JInko Graham

List of Publications by Year
in descending order

58 papers	1,468 citations	361413 20 h-index	345221 36 g-index
65 all docs	65 docs citations	65 times ranked	2569 citing authors

#	Article	IF	Citations
1	LDheatmap: AnRFunction for Graphical Display of Pairwise Linkage Disequilibria Between Single Nucleotide Polymorphisms. Journal of Statistical Software, 2006, 16, .	3.7	416
2	Genetic Effects on Age-Dependent Onset and Islet Cell Autoantibody Markers in Type 1 Diabetes. Diabetes, 2002, 51, 1346-1355.	0.6	203
3	Disequilibrium Likelihoods for Fine-Scale Mapping of a Rare Allele. American Journal of Human Genetics, 1998, 63, 1517-1530.	6.2	63
4	A discovery study of daunorubicin induced cardiotoxicity in a sample of acute myeloid leukemia patients prioritizes P450 oxidoreductase polymorphisms as a potential risk factor. Frontiers in Genetics, 2013, 4, 231.	2.3	57
5	elrm: Software Implementing Exact-like Inference for Logistic Regression Models. Journal of Statistical Software, 2007, 21, .	3.7	44
6	Identification of Novel Adenosine Deaminase 2 Gene Variants and Varied Clinical Phenotype in Pediatric Vasculitis. Arthritis and Rheumatology, 2019, 71, 1747-1755.	5.6	41
7	A Bayesian group sparse multi-task regression model for imaging genetics. Bioinformatics, 2017, 33, 2513-2522.	4.1	40
8	hapassoc: Software for Likelihood Inference of Trait Associations with SNP Haplotypes and Other Attributes. Journal of Statistical Software, 2006, 16, .	3.7	39
9	A Note on Inference of Trait Associations with SNP Haplotypes and Other Attributes in Generalized Linear Models. Human Heredity, 2004, 57, 200-206.	0.8	38
10	IA-2 autoantibodies in incident type I diabetes patients are associated with a polyadenylation signal polymorphism in GIMAP5. Genes and Immunity, 2007, 8, 503-512.	4.1	38
11	HLA associations in type 1 diabetes among patients not carrying highâ€risk DR3â€ĐQ2 or DR4â€ĐQ8 haplotypes. Tissue Antigens, 1999, 54, 543-551.	1.0	37
12	Recombinant human platelet-activating factor acetylhydrolase reduces the frequency of diabetes in the diabetes-prone BB rat. Diabetes, 1999, 48, 43-49.	0.6	35
13	Distributions of HLA-DRB1 /DQB1 alleles and haplotypes in the North-eastern Thai population: indicative of a distinct Thai population with Chinese admixtures in the Central Thais. International Journal of Immunogenetics, 1999, 26, 129-133.	1.2	35
14	Cell culture-induced aberrant methylation of the imprinted IG DMR in human lymphoblastoid cell lines. Epigenetics, 2010, 5, 50-60.	2.7	30
15	Glutamate Cysteine Ligase Catalytic Subunit Promoter Polymorphisms and Associations with Type 1 Diabetes Age-at-onset and GAD65 Autoantibody Levels. Experimental and Clinical Endocrinology and Diabetes, 2007, 115, 221-228.	1.2	24
16	Age-dependent variation of genotypes in MHC II transactivator gene (CIITA) in controls and association to type 1 diabetes. Genes and Immunity, 2012, 13, 632-640.	4.1	24
17	The Length of the CTLA-4 Microsatellite (AT)N-Repeat Affects the Risk for Type 1 Diabetes: For the Swedish Childhood Diabetes Study Group. Autoimmunity, 2000, 32, 173-180.	2.6	22
18	Single-Nucleotide Polymorphisms in Aldo-Keto and Carbonyl Reductase Genes Are Not Associated with Acute Cardiotoxicity after Daunorubicin Chemotherapy. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 2118-2120.	2.5	22

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19	D6S265*15 marks a DRB1*15, DQB1*0602 haplotype associated with attenuated protection from type 1 diabetes mellitus. Diabetologia, 2005, 48, 2540-2543.	6.3	21
20	Genetic Variation in Cell Death Genes and Risk of Non-Hodgkin Lymphoma. PLoS ONE, 2012, 7, e31560.	2.5	21
21	S100A12 Serum Levels and PMN Counts Are Elevated in Childhood Systemic Vasculitides Especially Involving Proteinase 3 Specific Anti-neutrophil Cytoplasmic Antibodies. Frontiers in Pediatrics, 2018, 6, 341.	1.9	16
22	Non-HLA type 1 diabetes genes modulate disease risk together with HLA-DQ and islet autoantibodies. Genes and Immunity, 2015, 16, 541-551.	4.1	15
23	Conditional Genotypic Probabilities for Microsatellite Loci. Genetics, 2000, 155, 1973-1980.	2.9	15
24	Stepwise detection of recombination breakpoints in sequence alignments. Bioinformatics, 2005, 21, 589-595.	4.1	12
25	A comparison of five methods for selecting tagging single-nucleotide polymorphisms. BMC Genetics, 2005, 6, S71.	2.7	11
26	A comparison of three statistical models for IDDM associations with HLA. Tissue Antigens, 1996, 48, 1-14.	1.0	9
27	The beta cell glucokinase promoter variant is an unlikely risk factor for diabetes mellitus. Diabetologia, 1997, 40, 959-962.	6.3	9
28	Negative association between type 1 diabetes and HLA DQB1*0602-DQA1*0102 is attenuated with age at onset. International Journal of Immunogenetics, 1999, 26, 117-127.	1.2	9
29	CrypticIBDcheck: an R package for checking cryptic relatedness in nominally unrelated individuals. Source Code for Biology and Medicine, 2013, 8, 5.	1.7	8
30	Multivariate association between single-nucleotide polymorphisms in Alzgene linkage regions and structural changes in the brain: discovery, refinement and validation. Statistical Applications in Genetics and Molecular Biology, 2017, 16, 349-365.	0.6	8
31	Analysis of quantitative risk factors for a common oligogenic disease. Genetic Epidemiology, 1995, 12, 759-764.	1.3	7
32	Costâ€“Effective Prediction of Gender-Labeling Errors and Estimation of Gender-Labeling Error Rates in Candidate-Gene Association Studies. Frontiers in Genetics, 2011, 2, 31.	2.3	7
33	Using Gene Genealogies to Detect Rare Variants Associated with Complex Traits. Human Heredity, 2014, 78, 117-130.	0.8	7
34	Nonrandom occurrence of lymphoid cancer types in 140 families. Leukemia and Lymphoma, 2017, 58, 2134-2143.	1.3	7
35	Different Disease Endotypes in Phenotypically Similar Vasculitides Affecting Small-to-Medium Sized Blood Vessels. Frontiers in Immunology, 2021, 12, 638571.	4.8	7
36	Simulating pedigrees ascertained for multiple disease-affected relatives. Source Code for Biology and Medicine, 2018, 13, 2.	1.7	6

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37	MHC Class I Chain-Related Gene-A Is Associated with IA2 and IAA but Not GAD in Swedish Type 1 Diabetes Mellitus. Annals of the New York Academy of Sciences, 2006, 1079, 229-239.	3.8	5
38	Adjusting for Spurious Gene-by-Environment Interaction Using Case-Parent Triads. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.6	5
39	Segregation and linkage analysis of a quantitative versus a qualitative trait in large pedigrees. Genetic Epidemiology, 1997, 14, 999-1004.	1.3	4
40	Single-Nucleotide Polymorphisms in Reductase Genes Are not Associated with Response to Daunorubicin-Based Remission Induction. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1918-1920.	2.5	4
41	Markov chain Monte Carlo sampling of gene genealogies conditional on unphased SNP genotype data. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 559-81.	0.6	4
42	Gene genealogies for genetic association mapping, with application to Crohn's disease. Frontiers in Genetics, 2013, 4, 260.	2.3	4
43	Sampletrees and Rsampletrees: sampling gene genealogies conditional on SNP genotype data. Bioinformatics, 2016, 32, 1580-1582.	4.1	4
44	Using Gene Genealogies to Localize Rare Variants Associated with Complex Traits in Diploid Populations. Human Heredity, 2018, 83, 30-39.	0.8	4
45	SimRVSequences: an R package to simulate genetic sequence data for pedigrees. Bioinformatics, 2020, 36, 2295-2297.	4.1	4
46	Case-Control Inference of Interaction between Genetic and Nongenetic Risk Factors under Assumptions on Their Distribution. Statistical Applications in Genetics and Molecular Biology, 2007, 6, Article13.	0.6	3
47	Secondary Analysis of Publicly Available Data Reveals Superoxide and Oxygen Radical Pathways are Enriched for Associations Between Type 2 Diabetes and Lowâ€Frequency Variants. Annals of Human Genetics, 2013, 77, 472-481.	0.8	3
48	A data-smoothing approach to explore and test gene-environment interaction in case-parent trios. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 159-71.	0.6	3
49	Simple Measures of Individual Cluster-Membership Certainty for Hard Partitional Clustering. American Statistician, 2019, 73, 70-79.	1.6	3
50	On the Use of Allelic Transmission Rates for Assessing Geneâ€byâ€Environment Interaction in Caseâ€Parent Trios. Annals of Human Genetics, 2010, 74, 439-451.	0.8	2
51	A statistical approach to high-throughput screening of predicted orthologs. Computational Statistics and Data Analysis, 2011, 55, 935-943.	1.2	2
52	perfectphyloR: An R package for reconstructing perfect phylogenies. BMC Bioinformatics, 2019, 20, 729.	2.6	2
53	The Contribution Plot: Decomposition and Graphical Display of the RV Coefficient, with Application to Genetic and Brain Imaging Biomarkers of Alzheimerâ€™s Disease. Human Heredity, 2019, 84, 59-72.	0.8	2
54	Small Sample Methods. , 2018, , 133-162.		2

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55	A Coalescent Model of Ancestry for a Rare Allele. Genetics, 2000, 156, 375-384.	2.9	2
56	A MARKOV CHAIN MONTE CARLO SAMPLER FOR GENE GENEALOGIES CONDITIONAL ON HAPLOTYPE DATA. , 2013, , .		2
57	Modeling Dependence beyond Correlation. , 2014, , 83-102.		0
58	Datasets for a simulated family-based exome-sequencing study. Data in Brief, 2022, 42, 108311.	1.0	0