Jean-Louis Foulley

List of Publications by Year
in descending order

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	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
2	Bayesian Analysis of Growth Curves Using Mixed Models Defined by Stochastic Differential Equations. Biometrics, 2010, 66, 733-741.	1.4	49
3	A Bayesian Outlier Criterion to Detect SNPs under Selection in Large Data Sets. PLoS ONE, 2010, 5, e11913.	2.5	19
4	Moderated effect size and *P*-value combinations for microarray meta-analyses. Bioinformatics, 2009, 25, 2692-2699.	4.1	139
5	A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. BMC Genomics, 2009, 10, 550.	2.8	186
6	A structural mixed model to shrink covariance matrices for time-course differential gene expression studies. Computational Statistics and Data Analysis, 2009, 53, 1630-1638.	1.2	2
7	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
8	Managing Genetic Diversity, Fitness and Adaptation of Farm Animal Genetic Resources. , 2009, , 201-227.		8
9	The Genome Response to Artificial Selection: A Case Study in Dairy Cattle. PLoS ONE, 2009, 4, e6595.	2.5	219
10	A structural mixed model for variances in differential gene expression studies. Genetical Research, 2007, 89, 19-25.	0.9	31
11	REML Estimation of Variance Parameters in Nonlinear Mixed Effects Models Using the SAEM Algorithm. Biometrical Journal, 2007, 49, 876-888.	1.0	16
12	Analysis of a simulated microarray dataset: Comparison of methods for data normalisation and detection of differential expression (Open Access publication). Genetics Selection Evolution, 2007, 39, 669.	3.0	5
13	Estimating allelic richness and its diversity. Livestock Science, 2006, 101, 150-158.	1.6	57
14	Genetic analysis of growth curves using the SAEM algorithm. Genetics Selection Evolution, 2006, 38, 583-600.	3.0	11
15	Aggregate diversity: New approach combining within- and between-breed genetic diversity. Livestock Science, 2005, 95, 247-254.	1.2	65
16	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. Conservation Genetics, 2005, 6, 729-741.	1.5	40
17	The PX-EM algorithm for fast stable fitting of Henderson's mixed model. Genetics Selection Evolution, 2000, 32, 143-63.	3.0	20
18	Genetic diversity of eleven European pig breeds. Genetics Selection Evolution, 2000, 32, 187-203.	3.0	182

#	Article	IF	Citations
19	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
20	An overview of the Weitzman approach to diversity. Genetics Selection Evolution, 1998, 30, 1.	3.0	70