

Jean-Louis Foulley

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,159
citations

623734

14
h-index

752698

20
g-index

21
all docs

21
docs citations

21
times ranked

1550
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Response to Artificial Selection: A Case Study in Dairy Cattle. PLoS ONE, 2009, 4, e6595.	2.5	219
2	A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. BMC Genomics, 2009, 10, 550.	2.8	186
3	Genetic diversity of eleven European pig breeds. Genetics Selection Evolution, 2000, 32, 187-203.	3.0	182
4	Moderated effect size and <i>P</i> -value combinations for microarray meta-analyses. Bioinformatics, 2009, 25, 2692-2699.	4.1	139
5	An overview of the Weitzman approach to diversity. Genetics Selection Evolution, 1998, 30, 1.	3.0	70
6	Aggregate diversity: New approach combining within- and between-breed genetic diversity. Livestock Science, 2005, 95, 247-254.	1.2	65
7	Estimating allelic richness and its diversity. Livestock Science, 2006, 101, 150-158.	1.6	57
8	Bayesian Analysis of Growth Curves Using Mixed Models Defined by Stochastic Differential Equations. Biometrics, 2010, 66, 733-741.	1.4	49
9	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. Conservation Genetics, 2005, 6, 729-741.	1.5	40
10	A structural mixed model for variances in differential gene expression studies. Genetical Research, 2007, 89, 19-25.	0.9	31
11	The PX-EM algorithm for fast stable fitting of Henderson's mixed model. Genetics Selection Evolution, 2000, 32, 143-63.	3.0	20
12	A Bayesian Outlier Criterion to Detect SNPs under Selection in Large Data Sets. PLoS ONE, 2010, 5, e11913.	2.5	19
13	REML Estimation of Variance Parameters in Nonlinear Mixed Effects Models Using the SAEM Algorithm. Biometrical Journal, 2007, 49, 876-888.	1.0	16
14	Genetic analysis of growth curves using the SAEM algorithm. Genetics Selection Evolution, 2006, 38, 583-600.	3.0	11
15	Estimation in the probit normal model for binary outcomes using the SAEM algorithm. Computational Statistics and Data Analysis, 2009, 53, 1350-1360.	1.2	10
16	Modelling and estimating heterogeneous variances in threshold models for ordinal discrete data via Winbugs/Openbugs. Computer Methods and Programs in Biomedicine, 2010, 97, 19-27.	4.7	10
17	Managing Genetic Diversity, Fitness and Adaptation of Farm Animal Genetic Resources. , 2009, , 201-227.		8
18	A quasi-score approach to the analysis of ordered categorical data via a mixed heteroskedastic threshold model. Genetics Selection Evolution, 1999, 31, 1.	3.0	5

#	ARTICLE	IF	CITATIONS
19	Analysis of a simulated microarray dataset: Comparison of methods for data normalisation and detection of differential expression (Open Access publication). <i>Genetics Selection Evolution</i> , 2007, 39, 669.	3.0	5
20	A structural mixed model to shrink covariance matrices for time-course differential gene expression studies. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1630-1638.	1.2	2