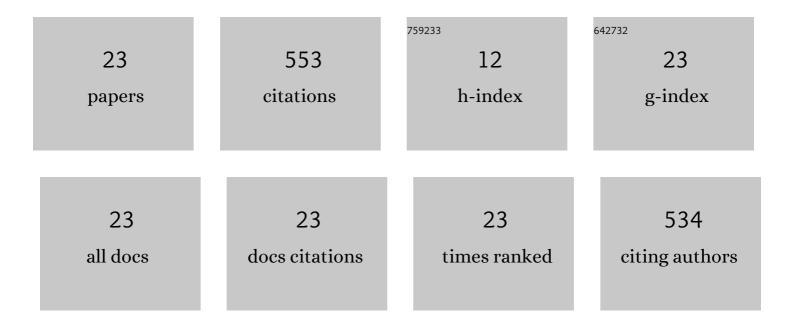
## Xiaonan Li

List of Publications by Year in descending order

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XIAONANLI

#	Article	IF	CITATIONS
1	Marker-Assisted Pyramiding of Genes for Multilocular Ovaries, Self-Compatibility, and Clubroot Resistance in Chinese Cabbage (Brassica rapa L. ssp. pekinensis). Horticulturae, 2022, 8, 139.	2.8	3
2	Identification and Characterization of Circular RNAs in Brassica rapa in Response to Plasmodiophora brassicae. International Journal of Molecular Sciences, 2022, 23, 5369.	4.1	4
3	Sugar Transporters in Plasmodiophora brassicae: Genome-Wide Identification and Functional Verification. International Journal of Molecular Sciences, 2022, 23, 5264.	4.1	6
4	Transferring of clubroot-resistant locus <i>CRd</i> from Chinese cabbage ( <i>Brassica) Tj ETQq( Breeding Science, 2022, , .</i>	0 0 0 rgBT 1.9	/Overlock 10 1
5	Development of a Sinitic Clubroot Differential Set for the Pathotype Classification of Plasmodiophora brassicae. Frontiers in Plant Science, 2020, 11, 568771.	3.6	29
6	Genome-wide identification and expression analysis of chitinase gene family in Brassica rapa reveals its role in clubroot resistance. Plant Science, 2018, 270, 257-267.	3.6	46
7	Mining of Brassica-Specific Genes (BSGs) and Their Induction in Different Developmental Stages and under Plasmodiophora brassicae Stress in Brassica rapa. International Journal of Molecular Sciences, 2018, 19, 2064.	4.1	14
8	Genome Wide Identification and Expression Profiling of SWEET Genes Family Reveals Its Role During Plasmodiophora brassicae-Induced Formation of Clubroot in Brassica rapa. Frontiers in Plant Science, 2018, 9, 207.	3.6	64
9	Identification and Mapping of the Clubroot Resistance Gene CRd in Chinese Cabbage (Brassica rapa ssp.) Tj ETQ	q110.78	94314 rgBT /O
10	Genome-wide identification and role of MKK and MPK gene families in clubroot resistance of Brassica rapa. PLoS ONE, 2018, 13, e0191015.	2.5	11
11	Natural variation in <i>CIRCADIAN CLOCK ASSOCIATED 1</i> is associated with flowering time in <i>Brassica rapa</i> . Genome, 2017, 60, 402-413.	2.0	4
12	Integrated analysis of leaf morphological and color traits in different populations of Chinese cabbage (Brassica rapa ssp. pekinensis). Theoretical and Applied Genetics, 2017, 130, 1617-1634.	3.6	9
13	Quantitative Trait Loci for Morphological Traits and their Association with Functional Genes in Raphanus sativus. Frontiers in Plant Science, 2016, 7, 255.	3.6	13
14	Genome-Wide Analysis and Characterization of Aux/IAA Family Genes in Brassica rapa. PLoS ONE, 2016, 11, e0151522.	2.5	29
15	Anatomic Characteristics Associated with Head Splitting in Cabbage (Brassica oleracea var. capitata) Tj ETQq1 1	0.78431 2.5	4 rgBT /Overlo
16	Construction of chromosome segment substitution lines enables QTL mapping for flowering and morphological traits in Brassica rapa. Frontiers in Plant Science, 2015, 6, 432.	3.6	34
17	Development of a leafy Brassica rapa fixed line collection for genetic diversity and population structure analysis. Molecular Breeding, 2015, 35, 1.	2.1	13
18	Mapping QTLs of resistance to head splitting in cabbage (Brassica oleracea L.var. capitata L.). Molecular Breeding, 2015, 35, 1.	2.1	11

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#	Article	IF	CITATIONS
19	Genetic detection of clubroot resistance loci in a new population of Brassica rapa. Horticulture Environment and Biotechnology, 2014, 55, 540-547.	2.1	33
20	Comparative genomics of Brassicaceae crops. Breeding Science, 2014, 64, 3-13.	1.9	25
21	Identification of candidate genes involved in the biosynthesis of carotenoids in Brassica rapa. Horticulture Environment and Biotechnology, 2014, 55, 342-351.	2.1	3
22	Quantitative Trait Loci Mapping in Brassica rapa Revealed the Structural and Functional Conservation of Genetic Loci Governing Morphological and Yield Component Traits in the A, B, and C Subgenomes of Brassica Species. DNA Research, 2013, 20, 1-16.	3.4	59
23	Development of a high density integrated reference genetic linkage map for the multinational Brassica rapa Genome Sequencing ProjectThis article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farmingâ€. Genome. 2010. 53. 939-947.	2.0	43