Alun Thomas

List of Publications by Year
in descending order

102 papers	5,615 citations	257101 24 h-index	79541 73 g-index
105 all docs	105 docs citations	105 times ranked	7925 citing authors

#	Article	IF	Citations
1	A Draft Sequence of the Rice Genome (Oryza sativa L. ssp. japonica). Science, 2002, 296, 92-100.	6.0	2,866
2	A candidate prostate cancer susceptibility gene at chromosome 17p. Nature Genetics, 2001, 27, 172-180.	9.4	504
3	Classification of rare missense substitutions, using risk surfaces, with genetic- and molecular-epidemiology applications. Human Mutation, 2008, 29, 1342-1354.	1.1	209
4	Forecasting Daily Patient Volumes in the Emergency Department. Academic Emergency Medicine, 2008, 15, 159-170.	0.8	203
5	Rare, Evolutionarily Unlikely Missense Substitutions in ATM Confer Increased Risk of Breast Cancer. American Journal of Human Genetics, 2009, 85, 427-446.	2.6	165
6	A multivariate time series approach to modeling and forecasting demand in the emergency department. Journal of Biomedical Informatics, 2009, 42, 123-139.	2.5	118
7	Multilocus linkage analysis by blocked Gibbs sampling. Statistics and Computing, 2000, 10, 259-269.	0.8	103
8	Calibration of Multiple In Silico Tools for Predicting Pathogenicity of Mismatch Repair Gene Missense Substitutions. Human Mutation, 2013, 34, 255-265.	1.1	80
9	Shared Genomic Segment Analysis. Mapping Disease Predisposition Genes in Extended Pedigrees Using SNP Genotype Assays. Annals of Human Genetics, 2008, 72, 279-287.	0.3	78
10	Rare, evolutionarily unlikely missense substitutions in CHEK2contribute to breast cancer susceptibility: results from a breast cancer family registry case-control mutation-screening study. Breast Cancer Research, 2011, 13, R6.	2.2	74
11	A probabilistic model for detecting coding regions in DNA sequences. Mathematical Medicine and Biology, 1994, 11, 149-160.	0.8	73
12	Evaluation of record linkage between a large healthcare provider and the Utah Population Database. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e54-e59.	2.2	59
13	Automated size selection for short cell-free DNA fragments enriches for circulating tumor DNA and improves error correction during next generation sequencing. PLoS ONE, 2018, 13, e0197333.	1.1	55
14	Linkage of body mass index to chromosome 20 in Utah pedigrees. Human Genetics, 2001, 109, 279-285.	1.8	51
15	Extending the Fellegiâ€“Sunter probabilistic record linkage method for approximate field comparators. Journal of Biomedical Informatics, 2010, 43, 24-30.	2.5	51
16	Graphical Modeling of the Joint Distribution of Alleles at Associated Loci. American Journal of Human Genetics, 2004, 74, 1088-1101.	2.6	38
17	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938.	1.8	37
18	Genomic mismatch scanning in pedigrees. Mathematical Medicine and Biology, 1994, 11, 1-16.	0.8	32

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19	An Analysis of Unclassified Missense Substitutions in Human BRCA1. Familial Cancer, 2006, 5, 77-88.	0.9	32
20	Cancer Risk in Families Fulfilling the Amsterdam Criteria for Lynch Syndrome. JAMA Oncology, 2017, 3, 1697.	3.4	32
21	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. PLoS Genetics, 2018, 14, e1007111.	1.5	30
22	Replication of the 10q11 and Xp11 Prostate Cancer Risk Variants: Results from a Utah Pedigree-Based Study. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1290-1294.	1.1	29
23	A Robust Multipoint Linkage Statistic (tlod) for Mapping Complex Trait Loci. Genetic Epidemiology, 2001, 21, S492-7.	0.6	24
24	GCHap: fast MLEs for haplotype frequencies by gene counting. Bioinformatics, 2003, 19, 2002-2003.	1.8	24
25	Population-based risk assessment for other cancers in relatives of hereditary prostate cancer (HPC) cases. Prostate, 2005, 64, 347-355.	1.2	24
26	A unique genome-wide association analysis in extended Utah high-risk pedigrees identifies a novel melanoma risk variant on chromosome arm 10q. Human Genetics, 2012, 131, 77-85.	1.8	24
27	Characterizing allelic associations from unphased diploid data by graphical modeling. Genetic Epidemiology, 2005, 29, 23-35.	0.6	23
28	A Nonsynonymous Variant in the GOLM1 Gene in Cutaneous Malignant Melanoma. Journal of the National Cancer Institute, 2018, 110, 1380-1385.	3.0	23
29	Optimal Computation of Probability Functions for Pedigree Analysis. Mathematical Medicine and Biology, 1986, 3, 167-178.	0.8	22
30	Familial Associations between Cancer Sites. Journal of Biomedical Informatics, 1999, 32, 517-529.	0.7	20
31	Enumerating the Junction Trees of a Decomposable Graph. Journal of Computational and Graphical Statistics, 2009, 18, 930-940.	0.9	18
32	Shared Genomic Segment Analysis: The Power to Find Rare Disease Variants. Annals of Human Genetics, 2012, 76, 500-509.	0.3	18
33	Characterization of linkage disequilibrium structure, mutation history, and tagging SNPs, and their use in association analyses:ELAC2 and familial early-onset prostate cancer. Genetic Epidemiology, 2005, 28, 232-243.	0.6	17
34	Evidence for Linkage on Chromosome 3q25â€“27 in a Large Autism Extended Pedigree. Human Heredity, 2005, 60, 220-226.	0.4	17
35	Identification of regions of positive selection using Shared Genomic Segment analysis. European Journal of Human Genetics, 2011, 19, 667-671.	1.4	17
36	Association Between Contact Precautions and Transmission of Methicillin-Resistant Staphylococcus aureus in Veterans Affairs Hospitals. JAMA Network Open, 2021, 4, e210971.	2.8	16

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37	Towards Linkage Analysis with Markers in Linkage Disequilibrium by Graphical Modelling. Human Heredity, 2007, 64, 16-26.	0.4	15
38	Software Trapping: A Strategy for Finding Genes in Large Genomic Regions. Journal of Biomedical Informatics, 1995, 28, 140-153.	0.7	14
39	GMCheck: Bayesian error checking for pedigreegenotypes and phenotypes. Bioinformatics, 2005, 21, 3187-3188.	1.8	14
40	Estimation of graphical models whose conditional independence graphs are interval graphs and its application to modelling linkage disequilibrium. Computational Statistics and Data Analysis, 2009, 53, 1818-1828.	0.7	14
41	Assessment of SNP streak statistics using gene drop simulation with linkage disequilibrium. Genetic Epidemiology, 2010, 34, 119-124.	0.6	13
42	Comparison of an exact and a simulation method for calculating gene extinction probabilities in pedigrees. Zoo Biology, 1990, 9, 259-274.	0.5	12
43	A New Nonparametric Linkage Statistic for Mapping Both Qualitative and Quantitative Trait Loci. Genetic Epidemiology, 2001, 21, S461-6.	0.6	12
44	Accelerated Gene Counting for Haplotype Frequency Estimation. Annals of Human Genetics, 2003, 67, 608-612.	0.3	12
45	Accuracy and Computational Efficiency of a Graphical Modeling Approach to Linkage Disequilibrium Estimation. Statistical Applications in Genetics and Molecular Biology, 2011, 10, Article 5.	0.2	12
46	Analysis of high-density single-nucleotide polymorphism data: three novel methods that control for linkage disequilibrium between markers in a linkage analysis. BMC Proceedings, 2007, 1, S160.	1.8	11
47	Creation of a national resource with linked genealogy and phenotypic data: the Veterans Genealogy Project. Genetics in Medicine, 2013, 15, 541-547.	1.1	11
48	Identification of specific Y chromosomes associated with increased prostate cancer risk. Prostate, 2014, 74, 991-998.	1.2	11
49	A Dynamic Transmission Model to Evaluate the Effectiveness of Infection Control Strategies. Open Forum Infectious Diseases, 2017, 4, ofw247.	0.4	11
50	The impact of a growing minority population on identification of duplicate records in an enterprise data warehouse. Studies in Health Technology and Informatics, 2010, 160, 1122-6.	0.2	11
51	Approximate Computation of Probability Functions for Pedigree Analysis. Mathematical Medicine and Biology, 1986, 3, 157-166.	0.8	10
52	Use of Strain Typing Data to Estimate Bacterial Transmission Rates in Healthcare Settings. Infection Control and Hospital Epidemiology, 2005, 26, 638-645.	1.0	10
53	A method and program for estimating graphical models for linkage disequilibrium that scale linearly with the number of loci, and their application to gene drop simulation. Bioinformatics, 2009, 25, 1287-1292.	1.8	10
54	Cold sore susceptibility gene-1 genotypes affect the expression of herpes labialis in unrelated human subjects. Human Genome Variation, 2014, 1, 14024.	0.4	10

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55	Efficient parameter estimation for models of healthcare-associated pathogen transmission in discrete and continuous time. Mathematical Medicine and Biology, 2015, 32, 81-100.	0.8	10
56	Extended models for nosocomial infection: parameter estimation and model selection. Mathematical Medicine and Biology, 2018, 35, i29-i49.	0.8	10
57	Maximum likelihood estimates of allele frequencies and error rates from samples of related individuals by gene counting. Bioinformatics, 2006, 22, 771-772.	1.8	9
58	A parallel genetic algorithm to discover patterns in genetic markers that indicate predisposition to multifactorial disease. Computers in Biology and Medicine, 2008, 38, 826-836.	3.9	9
59	Reparameterization of PAM50 Expression Identifies Novel Breast Tumor Dimensions and Leads to Discovery of a Genome-Wide Significant Breast Cancer Locus at 12q15. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 644-652.	1.1	9
60	Drawing Pedigrees. Mathematical Medicine and Biology, 1988, 5, 201-213.	0.8	8
61	Gene Hunting with Gradients of Likelihoods. Journal of the Royal Statistical Society Series B: Methodological, 1991, 53, 3-22.	0.8	8
62	Effectiveness of Contact Precautions to Prevent Transmission of Methicillin-Resistant Staphylococcus aureus and Vancomycin-Resistant Enterococci in Intensive Care Units. Clinical Infectious Diseases, 2021, 72, S42-S49.	2.9	8
63	A Linear Time Algorithm for Calculation of Multiple Pairwise Kinship Coefficients and the Genetic Index of Familiality. Journal of Biomedical Informatics, 1994, 27, 342-350.	0.7	7
64	Markov chain Monte Carlo methods for family trees using a parallel processor. Statistics and Computing, 1996, 6, 67-75.	0.8	7
65	Enumerating the decomposable neighbors of a decomposable graph under a simple perturbation scheme. Computational Statistics and Data Analysis, 2009, 53, 1232-1238.	0.7	6
66	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6
67	Effect of linkage disequilibrium on the identification of functional variants. Genetic Epidemiology, 2011, 35, S115-9.	0.6	6
68	Employing MCMC under the PPL framework to analyze sequence data in large pedigrees. Frontiers in Genetics, 2013, 4, 59.	1.1	6
69	Population genealogy resource shows evidence of familial clustering for Alzheimer disease. Neurology: Genetics, 2018, 4, e249.	0.9	6
70	The stochastic nature of errors in next-generation sequencing of circulating cell-free DNA. PLoS ONE, 2020, 15, e0229063.	1.1	6
71	Detection of circulating tumor DNA without a tumor-informed search using next-generation sequencing is a prognostic biomarker in pancreatic ductal adenocarcinoma. Neoplasia, 2021, 23, 859-869.	2.3	6
72	Comprehensive evaluation and efficient classification of BRCA1 RING domain missense substitutions. American Journal of Human Genetics, 2022, 109, 1153-1174.	2.6	6

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73	A chromosome 16 quantitative trait locus regulates allogeneic bone marrow engraftment in nonmyeloablated mice. Blood, 2009, 114, 202-210.	0.6	5
74	Detecting Pleiotropy and Epistasis Using Variance Components Linkage Analysis in jPAP. Human Heredity, 2011, 72, 258-263.	0.4	5
75	Linkage analysis on complex pedigrees by simulation. Mathematical Medicine and Biology, 1994, 11, 79-93.	0.8	4
76	Tests of association for rare variants: case control mutation screening. Nature Reviews Genetics, 2011, 12, 224-224.	7.7	4
77	Pairwise shared genomic segment analysis in high-risk pedigrees: application to Genetic Analysis Workshop 17 exome-sequencing SNP data. BMC Proceedings, 2011, 5, S9.	1.8	4
78	A structural Markov property for decomposable graph laws that allows control of clique intersections. Biometrika, 2018, 105, 19-29.	1.3	4
79	Peri-implantation intercourse does not lower fecundability. Human Reproduction, 2020, 35, 2107-2112.	0.4	4
80	Haplotype association analyses in resources of mixed structure using Monte Carlo testing. BMC Bioinformatics, 2010, 11, 592.	1.2	3
81	The conditional independences between variables derived from two independent identically distributed Markov random fields when pairwise order is ignored. Mathematical Medicine and Biology, 2010, 27, 283-288.	0.8	3
82	Fine mapping of the Bmgr5 quantitative trait locus for allogeneic bone marrow engraftment in mice. Immunogenetics, 2013, 65, 585-596.	1.2	3
83	Pathways analysis of differential gene expression induced by engrafting doses of total body irradiation for allogeneic bone marrow transplantation in mice. Immunogenetics, 2013, 65, 597-607.	1.2	3
84	Variation and trends in transmission dynamics of Methicillin-resistant Staphylococcus aureus in veterans affairs hospitals and nursing homes. Epidemics, 2019, 28, 100347.	1.5	3
85	A note on the four-colourability of pedigrees and its consequences for probability calculations. Statistics and Computing, 1993, 3, 51-54.	0.8	2
86	Alternative graphical representations of genotypes in a pedigree. Mathematical Medicine and Biology, 1994, 11, 217-228.	0.8	2
87	Genetic models for the inheritance of the silver colour mutation of foxes. Genetical Research, 1994, 64, 11-18.	0.3	2
88	Identification of a Major Susceptibility Locus for Lethal Graft-versus-Host Disease in MHC-Matched Mice. Journal of Immunology, 2009, 183, 462-469.	0.4	2
89	Automated construction and testing of multi-locus geneâ€“gene associations. Bioinformatics, 2011, 27, 134-136.	1.8	2
90	Enumeration and simulation of marriage node graphs on zero-loop pedigrees. Mathematical Medicine and Biology, 2003, 20, 261-275.	0.8	1

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91	Estimating the parameters of a model for proteinâ€“protein interaction graphs. Mathematical Medicine and Biology, 2006, 23, 279-295.	0.8	1
92	Case-control association testing by graphical modeling for the Genetic Analysis Workshop 17 mini-exome sequence data. BMC Proceedings, 2011, 5, S62.	1.8	1
93	Improved hidden Markov model for nosocomial infections. Mathematical Medicine and Biology, 2014, 31, 338-352.	0.8	1
94	Evidence for excess familial clustering of Post Traumatic Stress Disorder in the US Veterans Genealogy resource. Journal of Psychiatric Research, 2022, 150, 332-337.	1.5	1
95	Simulating realistic zero loop pedigrees using a bipartite Prufer code and graphical modelling. Mathematical Medicine and Biology, 2004, 21, 335-45.	0.8	1
96	Classifying, identifying and enumerating arbitrary relationships. Annals of Human Biology, 1988, 15, 229-235.	0.4	0
97	A class of perfect graphs in genetics. Mathematical Medicine and Biology, 1993, 10, 77-81.	0.8	0
98	Allelic Association in Large Pedigrees. Genetic Epidemiology, 2001, 21, S571-S575.	0.6	0
99	An Application of the Latent p Value Method to Assess Linkage in Asthma Pedigrees. Human Heredity, 2010, 70, 1-8.	0.4	0
100	Pairwise shared genomic segment analysis in three Utah high-risk breast cancer pedigrees. BMC Genomics, 2012, 13, 676.	1.2	0
101	Variation in Transmission and Clearance of Methicillin-Resistant Staphylococcus aureus Among Veteran Nursing Homes. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
102	1839. Contact Precautionsâ€™ Effects on MRSA Transmission in Department of Veterans Affairs Hospitals. Open Forum Infectious Diseases, 2019, 6, S46-S46.	0.4	0