

# Bárbara Salomé de Faria Müller

## List of Publications by Year in descending order

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

Version: 2024-02-01

12  
papers

552  
citations

933447

10  
h-index

1199594

12  
g-index

13  
all docs

13  
docs citations

13  
times ranked

767  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Genomic prediction of growth and wood quality traits in <i>Eucalyptus benthamii</i> using different genomic models and variable SNP genotyping density. <i>New Forests</i> , 2023, 54, 343-362.                  | 1.7  | 7         |
| 2  | Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 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. <i>Frontiers in Plant Science</i> , 2020, 11, 574674.                 | 3.6  | 24        |
| 4  | Competitive Growth Assay of Mutagenized <i>Chlamydomonas reinhardtii</i> Compatible With the International Space Station Veggie Plant Growth Chamber. <i>Frontiers in Plant Science</i> , 2020, 11, 631.         | 3.6  | 12        |
| 5  | Independent and Joint GWAS for growth traits in <i>Eucalyptus</i> by assembling genome-wide data for 3373 individuals across four breeding populations. <i>New Phytologist</i> , 2019, 221, 818-833.             | 7.3  | 62        |
| 6  | Quantitative Genetics and Genomics Converge to Accelerate Forest Tree Breeding. <i>Frontiers in Plant Science</i> , 2018, 9, 1693.   | 3.6  | 176       |
| 7  | In-depth genome characterization of a Brazilian common bean core collection using DArTseq high-density SNP genotyping. <i>BMC Genomics</i> , 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 <i>Eucalyptus</i> . <i>BMC Genomics</i> , 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. <i>Molecular Genetics and Genomics</i> , 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. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1697-1711.            | 1.8  | 20        |
| 11 | Analysis of BAC-end sequences in common bean ( <i>Phaseolus vulgaris</i> L.) towards the development and characterization of long motifs SSRs. <i>Plant Molecular Biology</i> , 2014, 86, 455-470.               | 3.9  | 14        |
| 12 | Differentially Expressed Genes during Flowering and Grain Filling in Common Bean ( <i>Phaseolus</i> ) Tj ETQqO O O rgBT /Overlock 10 Tf 50 307<br>438-451.   | 1.8  | 25        |