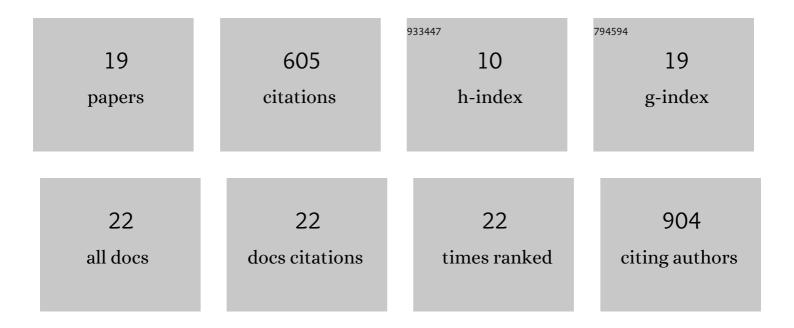
Prisca Viehöver

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. Genome Biology, 2015, 16, 184.	8.8	148
2	The Structural Features of Thousands of T-DNA Insertion Sites Are Consistent with a Double-Strand Break Repair-Based Insertion Mechanism. Molecular Plant, 2015, 8, 1651-1664.	8.3	80
3	Natural variation in flavonol accumulation in Arabidopsis is determined by the flavonol glucosyltransferase BGLU6. Journal of Experimental Botany, 2016, 67, 1505-1517.	4.8	67
4	A De Novo Genome Sequence Assembly of the Arabidopsis thaliana Accession Niederzenz-1 Displays Presence/Absence Variation and Strong Synteny. PLoS ONE, 2016, 11, e0164321.	2.5	63
5	High Contiguity de novo Genome Sequence Assembly of Trifoliate Yam (Dioscorea dumetorum) Using Long Read Sequencing. Genes, 2020, 11, 274.	2.4	54
6	Repeat Composition of CenH3-chromatin and H3K9me2-marked heterochromatin in Sugar Beet (Beta) Tj ETQq0	0	Overlock 10 T
7	Rapid gene identification in sugar beet using deep sequencing of DNA from phenotypic pools selected from breeding panels. BMC Genomics, 2016, 17, 236.	2.8	26

8 Selective egg cell polyspermy bypasses the triploid block. ELife, 2020, 9,	•
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9	Characterization of the Brassica napus Flavonol Synthase Gene Family Reveals Bifunctional Flavonol Synthases. Frontiers in Plant Science, 2021, 12, 733762.	3.6	24
10	Reliable In Silico Identification of Sequence Polymorphisms and Their Application for Extending the Genetic Map of Sugar Beet (Beta vulgaris). PLoS ONE, 2014, 9, e110113.	2.5	18
11	Twenty-Five Years of Propagation in Suspension Cell Culture Results in Substantial Alterations of the Arabidopsis Thaliana Genome. Genes, 2019, 10, 671.	2.4	15
12	Genome Sequencing of <i>Musa acuminata</i> Dwarf Cavendish Reveals a Duplication of a Large Segment of Chromosome 2. G3: Genes, Genomes, Genetics, 2020, 10, 37-42.	1.8	10
13	Complete pan-plastome sequences enable high resolution phylogenetic classification of sugar beet and closely related crop wild relatives. BMC Genomics, 2022, 23, 113.	2.8	10
14	Characterization of genes and alleles involved in the control of flowering time in grapevine. PLoS ONE, 2019, 14, e0214703.	2.5	9
15	Transcriptomic analysis of temporal shifts in berry development between two grapevine cultivars of the Pinot family reveals potential genes controlling ripening time. BMC Plant Biology, 2021, 21, 327.	3.6	8
16	RNA-Seq Time Series of Vitis vinifera Bud Development Reveals Correlation of Expression Patterns with the Local Temperature Profile. Plants, 2020, 9, 1548.	3.5	7
17	A Partially Phase-Separated Genome Sequence Assembly of the Vitis Rootstock â€~Börner' (Vitis riparia ×) ⁻ Science, 2020, 11, 156.	[j ETQq1 ∶ 3.6	1 0.78431 6

18Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar â€~Börner'. Microbiology
Resource Announcements, 2020, 9, .0.63

#	Article	IF	CITATIONS
19	Draft Genome Sequence of Pseudomonas aeruginosa Strain WS394, a Multidrug-Resistant and Highly Cytotoxic Wound Isolate from Chronic Ulcus Cruris. Genome Announcements, 2014, 2, .	0.8	1