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List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

18,981
citations

81434

41
h-index

134545

62
g-index

65
all docs

65
docs citations

65
times ranked

38216
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590. | 13.7 | 71 |
| 2 | Statistical Inference for the Evolutionary History of Cancer Genomes. <i>Statistical Science</i> , 2020, 35, . | 1.6 | 13 |
| 3 | Ancestral inference from haplotypes and mutations. <i>Theoretical Population Biology</i> , 2018, 122, 12-21. | 0.5 | 3 |
| 4 | HDTD: analyzing multi-tissue gene expression data. <i>Bioinformatics</i> , 2016, 32, 2193-2195. | 1.8 | 6 |
| 5 | Metabolomic changes during cellular transformation monitored by metabolite correlation analysis and correlated with gene expression. <i>Metabolomics</i> , 2015, 11, 1848-1863. | 1.4 | 14 |
| 6 | Genetic Mapping of Natural Variation in Schooling Tendency in the Threespine Stickleback. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 761-769. | 0.8 | 31 |
| 7 | Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. <i>Cancer Research</i> , 2015, 75, 194-202. | 0.4 | 48 |
| 8 | Testing the Mean Matrix in High-Dimensional Transposable Data. <i>Biometrics</i> , 2015, 71, 157-166. | 0.8 | 8 |
| 9 | Fkh1 and Fkh2 Bind Multiple Chromosomal Elements in the <i>S. cerevisiae</i> Genome with Distinct Specificities and Cell Cycle Dynamics. <i>PLoS ONE</i> , 2014, 9, e87647. | 1.1 | 45 |
| 10 | Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4009-4014. | 3.3 | 1,471 |
| 11 | Single-Molecule Genomic Data Delineate Patient-Specific Tumor Profiles and Cancer Stem Cell Organization. <i>Cancer Research</i> , 2013, 73, 41-49. | 0.4 | 68 |
| 12 | Assessing Senescence in <i>Drosophila</i> Using Video Tracking. <i>Methods in Molecular Biology</i> , 2013, 965, 501-516. | 0.4 | 2 |
| 13 | Transcriptional Dynamics Elicited by a Short Pulse of Notch Activation Involves Feed-Forward Regulation by E(spl)/Hes Genes. <i>PLoS Genetics</i> , 2013, 9, e1003162. | 1.5 | 62 |
| 14 | Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. <i>Molecular Cell</i> , 2012, 47, 203-214. | 4.5 | 258 |
| 15 | Calling Sample Mix-Ups in Cancer Population Studies. <i>PLoS ONE</i> , 2012, 7, e41815. | 1.1 | 6 |
| 16 | The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. <i>Nature</i> , 2012, 486, 346-352. | 13.7 | 4,708 |
| 17 | Dating Primate Divergences through an Integrated Analysis of Palaeontological and Molecular Data. <i>Systematic Biology</i> , 2011, 60, 16-31. | 2.7 | 195 |
| 18 | Spatial Coupling of mTOR and Autophagy Augments Secretory Phenotypes. <i>Science</i> , 2011, 332, 966-970. | 6.0 | 469 |

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|----|--|-----|-----------|
| 19 | Sparse Partitioning: Nonlinear regression with binary or tertiary predictors, with application to association studies. <i>Annals of Applied Statistics</i> , 2011, 5, . | 0.5 | 3 |
| 20 | Modeling Evolutionary Dynamics of Epigenetic Mutations in Hierarchically Organized Tumors. <i>PLoS Computational Biology</i> , 2011, 7, e1001132. | 1.5 | 53 |
| 21 | Data analysis issues for allele-specific expression using Illumina's GoldenGate assay. <i>BMC Bioinformatics</i> , 2010, 11, 280. | 1.2 | 4 |
| 22 | The cost of reducing starting RNA quantity for Illumina BeadArrays: A bead-level dilution experiment. <i>BMC Genomics</i> , 2010, 11, 540. | 1.2 | 4 |
| 23 | High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010, 11, 25. | 2.7 | 64 |
| 24 | A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, e17-e17. | 6.5 | 200 |
| 25 | The microRNA miR-124 controls gene expression in the sensory nervous system of <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2010, 38, 3780-3793. | 6.5 | 91 |
| 26 | Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4828-4833. | 3.3 | 134 |
| 27 | Estimating primate divergence times by using conditioned birth-and-death processes. <i>Theoretical Population Biology</i> , 2009, 75, 278-285. | 0.5 | 30 |
| 28 | Autophagy mediates the mitotic senescence transition. <i>Genes and Development</i> , 2009, 23, 798-803. | 2.7 | 883 |
| 29 | Hydrogen Peroxide Stimulates Activity and Alters Behavior in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2009, 4, e7580. | 1.1 | 29 |
| 30 | Simultaneous tracking of fly movement and gene expression using GFP. <i>BMC Biotechnology</i> , 2008, 8, 93. | 1.7 | 22 |
| 31 | A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785. | 9.4 | 619 |
| 32 | Piwi and piRNAs Act Upstream of an Endogenous siRNA Pathway to Suppress Tc3 Transposon Mobility in the <i>Caenorhabditis elegans</i> Germline. <i>Molecular Cell</i> , 2008, 31, 79-90. | 4.5 | 392 |
| 33 | Modifier Effects between Regulatory and Protein-Coding Variation. <i>PLoS Genetics</i> , 2008, 4, e1000244. | 1.5 | 33 |
| 34 | An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , 2008, 18, 1518-1529. | 2.4 | 350 |
| 35 | beadarray: R classes and methods for Illumina bead-based data. <i>Bioinformatics</i> , 2007, 23, 2183-2184. | 1.8 | 443 |
| 36 | The Stem Cell Population of the Human Colon Crypt: Analysis via Methylation Patterns. <i>PLoS Computational Biology</i> , 2007, 3, e28. | 1.5 | 85 |

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|----|---|------|-----------|
| 37 | Transcriptional profiling of MnSOD-mediated lifespan extension in <i>Drosophila</i> reveals a species-general network of aging and metabolic genes. <i>Genome Biology</i> , 2007, 8, R262. | 13.9 | 123 |
| 38 | High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. <i>Genome Biology</i> , 2007, 8, R215. | 13.9 | 275 |
| 39 | Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. <i>Science</i> , 2007, 315, 848-853. | 6.0 | 1,546 |
| 40 | Population genomics of human gene expression. <i>Nature Genetics</i> , 2007, 39, 1217-1224. | 9.4 | 1,072 |
| 41 | Modern computational approaches for analysing molecular genetic variation data. <i>Nature Reviews Genetics</i> , 2006, 7, 759-770. | 7.7 | 172 |
| 42 | A Unique Recent Origin of the Allotetraploid Species <i>Arabidopsis suecica</i> : Evidence from Nuclear DNA Markers. <i>Molecular Biology and Evolution</i> , 2006, 23, 1217-1231. | 3.5 | 119 |
| 43 | Genome-Wide Associations of Gene Expression Variation in Humans. <i>PLoS Genetics</i> , 2005, 1, e78. | 1.5 | 467 |
| 44 | Statistical Tests of the Coalescent Model Based on the Haplotype Frequency Distribution and the Number of Segregating Sites. <i>Genetics</i> , 2005, 169, 1763-1777. | 1.2 | 46 |
| 45 | Estimating a Nucleotide Substitution Rate for Maize from Polymorphism at a Major Domestication Locus. <i>Molecular Biology and Evolution</i> , 2005, 22, 2304-2312. | 3.5 | 82 |
| 46 | Similar gene expression patterns characterize aging and oxidative stress in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7663-7668. | 3.3 | 353 |
| 47 | Part I: Ancestral Inference in Population Genetics. <i>Lecture Notes in Mathematics</i> , 2004, , 1-188. | 0.1 | 38 |
| 48 | Approximate Bayesian Computation and MCMC. , 2004, , 99-113. | | 15 |
| 49 | Markov chain Monte Carlo without likelihoods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15324-15328. | 3.3 | 853 |
| 50 | Linkage disequilibrium: what history has to tell us. <i>Trends in Genetics</i> , 2002, 18, 83-90. | 2.9 | 472 |
| 51 | On a Test of Depaulis and Veuille. <i>Molecular Biology and Evolution</i> , 2001, 18, 1132-1133. | 3.5 | 19 |
| 52 | The Age of a Unique Event Polymorphism. <i>Genetics</i> , 2000, 156, 401-409. | 1.2 | 29 |
| 53 | The Effects of Rate Variation on Ancestral Inference in the Coalescent. <i>Genetics</i> , 2000, 156, 1427-1436. | 1.2 | 27 |
| 54 | The ages of mutations in gene trees. <i>Annals of Applied Probability</i> , 1999, 9, . | 0.6 | 48 |

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|----|--|-----|-----------|
| 55 | The age of a mutation in a general coalescent tree. <i>Stochastic Models</i> , 1998, 14, 273-295. | 0.3 | 215 |
| 56 | Inferring Coalescence Times From DNA Sequence Data. <i>Genetics</i> , 1997, 145, 505-518. | 1.2 | 678 |
| 57 | Coalescents and Genealogical Structure Under Neutrality. <i>Annual Review of Genetics</i> , 1995, 29, 401-421. | 3.2 | 378 |
| 58 | Unrooted genealogical tree probabilities in the infinitely-many-sites model. <i>Mathematical Biosciences</i> , 1995, 127, 77-98. | 0.9 | 92 |
| 59 | The ages of alleles and a coalescent. <i>Advances in Applied Probability</i> , 1986, 18, 1-19. | 0.4 | 183 |
| 60 | The ages of alleles and a coalescent. <i>Advances in Applied Probability</i> , 1986, 18, 1-19. | 0.4 | 91 |
| 61 | Line-of-descent and genealogical processes, and their applications in population genetics models. <i>Theoretical Population Biology</i> , 1984, 26, 119-164. | 0.5 | 547 |
| 62 | On the genealogy of nested subsamples from a haploid population. <i>Advances in Applied Probability</i> , 1984, 16, 471-491. | 0.4 | 108 |