

# Giang T H Vu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1626411/publications.pdf>

Version: 2024-02-01

22  
papers

714  
citations

567281

15  
h-index

677142

22  
g-index

22  
all docs

22  
docs citations

22  
times ranked

1222  
citing authors

#	ARTICLE	IF	CITATIONS
1	From Genome Sequencing to CRISPR-Based Genome Editing for Climate-Resilient Forest Trees. <i>International Journal of Molecular Sciences</i> , 2022, 23, 966.	4.1	16
2	Future Prospects of Duckweed Research and Applications. <i>Compendium of Plant Genomes</i> , 2020, , 179-185.	0.5	4
3	Cytogenetics, Epigenetics and Karyotype Evolution of Duckweeds. <i>Compendium of Plant Genomes</i> , 2020, , 47-57.	0.5	2
4	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
5	Deletion-bias in <i>double-strand break repair</i> differentially contributes to plant genome shrinkage. <i>New Phytologist</i> , 2017, 214, 1712-1721.	7.3	34
6	Endogenous sequence patterns predispose the repair modes of <i>CRISPR/Cas9-induced double-stranded breaks</i> in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 92, 57-67.	5.7	34
7	The Power of CRISPR-Cas9-Induced Genome Editing to Speed Up Plant Breeding. <i>International Journal of Genomics</i> , 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. <i>New Phytologist</i> , 2016, 209, 354-363.	7.3	40
9	Genome Stability and Evolution: Attempting a Holistic View. <i>Trends in Plant Science</i> , 2016, 21, 749-757.	8.8	125
10	Centromere and telomere sequence alterations reflect the rapid genome evolution within the carnivorous plant genus <i>Genlisea</i> . <i>Plant Journal</i> , 2015, 84, 1087-1099.	5.7	41
11	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.04.0021.	2.8	45
12	Metatranscriptome analysis reveals host-microbiome interactions in traps of carnivorous <i>Genlisea</i> species. <i>Frontiers in Microbiology</i> , 2015, 6, 526.	3.5	23
13	Chromatin organization and cytological features of carnivorous <i>Genlisea</i> species with large genome size differences. <i>Frontiers in Plant Science</i> , 2015, 6, 613.	3.6	5
14	Chromatin organisation in duckweed interphase nuclei in relation to the nuclear <i>DNA</i> content. <i>Plant Biology</i> , 2015, 17, 120-124.	3.8	18
15	Chromatin features of plant telomeric sequences at terminal vs. internal positions. <i>Frontiers in Plant Science</i> , 2014, 5, 593.	3.6	33
16	Repair of Site-Specific DNA Double-Strand Breaks in Barley Occurs via Diverse Pathways Primarily Involving the Sister Chromatid. <i>Plant Cell</i> , 2014, 26, 2156-2167.	6.6	55
17	Hidden genetic nature of epigenetic natural variation in plants. <i>Trends in Plant Science</i> , 2013, 18, 625-632.	8.8	39
18	Fine mapping and syntenic integration of the semi-dwarfing gene <i>sdw3</i> of barley. <i>Functional and Integrative Genomics</i> , 2010, 10, 509-521.	3.5	19

#	ARTICLE	IF	CITATIONS
19	Synteny between <i>Brachypodium distachyon</i> and <i>Hordeum vulgare</i> as revealed by FISH. <i>Chromosome Research</i> , 2010, 18, 841-850.	2.2	50
20	A simple, high throughput method to locate single copy sequences from Bacterial Artificial Chromosome (BAC) libraries using High Resolution Melt analysis. <i>BMC Genomics</i> , 2010, 11, 301.	2.8	7
21	BAC-HAPPY Mapping (BAP Mapping): A New and Efficient Protocol for Physical Mapping. <i>PLoS ONE</i> , 2010, 5, e9089.	2.5	6
22	Low-pass shotgun sequencing of the barley genome facilitates rapid identification of genes, conserved non-coding sequences and novel repeats. <i>BMC Genomics</i> , 2008, 9, 518.	2.8	75