Joost van Heerwaarden

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4769838/publications.pdf

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40 papers 3,095 citations

331538 21 h-index 276775 41 g-index

42 all docs 42 docs citations

42 times ranked 4995 citing authors

#	Article	IF	CITATIONS
1	Phylogeography and Symbiotic Effectiveness of Rhizobia Nodulating Chickpea (Cicer arietinum L.) in Ethiopia. Microbial Ecology, 2021, 81, 703-716.	1.4	6
2	Phylogeographic distribution of rhizobia nodulating common bean (<i>Phaseolus vulgaris</i> L.) in Ethiopia. FEMS Microbiology Ecology, 2021, 97, .	1.3	8
3	Quantifying the prevalence of (non)-response to fertilizers in sub-Saharan Africa using on-farm trial data. Nutrient Cycling in Agroecosystems, 2021, 121, 257-269.	1.1	6
4	Nutrient Deficiencies Are Key Constraints to Grain Legume Productivity on "Non-responsive―Soils in Sub-Saharan Africa. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	4
5	Symbiotic interactions between chickpea (Cicer arietinum L.) genotypes and Mesorhizobium strains. Symbiosis, 2020, 82, 235-248.	1.2	9
6	Tracing legume seed diffusion beyond demonstration trials: An exploration of sharing mechanisms. Outlook on Agriculture, 2020, 49, 29-38.	1.8	5
7	DO OPEN-POLLINATED MAIZE VARIETIES PERFORM BETTER THAN HYBRIDS IN AGROFORESTRY SYSTEMS?. Experimental Agriculture, 2019, 55, 649-661.	0.4	9
8	Maize crop nutrient input requirements for food security in sub-Saharan Africa. Global Food Security, 2019, 23, 9-21.	4.0	115
9	Genetic Interaction Studies Reveal Superior Performance of Rhizobium tropici CIAT899 on a Range of Diverse East African Common Bean (Phaseolus vulgaris L.) Genotypes. Applied and Environmental Microbiology, 2019, 85, .	1.4	29
10	Additive yield response of chickpea (Cicer arietinum L.) to rhizobium inoculation and phosphorus fertilizer across smallholder farms in Ethiopia. Agriculture, Ecosystems and Environment, 2018, 261, 144-152.	2.5	60
11	Soyabean response to rhizobium inoculation across sub-Saharan Africa: Patterns of variation and the role of promiscuity. Agriculture, Ecosystems and Environment, 2018, 261, 211-218.	2.5	38
12	Using household survey data to identify large-scale food security patterns across Uganda. PLoS ONE, 2018, 13, e0208714.	1.1	12
13	Conservation agriculture with trees amplifies negative effects of reduced tillage on maize performance in East Africa. Field Crops Research, 2018, 221, 238-244.	2.3	18
14	Natural variation in life history strategy of <i>Arabidopsis thaliana</i> determines stress responses to drought and insects of different feeding guilds. Molecular Ecology, 2017, 26, 2959-2977.	2.0	23
15	Genetic architecture of plant stress resistance: multiâ€trait genomeâ€wide association mapping. New Phytologist, 2017, 213, 1346-1362.	3.5	144
16	Water and radiation use efficiencies explain the effect of potassium on the productivity of cassava. European Journal of Agronomy, 2017, 83, 28-39.	1.9	22
17	Appropriate homoplasy metrics in linked SSRs to predict an underestimation of demographic expansion times. BMC Evolutionary Biology, 2017, 17, 213.	3.2	1
18	Performance of genomic prediction within and across generations in maritime pine. BMC Genomics, 2016, 17, 604.	1.2	82

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19	Whole-Genome Hitchhiking on an Organelle Mutation. Current Biology, 2016, 26, 1306-1311.	1.8	17
20	Understanding variability in soybean yield and response to P-fertilizer and rhizobium inoculants on farmers' fields in northern Nigeria. Field Crops Research, 2016, 186, 133-145.	2.3	119
21	Linkage and Association Mapping for Two Major Traits Used in the Maritime Pine Breeding Program: Height Growth and Stem Straightness. PLoS ONE, 2016, 11, e0165323.	1.1	36
22	Genome-Wide Association Analysis of Adaptation Using Environmentally Predicted Traits. PLoS Genetics, 2015, 11, e1005594.	1.5	7
23	Development of a <i><scp>N</scp>asonia vitripennis</i> outbred laboratory population for genetic analysis. Molecular Ecology Resources, 2014, 14, 578-587.	2.2	33
24	Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. BMC Genomics, 2014, 15, 171.	1.2	41
25	Maximizing genetic differentiation in core collections by PCA-based clustering of molecular marker data. Theoretical and Applied Genetics, 2013, 126, 763-772.	1.8	20
26	Improving Hierarchical Clustering of Genotypic Data via Principal Component Analysis. Crop Science, 2013, 53, 1546-1554.	0.8	22
27	Historical genomics of North American maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12420-12425.	3.3	151
28	New Genes in Traditional Seed Systems: Diffusion, Detectability and Persistence of Transgenes in a Maize Metapopulation. PLoS ONE, 2012, 7, e46123.	1.1	20
29	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	9.4	816
30	Determination of genetic structure of germplasm collections: are traditional hierarchical clustering methods appropriate for molecular marker data?. Theoretical and Applied Genetics, 2011, 123, 195-205.	1.8	103
31	Genetic signals of origin, spread, and introgression in a large sample of maize landraces. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1088-1092.	3.3	357
32	Statistical Techniques for Defining Reference Sets of Accessions and Microsatellite Markers. Crop Science, 2011, 51, 2401-2411.	0.8	22
33	Fine scale genetic structure in the wild ancestor of maize (<i>Zea mays</i> ssp. <i>parviglumis</i>). Molecular Ecology, 2010, 19, 1162-1173.	2.0	37
34	Genetic diversity in a crop metapopulation. Heredity, 2010, 104, 28-39.	1.2	42
35	Patterns of Population Structure and Environmental Associations to Aridity Across the Range of Loblolly Pine (<i>Pinus taeda</i> L., Pinaceae). Genetics, 2010, 185, 969-982.	1.2	332
36	Estimating maize genetic erosion in modernized smallholder agriculture. Theoretical and Applied Genetics, 2009, 119, 875-888.	1.8	48

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37	Transgenes in Mexican maize: molecular evidence and methodological considerations for GMO detection in landrace populations. Molecular Ecology, 2009, 18, 750-761.	2.0	113
38	Resolution of the Mexican transgene detection controversy: error sources and scientific practice in commercial and ecological contexts. Molecular Ecology, 2009, 18, 4145-4150.	2.0	14
39	Major histocompatibility genes in the Lake Tana African large barb species flock: evidence for complete partitioning of class II B, but not class I, genes among different species. Immunogenetics, 2005, 56, 894-908.	1.2	28
40	Unique haplotypes of co-segregating major histocompatibility class II A and class II B alleles in Atlantic salmon (Salmo salar) give rise to diverse class II genotypes. Immunogenetics, 2002, 54, 320-331.	1.2	124