genetics*, **1992**, 30, 233-46	2.4	16
33	Isolation and analysis of mRNAs from specific cell types of plants by ribosome immunopurification. *Methods in Molecular Biology*, **2013**, 959, 277-302	1.4	15
32	DHH1/DDX6-like RNA helicases maintain ephemeral half-lives of stress-response mRNAs. *Nature Plants*, **2020**, 6, 675-685	11.5	14
31	Evaluation of Translational Control Mechanisms in Response to Oxygen Deprivation in Maize. *Russian Journal of Plant Physiology*, **2003**, 50, 774-786	1.6	12
30	Searching for a Match: Structure, Function and Application of Sequence-Specific RNA-Binding Proteins. *Plant and Cell Physiology*, **2019**, 60, 1927-1938	4.9	10
29	The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. *Plant Physiology*, **2017**, 175, 1499-1509	6.6	10
28	Reprogramming of Root Cells during Nitrogen-Fixing Symbiosis Involves Dynamic Polysome Association of Coding and Noncoding RNAs. *Plant Cell*, **2020**, 32, 352-373	11.6	10
27	Innovation, conservation, and repurposing of gene function in root cell type development. *Cell*, **2021**, 184, 3333-3348.e19	56.2	9
26	Utilizing PacBio Iso-Seq for Novel Transcript and Gene Discovery of Abiotic Stress Responses in L. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	8
25	Vision, challenges and opportunities for a Plant Cell Atlas. *ELife*, **2021**, 10,	8.9	8
24	Improved Transformation and Regeneration of Rice: Disruption of as a Test Case via CRISPR-Cas9. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	7

23	Lighting the shadows: methods that expose nuclear and cytoplasmic gene regulatory control. *Current Opinion in Biotechnology*, **2018**, 49, 29-34	11.4	5
22	Selective mRNA Translation Tailors Low Oxygen Energetics. *Plant Cell Monographs*, **2014**, 95-115	0.6	5
21	Plant biology: An immunity boost combats crop disease. *Nature*, **2017**, 545, 420-421	50.4	4
20	Flexible Ion Barrier. *Cell*, **2016**, 164, 345-6	56.2	4
19	Rapid immunopurification of ribonucleoprotein complexes of plants. *Methods in Molecular Biology*, **2015**, 1284, 209-19	1.4	4
18	Flood resilience loci and interact in seedlings established underwater. *Plant Direct*, **2020**, 4, e00240	3.3	4
17	Genome-wide Analysis of Transcript Abundance and Translation in Arabidopsis Seedlings Subjected to Oxygen Deprivation. *Annals of Botany*, **2005**, 96, 1142-1142	4.1	3
16	Isolation of Nuclei in Tagged Cell Types (INTACT), RNA Extraction and Ribosomal RNA Degradation to Prepare Material for RNA-Seq. *Bio-protocol*, **2018**, 8, e2458	0.9	3
15	Conserved and nuanced hierarchy of gene regulatory response to hypoxia. *New Phytologist*, **2021**, 229, 71-78	9.8	3
14	Innovation, conservation and repurposing of gene function in plant root cell type development		2
13	Profiling of accessible chromatin regions across multiple plant species and cell types reveals common gene regulatory principles and new control modules		2
12	A stress recovery signaling network for enhanced flooding tolerance in Arabidopsis thaliana		2
11	Nitrogen-responsive transcription factor kinetics meter plant growth. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 13196-13198	11.5	1
10	Hypoxia and development: Air conditional. *Nature Plants*, **2015**, 1, 15095	11.5	1
9	Integrative analysis from the epigenome through translation exposes patterns of dominant nuclear regulation during transient stress		1
8	DHH1/DDX6-like RNA helicases maintain ephemeral half-lives of stress-response mRNAs associated with innate immunity and growth inhibition		1
7	Ethylene-mediated nitric oxide depletion pre-adapts plants to hypoxia stress		1
6	Nuclear transcriptomes at high resolution using retooled INTACT		1

5	The Plant Cell Atlas: Focusing New Technologies on the Kingdom that Nourishes the Planet.. *Plant Physiology*, **2021**,	6.6	1
4	Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2112516119	11.5	1
3	Gene regulatory circuitry of plant-environment interactions: scaling from cells to the field. *Current Opinion in Plant Biology*, **2021**, 65, 102122	9.9	0
2	???????????. *Nature Digest*, **2009**, 6, 28-29	0	
1	Expression and distribution of cytosolic 6-phosphogluconate dehydrogenase isozymes in maize. *Biochemical Genetics*, **1992**, 30, 233-246	2.4	