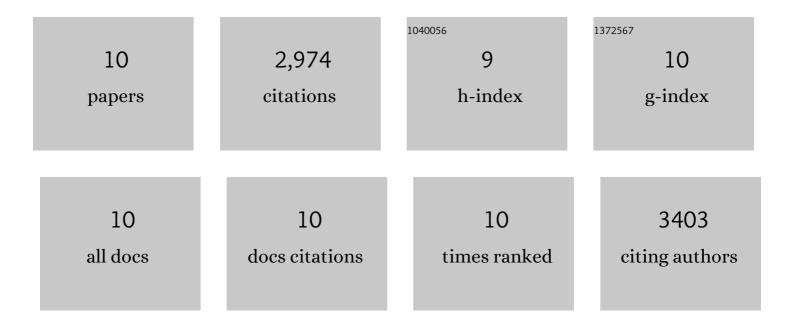
Ryan C Kirkbride

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
2	Global analysis of gene activity during <i>Arabidopsis</i> seed development and identification of seed-specific transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8063-8070.	7.1	509
3	Comprehensive developmental profiles of gene activity in regions and subregions of the <i>Arabidopsis</i> seed. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E435-44.	7.1	381
4	Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature Genetics, 2020, 52, 525-533.	21.4	249
5	Dosage-Dependent Deregulation of an AGAMOUS-LIKE Gene Cluster Contributes to Interspecific Incompatibility. Current Biology, 2009, 19, 1128-1132.	3.9	123
6	Maternal small RNAs mediate spatial-temporal regulation of gene expression, imprinting, and seed development in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2761-2766.	7.1	54
7	An Epigenetic Role for Disrupted Paternal Gene Expression in Postzygotic Seed Abortion in Arabidopsis Interspecific Hybrids. Molecular Plant, 2015, 8, 1766-1775.	8.3	39
8	Transcriptome atlas of the Arabidopsis funiculus – a study of maternal seed subregions. Plant Journal, 2015, 82, 41-53.	5.7	31
9	LEAFY COTYLEDON1, a Key Regulator of Seed Development, Is Expressed in Vegetative and Sexual Propagules of Selaginella moellendorffii. PLoS ONE, 2013, 8, e67971.	2.5	21
10	LCM and RNA-seq analyses revealed roles of cell cycle and translational regulation and homoeolog expression bias in cotton fiber cell initiation. BMC Genomics, 2021, 22, 309.	2.8	7