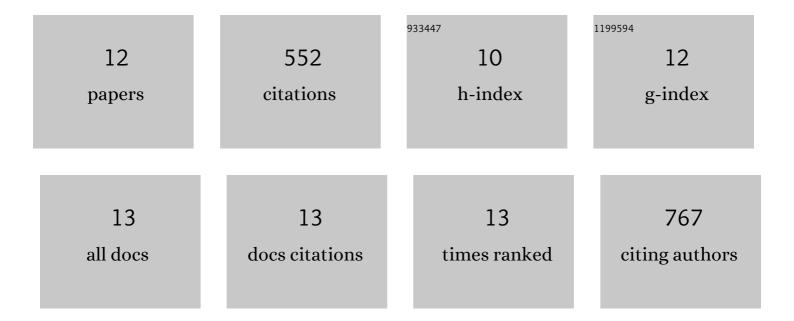
BÃ;rbara Salomão de Faria Müller

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4068503/publications.pdf

Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genomic prediction of growth and wood quality traits in Eucalyptus benthamii using different genomic models and variable SNP genotyping density. New Forests, 2023, 54, 343-362.	1.7	7
2	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. Nature Communications, 2021, 12, 1227.	12.8	37
3	Genome-Wide Association Studies Detect Multiple QTLs for Productivity in Mesoamerican Diversity Panel of Common Bean Under Drought Stress. Frontiers in Plant Science, 2020, 11, 574674.	3.6	24
4	Competitive Growth Assay of Mutagenized Chlamydomonas reinhardtii Compatible With the International Space Station Veggie Plant Growth Chamber. Frontiers in Plant Science, 2020, 11, 631.	3.6	12
5	Independent and Joint―GWAS for growth traits in Eucalyptus by assembling genomeâ€wide data for 3373 individuals across four breeding populations. New Phytologist, 2019, 221, 818-833.	7.3	62
6	Quantitative Genetics and Genomics Converge to Accelerate Forest Tree Breeding. Frontiers in Plant Science, 2018, 9, 1693.	3.6	176
7	In-depth genome characterization of a Brazilian common bean core collection using DArTseq high-density SNP genotyping. BMC Genomics, 2017, 18, 423.	2.8	81
8	Genomic prediction in contrast to a genome-wide association study in explaining heritable variation of complex growth traits in breeding populations of Eucalyptus. BMC Genomics, 2017, 18, 524.	2.8	76
9	SNP discovery in common bean by restriction-associated DNA (RAD) sequencing for genetic diversity and population structure analysis. Molecular Genetics and Genomics, 2016, 291, 1277-1291.	2.1	18
10	An Operational SNP Panel Integrated to SSR Marker for the Assessment of Genetic Diversity and Population Structure of the Common Bean. Plant Molecular Biology Reporter, 2015, 33, 1697-1711.	1.8	20
11	Analysis of BAC-end sequences in common bean (Phaseolus vulgaris L.) towards the development and characterization of long motifs SSRs. Plant Molecular Biology, 2014, 86, 455-470.	3.9	14

Differentially Expressed Genes during Flowering and Grain Filling in Common Bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 1.8 25 438-451.

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