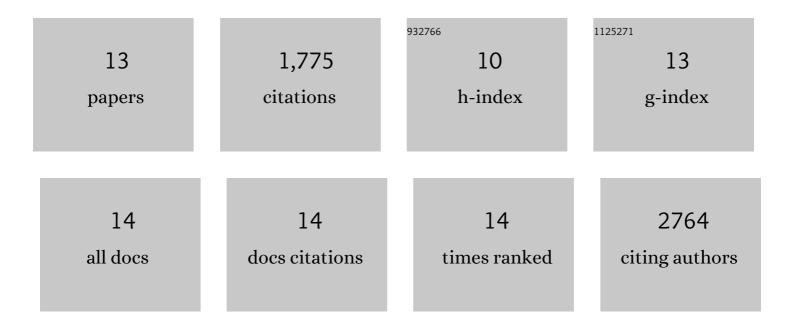
Sergei A Filichkin

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i> . Genome Research, 2010, 20, 45-58.	2.4	825
2	Alternative splicing in plants: directing traffic at the crossroads of adaptation and environmental stress. Current Opinion in Plant Biology, 2015, 24, 125-135.	3.5	215
3	Global Profiling of Rice and Poplar Transcriptomes Highlights Key Conserved Circadian-Controlled Pathways and cis-Regulatory Modules. PLoS ONE, 2011, 6, e16907.	1.1	188
4	Environmental Stresses Modulate Abundance andÂTiming of Alternatively Spliced Circadian Transcripts in Arabidopsis. Molecular Plant, 2015, 8, 207-227.	3.9	142
5	Unproductive alternative splicing and nonsense mRNAs: A widespread phenomenon among plant circadian clock genes. Biology Direct, 2012, 7, 20.	1.9	125
6	Abiotic Stresses Modulate Landscape of Poplar Transcriptome via Alternative Splicing, Differential Intron Retention, and Isoform Ratio Switching. Frontiers in Plant Science, 2018, 9, 5.	1.7	122
7	The cyclophilin A DIAGEOTROPICA gene affects auxin transport in both root and shoot to control lateral root formation. Development (Cambridge), 2015, 142, 712-21.	1.2	57
8	Small Genetic Circuits and MicroRNAs: Big Players in Polymerase II Transcriptional Control in Plants. Plant Cell, 2016, 28, 286-303.	3.1	38
9	Efficiency of gene silencing in Arabidopsis: direct inverted repeats vs. transitive RNAi vectors. Plant Biotechnology Journal, 2007, 5, 615-626.	4.1	23
10	Improved DNase-seq protocol facilitates high resolution mapping of DNase I hypersensitive sites in roots in Arabidopsis thaliana. Plant Methods, 2015, 11, 42.	1.9	20
11	Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in Arabidopsis. Molecular Plant, 2014, , .	3.9	9
12	Identification of transcription factors from NF-Y, NAC, and SPL families responding to osmotic stress in multiple tomato varieties. Plant Science, 2018, 274, 441-450.	1.7	9
13	DNase I SIM: A Simplified In-Nucleus Method for DNase I Hypersensitive Site Sequencing. Methods in Molecular Biology, 2017, 1629, 141-154.	0.4	1