

# Yuhong Li

## List of Publications by Year in descending order

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24  
papers

977  
citations

471509

17  
h-index

580821

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25  
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docs citations

25  
times ranked

700  
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#	ARTICLE	IF	CITATIONS
1	Genome-wide characterisation and expression analysis of cellulose synthase genes superfamily under various environmental stresses in <i>Cucumis sativus</i> L. <i>New Zealand Journal of Crop and Horticultural Science</i> , 2021, 49, 127-150.	1.3	11
2	CsKTN1 for a katanin p60 subunit is associated with the regulation of fruit elongation in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2429-2441.	3.6	15
3	A mutation in CsHY2 encoding a phytochromobilin (Pif <sup>B</sup> ) synthase leads to an elongated hypocotyl 1 (elh1) phenotype in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2639-2652.	3.6	8
4	HD-ZIP Gene Family: Potential Roles in Improving Plant Growth and Regulating Stress-Responsive Mechanisms in Plants. <i>Genes</i> , 2021, 12, 1256.	2.4	65
5	Quantitative trait loci for fruit size and flowering time-related traits under domestication and diversifying selection in cucumber ( <i>Cucumis sativus</i> ). <i>Plant Breeding</i> , 2020, 139, 176-191.	1.9	26
6	Genome wide identification, characterization and expression analysis of HD-ZIP gene family in <i>Cucumis sativus</i> L. under biotic and various abiotic stresses. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 502-520.	7.5	35
7	A mutation in CsHD encoding a histidine and aspartic acid domain-containing protein leads to yellow young leaf-1 (yyl-1) in cucumber ( <i>Cucumis sativus</i> L.). <i>Plant Science</i> , 2020, 293, 110407.	3.6	14
8	QTL for horticulturally important traits associated with pleiotropic andromonoecy and carpel number loci, and a paracentric inversion in cucumber. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2271-2290.	3.6	8
9	PINOID is required for lateral organ morphogenesis and ovule development in cucumber. <i>Journal of Experimental Botany</i> , 2019, 70, 5715-5730.	4.8	24
10	Cloning and molecular characterization of rutin degrading enzyme from tartary buckwheat ( <i>Fagopyrum tataricum</i> Gaertn.). <i>Plant Physiology and Biochemistry</i> , 2019, 143, 61-71.	5.8	9
11	HiSeq Base Molecular Characterization of Soil Microbial Community, Diversity Structure, and Predictive Functional Profiling in Continuous Cucumber Planted Soil Affected by Diverse Cropping Systems in an Intensive Greenhouse Region of Northern China. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2619.	4.1	56
12	A mutation in class III homeodomain-leucine zipper (HD-ZIP III) transcription factor results in curly leaf (cul) in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 113-123.	3.6	39
13	QTL Analysis for Downy Mildew Resistance in Cucumber Inbred Line PI 197088. <i>Plant Disease</i> , 2018, 102, 1240-1245.	1.4	33
14	High-Level Production of DNA-Specific Endonuclease AsEndI with Synonymous Codon and its Potential Utilization for Removing DNA Contamination. <i>Applied Biochemistry and Biotechnology</i> , 2018, 185, 641-654.	2.9	3
15	Mutations in CsPID encoding a Ser/Thr protein kinase are responsible for round leaf shape in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 1379-1389.	3.6	25
16	Melatonin and Its Effects on Plant Systems. <i>Molecules</i> , 2018, 23, 2352.	3.8	157
17	Fine mapping identifies CsGCN5 encoding a histone acetyltransferase as putative candidate gene for tendril-less1 mutation (td-1) in cucumber. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1549-1558.	3.6	39
18	Identification and functional characterization of APRR2 controlling green immature fruit color in cucumber ( <i>Cucumis sativus</i> L.). <i>Plant Growth Regulation</i> , 2017, 83, 233-243.	3.4	23

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19	The Cytochrome P450 Gene CsCYP85A1 Is a Putative Candidate for Super Compact-1 (Scp-1) Plant Architecture Mutation in Cucumber ( <i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 266.	3.6	60
20	SHORT HYPOCOTYL 1 Encodes a SMARCA3-like Chromatin Remodeling Factor Regulating Elongation. <i>Plant Physiology</i> , 2016, 172, pp.00501.2016.	4.8	22
21	The chlorophyll-deficient golden leaf mutation in cucumber is due to a single nucleotide substitution in CsChlI for magnesium chelatase I subunit. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1961-1973.	3.6	92
22	Map-based cloning, identification and characterization of the w gene controlling white immature fruit color in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2016, 129, 1247-1256.	3.6	87
23	Fine genetic mapping of the white immature fruit color gene w to a 33.0-kb region in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 2375-2385.	3.6	32
24	Fine mapping of the pleiotropic locus B for black spine and orange mature fruit color in cucumber identifies a 50Åkb region containing a R2R3-MYB transcription factor. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2187-2196.	3.6	92