

ArÅ«nas P Verbyla

List of Publications by Year in descending order

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33
papers

1,983
citations

430874

18
h-index

454955

30
g-index

34
all docs

34
docs citations

34
times ranked

2232
citing authors

#	ARTICLE	IF	CITATIONS
1	The Analysis of Designed Experiments and Longitudinal Data by Using Smoothing Splines. Journal of the Royal Statistical Society Series C: Applied Statistics, 1999, 48, 269-311.	1.0	506
2	MAGIC populations in crops: current status and future prospects. Theoretical and Applied Genetics, 2015, 128, 999-1017.	3.6	230
3	Joint modeling of additive and non-additive genetic line effects in single field trials. Theoretical and Applied Genetics, 2006, 113, 809-819.	3.6	170
4	Spatial Analysis of Multi-Environment Early Generation Variety Trials. Biometrics, 1998, 54, 1.	1.4	125
5	Transcriptomic analysis of wheat near-isogenic lines identifies PM19-A1 and A2 as candidates for a major dormancy QTL. Genome Biology, 2015, 16, 93.	8.8	125
6	Quantitative trait loci analysis of zinc efficiency and grain zinc concentration in wheat using whole genome average interval mapping. Plant and Soil, 2009, 314, 49-66.	3.7	101
7	Use of a large multiparent wheat mapping population in genomic dissection of coleoptile and seedling growth. Plant Biotechnology Journal, 2014, 12, 219-230.	8.3	86
8	The analysis of QTL by simultaneous use of the full linkage map. Theoretical and Applied Genetics, 2007, 116, 95-111.	3.6	82
9	Adjusted likelihood methods for modelling dispersion in generalized linear models. , 1999, 10, 695-709.		81
10	Joint modeling of additive and non-additive (genetic line) effects in multi-environment trials. Theoretical and Applied Genetics, 2007, 114, 1319-1332.	3.6	70
11	Whole-genome QTL analysis for MAGIC. Theoretical and Applied Genetics, 2014, 127, 1753-1770.	3.6	49
12	The analysis of quantitative trait loci in multi-environment trials using a multiplicative mixed model. Australian Journal of Agricultural Research, 2003, 54, 1395.	1.5	42
13	Statistical methods for analysis of multi-harvest data from perennial pasture variety selection trials. Crop and Pasture Science, 2015, 66, 947.	1.5	38
14	Anisotropic MatÅ©rn correlation and spatial prediction using REML. Journal of Agricultural, Biological, and Environmental Statistics, 2007, 12, 147-160.	1.4	34
15	RWGAIM: an efficient high-dimensional random whole genome average (QTL) interval mapping approach. Genetical Research, 2012, 94, 291-306.	0.9	31
16	Whole-Genome Analysis of Multienvironment or Multitrait QTL in MAGIC. G3: Genes, Genomes, Genetics, 2014, 4, 1569-1584.	1.8	31
17	Exact and approximate REML for heteroscedastic regression. Statistical Modelling, 2001, 1, 161-175.	1.1	29
18	<i>R</i> Package wgaim : QTL Analysis in Bi-Parental Populations Using Linear Mixed Models. Journal of Statistical Software, 2011, 40, .	3.7	29

#	ARTICLE	IF	CITATIONS
19	Incorporating LASSO effects into a mixed model for quantitative trait loci detection. Journal of Agricultural, Biological, and Environmental Statistics, 2007, 12, 300-314.	1.4	18
20	Multivariate whole genome average interval mapping: QTL analysis for multiple traits and/or environments. Theoretical and Applied Genetics, 2012, 125, 933-953.	3.6	16
21	Residual Variance–Covariance Modelling in Analysis of Multivariate Data from Variety Selection Trials. Journal of Agricultural, Biological, and Environmental Statistics, 2017, 22, 1-22.	1.4	16
22	QTL identified for stay-green in a multi-reference nested association mapping population of wheat exhibit context dependent expression and parent-specific alleles. Field Crops Research, 2021, 270, 108181.	5.1	16
23	Modelling temporal genetic and spatio-temporal residual effects for high-throughput phenotyping data*. Australian and New Zealand Journal of Statistics, 2021, 63, 284-308.	0.9	12
24	Tensor Cubic Smoothing Splines in Designed Experiments Requiring Residual Modelling. Journal of Agricultural, Biological, and Environmental Statistics, 2018, 23, 478-508.	1.4	11
25	A random model approach for the LASSO. Computational Statistics, 2008, 23, 217-233.	1.5	10
26	Variable Selection in Linear Mixed Models Using an Extended Class of Penalties. Australian and New Zealand Journal of Statistics, 2012, 54, 427-449.	0.9	9
27	WGNAM: whole-genome nested association mapping. Theoretical and Applied Genetics, 2022, 135, 2213-2232.	3.6	5
28	ESTIMATION, PREDICTION AND INFERENCE FOR THE LASSO RANDOM EFFECTS MODEL. Australian and New Zealand Journal of Statistics, 2009, 51, 43-61.	0.9	3
29	Estimating a Single Shelf-Life for Multiple Batches. Australian and New Zealand Journal of Statistics, 2012, 54, 343-358.	0.9	3
30	Eagle: multi-locus association mapping on a genome-wide scale made routine. Bioinformatics, 2020, 36, 1509-1516.	4.1	2
31	A spatio-temporal analysis of a field trial. , 2000, , 161-172.		1
32	LEVERAGE ADJUSTMENTS FOR DISPERSION MODELLING IN GENERALIZED NONLINEAR MODELS. Australian and New Zealand Journal of Statistics, 2009, 51, 433-448.	0.9	1
33	Eagle for better genome-wide association mapping. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	0