Paul Marjoram

List of Publications by Year
in descending order

48 papers	6,262 citations	257450 24 h-index	233421 45 g-index
49 all docs	49 docs citations	49 times ranked	9555 citing authors

#	Article	IF	Citations
1	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. Nature, 2010, 465, 627-631.	27.8	1,651
2	A Big Bang model of human colorectal tumor growth. Nature Genetics, 2015, 47, 209-216.	21.4	867
3	Markov chain Monte Carlo without likelihoods. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15324-15328.	7.1	853
4	An Arabidopsis Example of Association Mapping in Structured Samples. PLoS Genetics, 2007, 3, e4.	3.5	625
5	Genome-Wide Association Mapping in Arabidopsis Identifies Previously Known Flowering Time and Pathogen Resistance Genes. PLoS Genetics, 2005, 1, e60.	3.5	378
6	Fast and flexible simulation of DNA sequence data. Genome Research, 2009, 19, 136-142.	5.5	358
7	Fast "coalescent" simulation. BMC Genetics, 2006, 7, 16.	2.7	203
8	Modern computational approaches for analysing molecular genetic variation data. Nature Reviews Genetics, 2006, 7, 759-770.	16.3	172
9	Approximately Sufficient Statistics and Bayesian Computation. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article26.	0.6	151
10	Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4828-4833.	7.1	134
11	Fine-Scale Mapping of Disease Genes with Multiple Mutations via Spatial Clustering Techniques. American Journal of Human Genetics, 2003, 73, 1368-1384.	6.2	91
12	Haplotype Structure and Phenotypic Associations in the Chromosomal Regions Surrounding Two Arabidopsis thaliana Flowering Time LociSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY781906, AY785055.. Genetics, 2004, 168, 1627-1638.	2.9	67
13	A multigene expression panel for the molecular diagnosis of Barrett's esophagus and Barrett's adenocarcinoma of the esophagus. Oncogene, 2004, 23, 4780-4788.	5.9	65
14	Critical Role of Nuclear Calcium/Calmodulin-dependent Protein Kinase IIÎ´B in Cardiomyocyte Survival in Cardiomyopathy. Journal of Biological Chemistry, 2009, 284, 24857-24868.	3.4	56
15	Brief episode of ischemia activates protective genetic program in rat heart: a gene chip study. Cardiovascular Research, 2003, 59, 450-459.	3.8	50
16	Exploring Population Genetic Models With Recombination Using Efficient Forward-Time Simulations. Genetics, 2008, 178, 2417-2427.	2.9	48
17	Estimating the Rate of Gene Conversion on Human Chromosome 21. American Journal of Human Genetics, 2004, 75, 386-397.	6.2	42
18	Application of Bayesian spatial statistical methods to analysis of haplotypes effects and gene mapping. Genetic Epidemiology, 2003, 25, 95-105.	1.3	40

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19	Age-related changes of cardiac gene expression following myocardial ischemia/reperfusion. Archives of Biochemistry and Biophysics, 2003, 420, 268-278.	3.0	36
20	The Molecular Signature of Normal Squamous Esophageal Epithelium Identifies the Presence of a Field Effect and Can Discriminate between Patients with Barrett's Esophagus and Patients with Barrett's-Associated Adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2113-2117.	2.5	36
21	Association Mapping With Single-Feature Polymorphisms. Genetics, 2006, 173, 1125-1133.	2.9	31
22	Many private mutations originate from the first few divisions of a human colorectal adenoma. Journal of Pathology, 2015, 237, 355-362.	4.5	30
23	Many colorectal cancers are â€œflatâ€•clonal expansions. Cell Cycle, 2009, 8, 2187-2193.	2.6	29
24	The Age of a Unique Event Polymorphism. Genetics, 2000, 156, 401-409.	2.9	29
25	Estimating Recombination Rates From Single-Nucleotide Polymorphisms Using Summary Statistics. Genetics, 2006, 174, 1517-1528.	2.9	28
26	The Effects of Rate Variation on Ancestral Inference in the Coalescent. Genetics, 2000, 156, 1427-1436.	2.9	27
27	Social effects for locomotion vary between environments inDrosophila melanogasterfemales. Evolution; International Journal of Organic Evolution, 2017, 71, 1765-1775.	2.3	24
28	High DNA Methylation Pattern Intratumoral Diversity Implies Weak Selection in Many Human Colorectal Cancers. PLoS ONE, 2011, 6, e21657.	2.5	18
29	Choice of Summary Statistic Weights in Approximate Bayesian Computation. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	17
30	A Bayesian Approach to Social Structure Uncovers Cryptic Regulation of Group Dynamics in Drosophila melanogaster. American Naturalist, 2015, 185, 797-808.	2.1	12
31	Approximation Bayesian computation. OA Genetics, 2013, 1, 853.	0.0	11
32	Using DNA Methylation Patterns to Infer Tumor Ancestry. PLoS ONE, 2010, 5, e12002.	2.5	10
33	Conservation of social effects (Î¨) between two species of Drosophila despite reversal of sexual dimorphism. Ecology and Evolution, 2017, 7, 10031-10041.	1.9	10
34	Ancestral inference in tumors: How much can we know?. Journal of Theoretical Biology, 2014, 359, 136-145.	1.7	9
35	WhoGEM: an admixture-based prediction machine accurately predicts quantitative functional traits in plants. Genome Biology, 2019, 20, 106.	8.8	9
36	A survey of current Bayesian gene mapping method. Human Genomics, 2004, 1, 371-4.	2.9	7

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37	Inferring Population Parameters From Single-Feature Polymorphism Data. Genetics, 2006, 173, 2257-2267.	2.9	7
38	Fine mapping â€“ 19th century style. BMC Genetics, 2005, 6, S63.	2.7	6
39	Towards the Molecular Characterization of Disease: Comparison of Molecular and Histological Analysis of Esophageal Epithelia. Journal of Gastrointestinal Surgery, 2007, 11, 1095-1104.	1.7	5
40	Translating natural genetic variation to gene expression in a computational model of the Drosophila gap gene regulatory network. PLoS ONE, 2017, 12, e0184657.	2.5	5
41	Genome-wide association mapping using mixed-models: application to GAW15 Problem 3. BMC Proceedings, 2007, 1, S164.	1.6	4
42	Practical Implications of Coalescent Theory. , 2010, , 63-84.		4
43	Cladistic analysis of genotype data-application to GAW15 Problem 3. BMC Proceedings, 2007, 1, S125.	1.6	2
44	al3c: high-performance software for parameter inference using Approximate Bayesian Computation: Table 1.. Bioinformatics, 2015, 31, 3549-3551.	4.1	2
45	Exact likelihood-free Markov chain Monte Carlo for elliptically contoured distributions. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 317-32.	0.6	1
46	Early mutation bursts in colorectal tumors. PLoS ONE, 2017, 12, e0172516.	2.5	1
47	Simulation-based Bayesian Analysis of Complex Data. , 2015, 47, 176-183.		1
48	Spatial Modeling of Multilocus Data. , 2005, , 471-487.		0