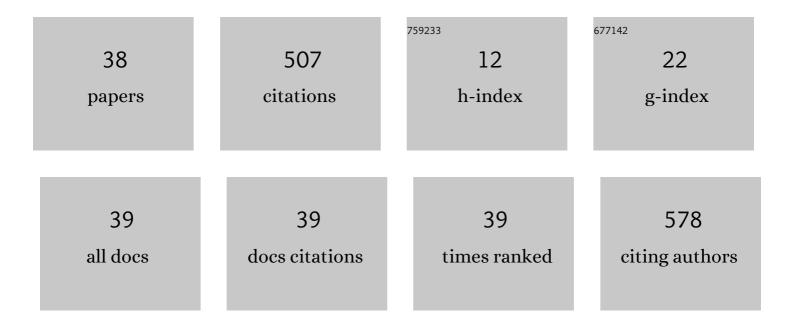
Wojciech Plader

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5108353/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The Genome Sequence of the North-European Cucumber (Cucumis sativus L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728.	2.5	112
2	The complete structure of the cucumber (Cucumis sativus L.) chloroplast genome: Its composition and comparative analysis. Cellular and Molecular Biology Letters, 2007, 12, 584-94.	7.0	41
3	Next generation sequencing and omics in cucumber (Cucumis sativus L.) breeding directed research. Plant Science, 2016, 242, 77-88.	3.6	35
4	Genetic and molecular bases of cucumber (Cucumis sativus L.) sex determination. Molecular Breeding, 2019, 39, 1.	2.1	34
5	Xyloglucan endotransglucosylase/hydrolase genes in cucumber (Cucumis sativus) - differential expression during somatic embryogenesis+. Physiologia Plantarum, 2004, 120, 678-685.	5.2	30
6	A high-quality cucumber genome assembly enhances computational comparative genomics. Molecular Genetics and Genomics, 2020, 295, 177-193.	2.1	30
7	The Shine-Dalgarno-like sequence is a negative regulatory element for translation of tobacco chloroplast rps2 mRNA: an additional mechanism for translational control in chloroplasts. Plant Journal, 2003, 34, 377-382.	5.7	29
8	Cucumber, melon, pumpkin, and squash: Are rules of editing in flowering plants chloroplast genes so well known indeed?. Gene, 2009, 434, 1-8.	2.2	25
9	Comparative transcriptome analysis reveals new molecular pathways for cucumber genes related to sex determination. Plant Reproduction, 2019, 32, 193-216.	2.2	25
10	The metabolic profiles of transgenic cucumber lines vary with different chromosomal locations of the transgene. Cellular and Molecular Biology Letters, 2005, 10, 697-710.	7.0	15
11	A tiling microarray for global analysis of chloroplast genome expression in cucumber and other plants. Plant Methods, 2011, 7, 29.	4.3	14
12	Molecular insight into somaclonal variation phenomena from transcriptome profiling of cucumber (Cucumis sativus L.) lines. Plant Cell, Tissue and Organ Culture, 2021, 145, 239-259.	2.3	14
13	Characterization of Lebanese Germplasm of Snake Melon (Cucumis melo subsp. melo var. flexuosus) Using Morphological Traits and SSR Markers. Agronomy, 2020, 10, 1293.	3.0	12
14	Chromosomal Polymorphism of Two Pickling Cucumbers (Cucumis sativus L.) Revealed by Fluorescent Staining with CMA and DAPI. Cytologia, 2008, 73, 41-48.	0.6	11
15	Molecular Cytogenetic Analysis of <i>Cucumis</i> Wild Species Distributed in Southern Africa: Physical Mapping of 5S and 45S rDNA with DAPI. Cytogenetic and Genome Research, 2015, 146, 80-87.	1.1	10
16	Genome-wide discovery of DNA variants in cucumber somaclonal lines. Gene, 2020, 736, 144412.	2.2	10
17	Cytogenetic comparison among three cultivars of cucumber (Cucumis sativus L.) by using post-heated DAPI band, 45S and 5S rDNA sites. Chromosome Botany, 2009, 4, 19-23.	0.2	8
18	Karyotype Analysis and Chromosomal Distribution of Repetitive DNA Sequences of <i>Cucumis metuliferus</i> Using Fluorescence in situ Hybridization. Cytogenetic and Genome Research, 2014, 144, 237-242.	1.1	8

WOJCIECH PLADER

#	Article	IF	CITATIONS
19	A Comparative Study of the Three Cucumber Cultivars Using Fluorescent Staining and Fluorescence In Situ Hybridization. Cytologia, 2011, 76, 3-10.	0.6	7
20	Biological significance, computational analysis, and applications of plant microRNAs. Acta Physiologiae Plantarum, 2018, 40, 1.	2.1	7
21	Effect of Transgenesis on mRNA and miRNA Profiles in Cucumber Fruits Expressing Thaumatin II. Genes, 2020, 11, 334.	2.4	7
22	Chloroplast transformation reveals that tobacco ycf5 is involved in photosynthesis. Acta Physiologiae Plantarum, 2006, 28, 365-372.	2.1	5
23	Identification and bioinformatics comparison of two novel phosphatases in monoecious and gynoecious cucumber lines. Proceedings of SPIE, 2016, , .	0.8	4
24	miRNA Profiling and Its Role in Multi-Omics Regulatory Networks Connected with Somaclonal Variation in Cucumber (Cucumis sativus L.). International Journal of Molecular Sciences, 2022, 23, 4317.	4.1	4
25	The utility of optical detection system (qPCR) and bioinformatics methods in reference gene expression analysis. Proceedings of SPIE, 2016, , .	0.8	3
26	Advantages and disadvantages in usage of bioinformatic programs in promoter region analysis. Proceedings of SPIE, 2015, , .	0.8	1
27	Bioinformatic investigation of the role of ubiquitins in cucumber flower morphogenesis. Proceedings of SPIE, 2016, , .	0.8	1
28	Comparison of de novo assembly statistics ofCucumis sativus L., , 2017, , .		1
29	Assembly of cucumber (Cucumis sativus L.) somaclones. , 2017, , .		1
30	Bioinformatics and expressional analysis of cDNA clones from floral buds. Proceedings of SPIE, 2017, ,	0.8	1
31	Laser capture microdissection to study flower morphogenesis. Proceedings of SPIE, 2017, , .	0.8	1
32	Influence of transgenesis on genome variability in cucumber lines with aÂthaumatin II gene. Physiology and Molecular Biology of Plants, 2021, 27, 985-996.	3.1	1
33	The Effects of DNA Synthesis Inhibitors on Cell Cycle Synchronization in Cucumber (Cucumis sativus) Tj ETQq1	1 0.78431	.4 rgBT /Over
34	Bioinformatics pipeline for functional identification and characterization of proteins. Proceedings of SPIE, 2015, , .	0.8	0
35	Detection of genomic rearrangements in cucumber using genomecmp software. Proceedings of SPIE, 2017, , .	0.8	0
36	The construction of genomic libraries in BAC and its practical application and bioinformatic usage. , 2018, , .		0

#	Article	IF	CITATIONS
37	Application of bioinformatics techniques for protein interaction analysis. , 2018, , .		Ο
38	Comparison of bioinformatics programs for analysis of single nucleotide variants. , 2018, , .		0