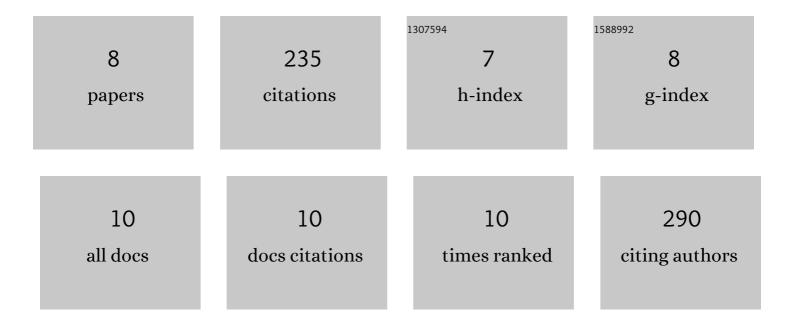
Xilong Chen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7941668/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The East Asian wild apples, <i>Malus baccata</i> (L.) Borkh and <i>Malus hupehensis</i> (Pamp.) Rehder., are additional contributors to the genomes of cultivated European and Chinese varieties. Molecular Ecology, 2023, 32, 5125-5139.	3.9	3
2	Population genomics of apricots unravels domestication history and adaptive events. Nature Communications, 2021, 12, 3956.	12.8	45
3	Sequencing of a Wild Apple (<i>Malus baccata</i>) Genome Unravels the Differences Between Cultivated and Wild Apple Species Regarding Disease Resistance and Cold Tolerance. G3: Genes, Genomes, Genetics, 2019, 9, 2051-2060.	1.8	47
4	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. Frontiers in Plant Science, 2019, 10, 616.	3.6	38
5	Transcription profiles reveal the regulatory mechanisms of spur bud changes and flower induction in response to shoot bending in apple (Malus domestica Borkh.). Plant Molecular Biology, 2019, 99, 45-66.	3.9	21
6	Identification and expression analysis of the IPT and CKX gene families during axillary bud outgrowth in apple (Malus domestica Borkh.). Gene, 2018, 651, 106-117.	2.2	46
7	Comparative RNA-sequencing-based transcriptome profiling of buds from profusely flowering â€~Qinguan' and weakly flowering â€~Nagafu no. 2â€M apple varieties reveals novel insights into the regulatory mechanisms underlying floral induction. BMC Plant Biology, 2018, 18, 370.	3.6	19
8	Identification and Characterization of miRNAs in Self-Rooted and Grafted Malus Reveals Critical Networks Associated with Flowering. International Journal of Molecular Sciences, 2018, 19, 2384.	4.1	13