

# Giang T H Vu

## List of Publications by Year in descending order

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22  
papers

714  
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567281  
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677142  
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22  
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22  
docs citations

22  
times ranked

1222  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Stability and Evolution: Attempting a Holistic View. Trends in Plant Science, 2016, 21, 749-757.	8.8	125
2	Low-pass shotgun sequencing of the barley genome facilitates rapid identification of genes, conserved non-coding sequences and novel repeats. BMC Genomics, 2008, 9, 518.	2.8	75
3	Repair of Site-Specific DNA Double-Strand Breaks in Barley Occurs via Diverse Pathways Primarily Involving the Sister Chromatid. Plant Cell, 2014, 26, 2156-2167.	6.6	55
4	Syteny between Brachypodium distachyon and Hordeum vulgare as revealed by FISH. Chromosome Research, 2010, 18, 841-850.	2.2	50
5	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. Plant Genome, 2015, 8, eplantgenome2015.04.0021.	2.8	45
6	Centromere and telomere sequence alterations reflect the rapid genome evolution within the carnivorous plant genus <i>Genlisea</i> . Plant Journal, 2015, 84, 1087-1099.	5.7	41
7	The Power of CRISPR-Cas9-Induced Genome Editing to Speed Up Plant Breeding. International Journal of Genomics, 2016, 2016, 1-10.	1.6	40
8	The map-based genome sequence of <i>Spirodela polyrhiza</i> aligned with its chromosomes, a reference for karyotype evolution. New Phytologist, 2016, 209, 354-363.	7.3	40
9	Hidden genetic nature of epigenetic natural variation in plants. Trends in Plant Science, 2013, 18, 625-632.	8.8	39
10	Deletion bias in DNA double-strand break repair differentially contributes to plant genome shrinkage. New Phytologist, 2017, 214, 1712-1721.	7.3	34
11	Endogenous sequence patterns predispose the repair modes of CRISPR/Cas9-induced DNA double-stranded breaks in <i>Arabidopsis thaliana</i> . Plant Journal, 2017, 92, 57-67.	5.7	34
12	Chromatin features of plant telomeric sequences at terminal vs. internal positions. Frontiers in Plant Science, 2014, 5, 593.	3.6	33
13	Metatranscriptome analysis reveals host-microbiome interactions in traps of carnivorous <i>Genlisea</i> species. Frontiers in Microbiology, 2015, 6, 526.	3.5	23
14	Fine mapping and syntenic integration of the semi-dwarfing gene sdw3 of barley. Functional and Integrative Genomics, 2010, 10, 509-521.	3.5	19
15	Chromatin organisation in duckweed interphase nuclei in relation to the nuclear DNA content. Plant Biology, 2015, 17, 120-124.	3.8	18
16	From Genome Sequencing to CRISPR-Based Genome Editing for Climate-Resilient Forest Trees. International Journal of Molecular Sciences, 2022, 23, 966.	4.1	16
17	A simple, high throughput method to locate single copy sequences from Bacterial Artificial Chromosome (BAC) libraries using High Resolution Melt analysis. BMC Genomics, 2010, 11, 301.	2.8	7
18	BAC-HAPPY Mapping (BAP Mapping): A New and Efficient Protocol for Physical Mapping. PLoS ONE, 2010, 5, e9089.	2.5	6

#	ARTICLE	IF	CITATIONS
19	Chromatin organization and cytological features of carnivorous Genlisea species with large genome size differences. <i>Frontiers in Plant Science</i> , 2015, 6, 613.	3.6	5
20	Future Prospects of Duckweed Research and Applications. <i>Compendium of Plant Genomes</i> , 2020, , 179-185.	0.5	4
21	Genome invasion by a hypomethylated satellite repeat in Australian crucifer <i>Ballantinia antipoda</i> . <i>Plant Journal</i> , 2019, 99, 1066-1079.	5.7	3
22	Cytogenetics, Epigenetics and Karyotype Evolution of Duckweeds. <i>Compendium of Plant Genomes</i> , 2020, , 47-57.	0.5	2