

# 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	WG NAM: whole-genome nested association mapping. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2213-2232.	3.6	5
2	Modelling temporal genetic and spatio-temporal residual effects for high-throughput phenotyping data*. <i>Australian and New Zealand Journal of Statistics</i> , 2021, 63, 284-308.	0.9	12
3	Eagle for better genome-wide association mapping. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
4	QTL identified for stay-green in a multi-reference nested association mapping population of wheat exhibit context dependent expression and parent-specific alleles. <i>Field Crops Research</i> , 2021, 270, 108181.	5.1	16
5	Eagle: multi-locus association mapping on a genome-wide scale made routine. <i>Bioinformatics</i> , 2020, 36, 1509-1516.	4.1	2
6	Tensor Cubic Smoothing Splines in Designed Experiments Requiring Residual Modelling. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2018, 23, 478-508.	1.4	11
7	Residual Variance-Covariance Modelling in Analysis of Multivariate Data from Variety Selection Trials. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2017, 22, 1-22.	1.4	16
8	Transcriptomic analysis of wheat near-isogenic lines identifies PM19-A1 and A2 as candidates for a major dormancy QTL. <i>Genome Biology</i> , 2015, 16, 93.	8.8	125
9	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015, 128, 999-1017.	3.6	230
10	Statistical methods for analysis of multi-harvest data from perennial pasture variety selection trials. <i>Crop and Pasture Science</i> , 2015, 66, 947.	1.5	38
11	Whole-Genome Analysis of Multi-environment or Multitrait QTL in MAGIC. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1569-1584.	1.8	31
12	Use of a large multiparent wheat mapping population in genomic dissection of coleoptile and seedling growth. <i>Plant Biotechnology Journal</i> , 2014, 12, 219-230.	8.3	86
13	Whole-genome QTL analysis for MAGIC. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1753-1770.	3.6	49
14	RWGAIM: an efficient high-dimensional random whole genome average (QTL) interval mapping approach. <i>Genetical Research</i> , 2012, 94, 291-306.	0.9	31
15	Multivariate whole genome average interval mapping: QTL analysis for multiple traits and/or environments. <i>Theoretical and Applied Genetics</i> , 2012, 125, 933-953.	3.6	16
16	Estimating a Single Shelf-Life for Multiple Batches. <i>Australian and New Zealand Journal of Statistics</i> , 2012, 54, 343-358.	0.9	3
17	Variable Selection in Linear Mixed Models Using an Extended Class of Penalties. <i>Australian and New Zealand Journal of Statistics</i> , 2012, 54, 427-449.	0.9	9
18	<i>R</i> Package <i>wgaim</i> : QTL Analysis in Bi-Parental Populations Using Linear Mixed Models. <i>Journal of Statistical Software</i> , 2011, 40, .	3.7	29

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19	Quantitative trait loci analysis of zinc efficiency and grain zinc concentration in wheat using whole genome average interval mapping. <i>Plant and Soil</i> , 2009, 314, 49-66.	3.7	101
20	ESTIMATION, PREDICTION AND INFERENCE FOR THE LASSO RANDOM EFFECTS MODEL. <i>Australian and New Zealand Journal of Statistics</i> , 2009, 51, 43-61.	0.9	3
21	LEVERAGE ADJUSTMENTS FOR DISPERSION MODELLING IN GENERALIZED NONLINEAR MODELS. <i>Australian and New Zealand Journal of Statistics</i> , 2009, 51, 433-448.	0.9	1
22	A random model approach for the LASSO. <i>Computational Statistics</i> , 2008, 23, 217-233.	1.5	10
23	Anisotropic MatÅ©rn correlation and spatial prediction using REML. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2007, 12, 147-160.	1.4	34
24	Incorporating LASSO effects into a mixed model for quantitative trait loci detection. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2007, 12, 300-314.	1.4	18
25	Joint modeling of additive and non-additive (genetic line) effects in multi-environment trials. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1319-1332.	3.6	70
26	The analysis of QTL by simultaneous use of the full linkage map. <i>Theoretical and Applied Genetics</i> , 2007, 116, 95-111.	3.6	82
27	Joint modeling of additive and non-additive genetic line effects in single field trials. <i>Theoretical and Applied Genetics</i> , 2006, 113, 809-819.	3.6	170
28	The analysis of quantitative trait loci in multi-environment trials using a multiplicative mixed model. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 1395.	1.5	42
29	Exact and approximate REML for heteroscedastic regression. <i>Statistical Modelling</i> , 2001, 1, 161-175.	1.1	29
30	A spatio-temporal analysis of a field trial. , 2000, , 161-172.		1
31	The Analysis of Designed Experiments and Longitudinal Data by Using Smoothing Splines. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 1999, 48, 269-311.	1.0	506
32	Adjusted likelihood methods for modelling dispersion in generalized linear models. , 1999, 10, 695-709.		81
33	Spatial Analysis of Multi-Environment Early Generation Variety Trials. <i>Biometrics</i> , 1998, 54, 1.	1.4	125