## Rongmei Wu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/494684/publications.pdf Version: 2024-02-01

		759233	1199594
12	1,813	12	12
papers	citations	h-index	g-index
12	12	12	2699
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	A MADSâ€box gene with similarity to <i>FLC</i> is induced by cold and correlated with epigenetic changes to control budbreak in kiwifruit. New Phytologist, 2022, 233, 2111-2126.	7.3	25
2	Histone modification and activation by SOC1-like and drought stress-related transcription factors may regulate AcSVP2 expression during kiwifruit winter dormancy. Plant Science, 2019, 281, 242-250.	3.6	28
3	A manually annotated Actinidia chinensis var. chinensis (kiwifruit) genome highlights the challenges associated with draft genomes and gene prediction in plants. BMC Genomics, 2018, 19, 257.	2.8	167
4	Kiwifruit SVP2 controls developmental and drought-stress pathways. Plant Molecular Biology, 2018, 96, 233-244.	3.9	17
5	Overexpression of both AcSVP1 and AcSVP4 delays budbreak in kiwifruit A. chinensis var. deliciosa, but only AcSVP1 delays flowering in model plants. Environmental and Experimental Botany, 2018, 153, 262-270.	4.2	14
6	Kiwifruit SVP2 gene prevents premature budbreak during dormancy. Journal of Experimental Botany, 2017, 68, 1071-1082.	4.8	62
7	SVP-like MADS Box Genes Control Dormancy and Budbreak in Apple. Frontiers in Plant Science, 2017, 08, 477.	3.6	121
8	Overexpression of the kiwifruit SVP3 gene affects reproductive development and suppresses anthocyanin biosynthesis in petals, but has no effect on vegetative growth, dormancy, or flowering time. Journal of Experimental Botany, 2014, 65, 4985-4995.	4.8	59
9	Kiwifruit floral gene APETALA2 is alternatively spliced and accumulates in aberrant indeterminate flowers in the absence of miR172. Plant Molecular Biology, 2012, 78, 417-429.	3.9	51
10	Identification and characterization of flowering genes in kiwifruit: sequence conservation and role in kiwifruit flower development. BMC Plant Biology, 2011, 11, 72.	3.6	43
11	Analysis of expressed sequence tags from Actinidia: applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. BMC Genomics, 2008, 9, 351.	2.8	178
12	Protocol: a highly sensitive RT-PCR method for detection and quantification of microRNAs. Plant Methods, 2007, 3, 12.	4.3	1,048