

# Jörn Me Bartholomäus

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2804392/publications.pdf>

Version: 2024-02-01

21  
papers

1,022  
citations

567281

15  
h-index

713466

21  
g-index

24  
all docs

24  
docs citations

24  
times ranked

1571  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Prediction: Progress and Perspectives for Rice Improvement. <i>Methods in Molecular Biology</i> , 2022, 2467, 569-617.	0.9	10
2	Impact of early genomic prediction for recurrent selection in an upland rice synthetic population. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	13
3	Identification of an Elite Core Panel as a Key Breeding Resource to Accelerate the Rate of Genetic Improvement for Irrigated Rice. <i>Rice</i> , 2021, 14, 92.	4.0	19
4	The genetics of exapted resistance to two exotic pathogens in pedunculate oak. <i>New Phytologist</i> , 2020, 226, 1088-1103.	7.3	20
5	The pulse of the tree is under genetic control: eucalyptus as a case study. <i>Plant Journal</i> , 2020, 103, 338-356.	5.7	7
6	Genomic selection in rice: empirical results and implications for breeding.. , 2020, , 243-258.		9
7	Selection of trait-specific markers and multi-environment models improve genomic predictive ability in rice. <i>PLoS ONE</i> , 2019, 14, e0208871.	2.5	46
8	Fine Scale Genomic Signals of Admixture and Alien Introgression among Asian Rice Landraces. <i>Genome Biology and Evolution</i> , 2019, 11, 1358-1373.	2.5	32
9	Rice diversity panel provides accurate genomic predictions for complex traits in the progenies of biparental crosses involving members of the panel. <i>Theoretical and Applied Genetics</i> , 2018, 131, 417-435.	3.6	29
10	Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2319-2332.	1.8	30
11	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
12	High-density SNP assay development for genetic analysis in maritime pine ( <i>Pinus pinaster</i> ). <i>Molecular Ecology Resources</i> , 2016, 16, 574-587.	4.8	53
13	Performance of genomic prediction within and across generations in maritime pine. <i>BMC Genomics</i> , 2016, 17, 604.	2.8	82
14	Genomic selection in maritime pine. <i>Plant Science</i> , 2016, 242, 108-119.	3.6	99
15	Linkage and Association Mapping for Two Major Traits Used in the Maritime Pine Breeding Program: Height Growth and Stem Straightness. <i>PLoS ONE</i> , 2016, 11, e0165323.	2.5	36
16	Evidence of intense chromosomal shuffling during conifer evolution. <i>Genome Biology and Evolution</i> , 2015, 7, evv185.	2.5	26
17	Genetic architecture of carbon isotope composition and growth in <i>Eucalyptus</i> across multiple environments. <i>New Phytologist</i> , 2015, 206, 1437-1449.	7.3	20
18	Quantitative Proteomic and Phosphoproteomic Approaches for Deciphering the Signaling Pathway for Tension Wood Formation in Poplar. <i>Journal of Proteome Research</i> , 2015, 14, 3188-3203.	3.7	12

#	ARTICLE	IF	CITATIONS
19	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	2.8	49
20	High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. New Phytologist, 2015, 206, 1283-1296.	7.3	90
21	Plasticity of primary and secondary growth dynamics in Eucalyptus hybrids: a quantitative genetics and QTL mapping perspective. BMC Plant Biology, 2013, 13, 120.	3.6	33