Simon Boitard

List of Publications by Year
in descending order

33 papers	3,585 citations	361413 20 h-index	395702 33 g-index
42 all docs	42 docs citations	42 times ranked	5295 citing authors

#	Article	IF	Citations
1	Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. PLoS Biology, 2012, 10, e1001258.	5.6	719
2	Sparse PLS discriminant analysis: biologically relevant feature selection and graphical displays for multiclass problems. BMC Bioinformatics, 2011, 12, 253.	2.6	699
3	Detecting Signatures of Selection Through Haplotype Differentiation Among Hierarchically Structured Populations. Genetics, 2013, 193, 929-941.	2.9	340
4	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	21.4	286
5	Detecting Selection in Population Trees: The Lewontin and Krakauer Test Extended. Genetics, 2010, 186, 241-262.	2.9	243
6	Selection Signatures in Worldwide Sheep Populations. PLoS ONE, 2014, 9, e103813.	2.5	197
7	Inferring Population Size History from Large Samples of Genome-Wide Molecular Data - An Approximate Bayesian Computation Approach. PLoS Genetics, 2016, 12, e1005877.	3.5	144
8	Detecting Selection in Population Trees: The Lewontin and Krakauer Test Extended. Genetics, 2010, 186, 241-262.	2.9	122
9	Uncovering Adaptation from Sequence Data: Lessons from Genome Resequencing of Four Cattle Breeds. Genetics, 2016, 203, 433-450.	2.9	93
10	Detecting Selective Sweeps from Pooled Next-Generation Sequencing Samples. Molecular Biology and Evolution, 2012, 29, 2177-2186.	8.9	75
11	The IICR (inverse instantaneous coalescence rate) as a summary of genomic diversity: insights into demographic inference and model choice. Heredity, 2018, 120, 13-24.	2.6	74
12	Accounting for linkage disequilibrium in genome scans for selection without individual genotypes: The local score approach. Molecular Ecology, 2017, 26, 3700-3714.	3.9	65
13	Pool€hmm: a Python program for estimating the allele frequency spectrum and detecting selective sweeps from next generation sequencing of pooled samples. Molecular Ecology Resources, 2013, 13, 337-340.	4.8	55
14	Mapping QTL for white striping in relation to breast muscle yield and meat quality traits in broiler chickens. BMC Genomics, 2018, 19, 202.	2.8	53
15	Genomic Signature of Selective Sweeps Illuminates Adaptation of *Medicago truncatula* to Root-Associated Microorganisms. Molecular Biology and Evolution, 2015, 32, 2097-2110.	8.9	51
16	Detecting Selective Sweeps: A New Approach Based on Hidden Markov Models. Genetics, 2009, 181, 1567-1578.	2.9	48
17	The quail genome: insights into social behaviour, seasonal biology and infectious disease response. BMC Biology, 2020, 18, 14.	3.8	40
18	Epilepsy Caused by an Abnormal Alternative Splicing with Dosage Effect of the SV2A Gene in a Chicken Model. PLoS ONE, 2011, 6, e26932.	2.5	37

#	Article	IF	Citations
19	The IICR and the non-stationary structured coalescent: towards demographic inference with arbitrary changes in population structure. Heredity, 2018, 121, 663-678.	2.6	32
20	An ABC Method for Whole-Genome Sequence Data: Inferring Paleolithic and Neolithic Human Expansions. Molecular Biology and Evolution, 2019, 36, 1565-1579.	8.9	27
21	A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. Molecular Ecology Resources, 2019, 19, 997-1014.	4.8	24
22	Inferring number of populations and changes in connectivity under the n-island model. Heredity, 2021, 126, 896-912.	2.6	20
23	Functional investigation of a QTL affecting resistance to Haemonchus contortus in sheep. Veterinary Research, 2014, 45, 68.	3.0	18
24	Identification of genomic regions and candidate genes for chicken meat ultimate pH by combined detection of selection signatures and QTL. BMC Genomics, 2018, 19, 294.	2.8	18
25	Inference of Selection from Genetic Time Series Using Various Parametric Approximations to the Wright-Fisher Model. G3: Genes, Genomes, Genetics, 2019, 9, 4073-4086.	1.8	18
26	Combined QTL and Selective Sweep Mappings with Coding SNP Annotation and *cis*-eQTL Analysis Revealed *PARK2* and *JAG2* as New Candidate Genes for Adiposity Regulation. G3: Genes, Genomes, Genetics, 2015, 5, 517-529.	1.8	17
27	Genetic characterization of the Blonde d'Aquitaine cattle breed using microsatellite markers and relationship with three other French cattle populations. Journal of Animal Breeding and Genetics, 2011, 128, 201-208.	2.0	16
28	Coalescence times for three genes provide sufficient information to distinguish population structure from population size changes. Journal of Mathematical Biology, 2019, 78, 189-224.	1.9	10
29	Heterogeneity in effective size across the genome: effects on the inverse instantaneous coalescence rate (IICR) and implications for demographic inference under linked selection. Genetics, 2022, 220, .	2.9	10
30	Linkage disequilibrium interval mapping of quantitative trait loci. BMC Genomics, 2006, 7, 54.	2.8	7
31	Probability distribution of haplotype frequencies under the two-locus Wright–Fisher model by diffusion approximation. Theoretical Population Biology, 2007, 71, 380-391.	1.1	6
32	Gene Banks as Reservoirs to Detect Recent Selection: The Example of the Asturiana de los Valles Bovine Breed. Frontiers in Genetics, 2021, 12, 575405.	2.3	6
33	Asymptotic Distribution of the "Orthogonal" Quantitative Transmission Disequilibrium Test in a Structured Population: Exact Formula. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article 11.	0.6	1