

# Alun Thomas

## List of Publications by Year in descending order

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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	Evidence for excess familial clustering of Post Traumatic Stress Disorder in the US Veterans Genealogy resource. <i>Journal of Psychiatric Research</i> , 2022, 150, 332-337.	1.5	1
2	Comprehensive evaluation and efficient classification of BRCA1 RING domain missense substitutions. <i>American Journal of Human Genetics</i> , 2022, 109, 1153-1174.	2.6	6
3	Effectiveness of Contact Precautions to Prevent Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> and Vancomycin-Resistant Enterococci in Intensive Care Units. <i>Clinical Infectious Diseases</i> , 2021, 72, S42-S49.	2.9	8
4	Association Between Contact Precautions and Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> in Veterans Affairs Hospitals. <i>JAMA Network Open</i> , 2021, 4, e210971.	2.8	16
5	Detection of circulating tumor DNA without a tumor-informed search using next-generation sequencing is a prognostic biomarker in pancreatic ductal adenocarcinoma. <i>Neoplasia</i> , 2021, 23, 859-869.	2.3	6
6	Peri-implantation intercourse does not lower fecundability. <i>Human Reproduction</i> , 2020, 35, 2107-2112.	0.4	4
7	The stochastic nature of errors in next-generation sequencing of circulating cell-free DNA. <i>PLoS ONE</i> , 2020, 15, e0229063.	1.1	6
8	Variation and trends in transmission dynamics of Methicillin-resistant <i>Staphylococcus aureus</i> in veterans affairs hospitals and nursing homes. <i>Epidemics</i> , 2019, 28, 100347.	1.5	3
9	1839. Contact Precautions™ Effects on MRSA Transmission in Department of Veterans Affairs Hospitals. <i>Open Forum Infectious Diseases</i> , 2019, 6, S46-S46.	0.4	0
10	A Nonsynonymous Variant in the GOLM1 Gene in Cutaneous Malignant Melanoma. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1380-1385.	3.0	23
11	Reparameterization of PAM50 Expression Identifies Novel Breast Tumor Dimensions and Leads to Discovery of a Genome-Wide Significant Breast Cancer Locus at <i>12q15</i> . <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 644-652.	1.1	9
12	Extended models for nosocomial infection: parameter estimation and model selection. <i>Mathematical Medicine and Biology</i> , 2018, 35, i29-i49.	0.8	10
13	A structural Markov property for decomposable graph laws that allows control of clique intersections. <i>Biometrika</i> , 2018, 105, 19-29.	1.3	4
14	Automated size selection for short cell-free DNA fragments enriches for circulating tumor DNA and improves error correction during next generation sequencing. <i>PLoS ONE</i> , 2018, 13, e0197333.	1.1	55
15	Population genealogy resource shows evidence of familial clustering for Alzheimer disease. <i>Neurology: Genetics</i> , 2018, 4, e249.	0.9	6
16	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. <i>PLoS Genetics</i> , 2018, 14, e1007111.	1.5	30
17	Cancer Risk in Families Fulfilling the Amsterdam Criteria for Lynch Syndrome. <i>JAMA Oncology</i> , 2017, 3, 1697.	3.4	32
18	A Dynamic Transmission Model to Evaluate the Effectiveness of Infection Control Strategies. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofw247.	0.4	11

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19	Variation in Transmission and Clearance of Methicillin-Resistant Staphylococcus aureus Among Veteran Nursing Homes. Open Forum Infectious Diseases, 2016, 3, .	0.4	0
20	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
21	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
22	Identification of specific Y chromosomes associated with increased prostate cancer risk. Prostate, 2014, 74, 991-998.	1.2	11
23	Improved hidden Markov model for nosocomial infections. Mathematical Medicine and Biology, 2014, 31, 338-352.	0.8	1
24	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
25	Fine mapping of the Bmgrp5 quantitative trait locus for allogeneic bone marrow engraftment in mice. Immunogenetics, 2013, 65, 585-596.	1.2	3
26	Calibration of Multiple In Silico Tools for Predicting Pathogenicity of Mismatch Repair Gene Missense Substitutions. Human Mutation, 2013, 34, 255-265.	1.1	80
27	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
28	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
29	Employing MCMC under the PPL framework to analyze sequence data in large pedigrees. Frontiers in Genetics, 2013, 4, 59.	1.1	6
30	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
31	Shared Genomic Segment Analysis: The Power to Find Rare Disease Variants. Annals of Human Genetics, 2012, 76, 500-509.	0.3	18
32	Pairwise shared genomic segment analysis in three Utah high-risk breast cancer pedigrees. BMC Genomics, 2012, 13, 676.	1.2	0
33	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
34	Rare, evolutionarily unlikely missense substitutions in CHEK2 contribute 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
35	Tests of association for rare variants: case control mutation screening. Nature Reviews Genetics, 2011, 12, 224-224.	7.7	4
36	Identification of regions of positive selection using Shared Genomic Segment analysis. European Journal of Human Genetics, 2011, 19, 667-671.	1.4	17

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37	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6
38	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
39	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
40	Effect of linkage disequilibrium on the identification of functional variants. Genetic Epidemiology, 2011, 35, S115-9.	0.6	6
41	Automated construction and testing of multi-locus gene-gene associations. Bioinformatics, 2011, 27, 134-136.	1.8	2
42	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
43	Detecting Pleiotropy and Epistasis Using Variance Components Linkage Analysis in jPAP. Human Heredity, 2011, 72, 258-263.	0.4	5
44	Haplotype association analyses in resources of mixed structure using Monte Carlo testing. BMC Bioinformatics, 2010, 11, 592.	1.2	3
45	Extending the Fellegi-Sunter probabilistic record linkage method for approximate field comparators. Journal of Biomedical Informatics, 2010, 43, 24-30.	2.5	51
46	Assessment of SNP streak statistics using gene drop simulation with linkage disequilibrium. Genetic Epidemiology, 2010, 34, 119-124.	0.6	13
47	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
48	An Application of the Latent p Value Method to Assess Linkage in Asthma Pedigrees. Human Heredity, 2010, 70, 1-8.	0.4	0
49	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
50	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
51	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
52	Enumerating the Junction Trees of a Decomposable Graph. Journal of Computational and Graphical Statistics, 2009, 18, 930-940.	0.9	18
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	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

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55	Estimation of graphical models whose conditional independence graphs are interval graphs and its application to modelling linkage disequilibrium. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1818-1828.	0.7	14
56	Enumerating the decomposable neighbors of a decomposable graph under a simple perturbation scheme. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1232-1238.	0.7	6
57	Rare, Evolutionarily Unlikely Missense Substitutions in ATM Confer Increased Risk of Breast Cancer. <i>American Journal of Human Genetics</i> , 2009, 85, 427-446.	2.6	165
58	A chromosome 16 quantitative trait locus regulates allogeneic bone marrow engraftment in nonmyeloablated mice. <i>Blood</i> , 2009, 114, 202-210.	0.6	5
59	Classification of rare missense substitutions, using risk surfaces, with genetic- and molecular-epidemiology applications. <i>Human Mutation</i> , 2008, 29, 1342-1354.	1.1	209
60	A parallel genetic algorithm to discover patterns in genetic markers that indicate predisposition to multifactorial disease. <i>Computers in Biology and Medicine</i> , 2008, 38, 826-836.	3.9	9
61	Forecasting Daily Patient Volumes in the Emergency Department. <i>Academic Emergency Medicine</i> , 2008, 15, 159-170.	0.8	203
62	Shared Genomic Segment Analysis. Mapping Disease Predisposition Genes in Extended Pedigrees Using SNP Genotype Assays. <i>Annals of Human Genetics</i> , 2008, 72, 279-287.	0.3	78
63	Towards Linkage Analysis with Markers in Linkage Disequilibrium by Graphical Modelling. <i>Human Heredity</i> , 2007, 64, 16-26.	0.4	15
64	Analysis of high-density single-nucleotide polymorphism data: three novel methods that control for linkage disequilibrium between markers in a linkage analysis. <i>BMC Proceedings</i> , 2007, 1, S160.	1.8	11
65	An Analysis of Unclassified Missense Substitutions in Human BRCA1. <i>Familial Cancer</i> , 2006, 5, 77-88.	0.9	32
66	Estimating the parameters of a model for protein-protein interaction graphs. <i>Mathematical Medicine and Biology</i> , 2006, 23, 279-295.	0.8	1
67	Maximum likelihood estimates of allele frequencies and error rates from samples of related individuals by gene counting. <i>Bioinformatics</i> , 2006, 22, 771-772.	1.8	9
68	Characterization of linkage disequilibrium structure, mutation history, and tagging SNPs, and their use in association analyses: ELAC2 and familial early-onset prostate cancer. <i>Genetic Epidemiology</i> , 2005, 28, 232-243.	0.6	17
69	Characterizing allelic associations from unphased diploid data by graphical modeling. <i>Genetic Epidemiology</i> , 2005, 29, 23-35.	0.6	23
70	Population-based risk assessment for other cancers in relatives of hereditary prostate cancer (HPC) cases. <i>Prostate</i> , 2005, 64, 347-355.	1.2	24
71	GMCheck: Bayesian error checking for pedigreegenotypes and phenotypes. <i>Bioinformatics</i> , 2005, 21, 3187-3188.	1.8	14
72	Evidence for Linkage on Chromosome 3q25-27 in a Large Autism Extended Pedigree. <i>Human Heredity</i> , 2005, 60, 220-226.	0.4	17

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73	Use of Strain Typing Data to Estimate Bacterial Transmission Rates in Healthcare Settings. <i>Infection Control and Hospital Epidemiology</i> , 2005, 26, 638-645.	1.0	10
74	Graphical Modeling of the Joint Distribution of Alleles at Associated Loci. <i>American Journal of Human Genetics</i> , 2004, 74, 1088-1101.	2.6	38
75	Simulating realistic zero loop pedigrees using a bipartite Prufer code and graphical modelling. <i>Mathematical Medicine and Biology</i> , 2004, 21, 335-45.	0.8	1
76	Accelerated Gene Counting for Haplotype Frequency Estimation. <i>Annals of Human Genetics</i> , 2003, 67, 608-612.	0.3	12
77	GCHap: fast MLEs for haplotype frequencies by gene counting. <i>Bioinformatics</i> , 2003, 19, 2002-2003.	1.8	24
78	Enumeration and simulation of marriage node graphs on zero-loop pedigrees. <i>Mathematical Medicine and Biology</i> , 2003, 20, 261-275.	0.8	1
79	A Draft Sequence of the Rice Genome ( <i>Oryza sativa</i> L. ssp. <i>japonica</i> ). <i>Science</i> , 2002, 296, 92-100.	6.0	2,866
80	A Robust Multipoint Linkage Statistic (tlod) for Mapping Complex Trait Loci. <i>Genetic Epidemiology</i> , 2001, 21, S492-7.	0.6	24
81	Allelic Association in Large Pedigrees. <i>Genetic Epidemiology</i> , 2001, 21, S571-S575.	0.6	0
82	A New Nonparametric Linkage Statistic for Mapping Both Qualitative and Quantitative Trait Loci. <i>Genetic Epidemiology</i> , 2001, 21, S461-6.	0.6	12
83	Linkage of body mass index to chromosome 20 in Utah pedigrees. <i>Human Genetics</i> , 2001, 109, 279-285.	1.8	51
84	A candidate prostate cancer susceptibility gene at chromosome 17p. <i>Nature Genetics</i> , 2001, 27, 172-180.	9.4	504
85	Multilocus linkage analysis by blocked Gibbs sampling. <i>Statistics and Computing</i> , 2000, 10, 259-269.	0.8	103
86	Familial Associations between Cancer Sites. <i>Journal of Biomedical Informatics</i> , 1999, 32, 517-529.	0.7	20
87	Markov chain Monte Carlo methods for family trees using a parallel processor. <i>Statistics and Computing</i> , 1996, 6, 67-75.	0.8	7
88	Software Trapping: A Strategy for Finding Genes in Large Genomic Regions. <i>Journal of Biomedical Informatics</i> , 1995, 28, 140-153.	0.7	14
89	A probabilistic model for detecting coding regions in DNA sequences. <i>Mathematical Medicine and Biology</i> , 1994, 11, 149-160.	0.8	73
90	Linkage analysis on complex pedigrees by simulation. <i>Mathematical Medicine and Biology</i> , 1994, 11, 79-93.	0.8	4

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91	Alternative graphical representations of genotypes in a pedigree. <i>Mathematical Medicine and Biology</i> , 1994, 11, 217-228.	0.8	2
92	Genomic mismatch scanning in pedigrees. <i>Mathematical Medicine and Biology</i> , 1994, 11, 1-16.	0.8	32
93	A Linear Time Algorithm for Calculation of Multiple Pairwise Kinship Coefficients and the Genetic Index of Familiarity. <i>Journal of Biomedical Informatics</i> , 1994, 27, 342-350.	0.7	7
94	Genetic models for the inheritance of the silver colour mutation of foxes. <i>Genetical Research</i> , 1994, 64, 11-18.	0.3	2
95	A note on the four-colourability of pedigrees and its consequences for probability calculations. <i>Statistics and Computing</i> , 1993, 3, 51-54.	0.8	2
96	A class of perfect graphs in genetics. <i>Mathematical Medicine and Biology</i> , 1993, 10, 77-81.	0.8	0
97	Gene Hunting with Gradients of Likelihoods. <i>Journal of the Royal Statistical Society Series B: Methodological</i> , 1991, 53, 3-22.	0.8	8
98	Comparison of an exact and a simulation method for calculating gene extinction probabilities in pedigrees. <i>Zoo Biology</i> , 1990, 9, 259-274.	0.5	12
99	Classifying, identifying and enumerating arbitrary relationships. <i>Annals of Human Biology</i> , 1988, 15, 229-235.	0.4	0
100	Drawing Pedigrees. <i>Mathematical Medicine and Biology</i> , 1988, 5, 201-213.	0.8	8
101	Approximate Computation of Probability Functions for Pedigree Analysis. <i>Mathematical Medicine and Biology</i> , 1986, 3, 157-166.	0.8	10
102	Optimal Computation of Probability Functions for Pedigree Analysis. <i>Mathematical Medicine and Biology</i> , 1986, 3, 167-178.	0.8	22