## Xilong Chen

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7941668/publications.pdf

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8	235	7	8
papers	citations	h-index	g-index
10	10	10	290 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	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
2	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
3	Population genomics of apricots unravels domestication history and adaptive events. Nature Communications, 2021, 12, 3956.	12.8	45
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	Comparative RNA-sequencing-based transcriptome profiling of buds from profusely flowering  Qinguan' and weakly flowering  Nagafu no. 2' apple varieties reveals novel insights into the regulatory mechanisms underlying floral induction. BMC Plant Biology, 2018, 18, 370.	3.6	19
7	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
8	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