Jason H Moore

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

580 papers	26,332 citations	75 h-index	149 g-index
667 ext. papers	30,534 ext. citations	5 avg, IF	7.28 L-index

#	Paper	IF	Citations
580	Multifactor-dimensionality reduction reveals high-order interactions among estrogen-metabolism genes in sporadic breast cancer. *American Journal of Human Genetics*, **2001**, 69, 138-47	11	1496
579	Missing heritability and strategies for finding the underlying causes of complex disease. *Nature Reviews Genetics*, **2010**, 11, 446-50	30.1	1230
578	The genetic structure and history of Africans and African Americans. *Science*, **2009**, 324, 1035-44	33.3	1042
577	Multifactor dimensionality reduction software for detecting gene-gene and gene-environment interactions. *Bioinformatics*, **2003**, 19, 376-82	7.2	951
576	Chapter 11: Genome-wide association studies. *PLoS Computational Biology*, **2012**, 8, e1002822	5	708
575	Characterization of microRNA expression levels and their biological correlates in human cancer cell lines. *Cancer Research*, **2007**, 67, 2456-68	10.1	617
574	The ubiquitous nature of epistasis in determining susceptibility to common human diseases. *Human Heredity*, **2003**, 56, 73-82	1.1	582
573	Proteomic patterns of tumour subsets in non-small-cell lung cancer. *Lancet, The*, **2003**, 362, 433-9	40	539
572	A flexible computational framework for detecting, characterizing, and interpreting statistical patterns of epistasis in genetic studies of human disease susceptibility. *Journal of Theoretical Biology*, **2006**, 241, 252-61	2.3	497
571	Power of multifactor dimensionality reduction for detecting gene-gene interactions in the presence of genotyping error, missing data, phenocopy, and genetic heterogeneity. *Genetic Epidemiology*, **2003**, 24, 150-7	2.6	464
570	Bioinformatics challenges for genome-wide association studies. *Bioinformatics*, **2010**, 26, 445-55	7.2	401
569	A high-density admixture map for disease gene discovery in african americans. *American Journal of Human Genetics*, **2004**, 74, 1001-13	11	379
568	Relief-based feature selection: Introduction and review. *Journal of Biomedical Informatics*, **2018**, 85, 189-203	2.2	352
567	New strategies for identifying gene-gene interactions in hypertension. *Annals of Medicine*, **2002**, 34, 88-95	3.5	337
566	Renin-angiotensin system gene polymorphisms and atrial fibrillation. *Circulation*, **2004**, 109, 1640-6	16.7	304
565	Breast cancer risk-associated SNPs modulate the affinity of chromatin for FOXA1 and alter gene expression. *Nature Genetics*, **2012**, 44, 1191-8	36.3	287
564	Alzheimer's Disease Neuroimaging Initiative biomarkers as quantitative phenotypes: Genetics core aims, progress, and plans. *Alzheimer's and Dementia*, **2010**, 6, 265-73	1.2	279

563	Whole genome association study of brain-wide imaging phenotypes for identifying quantitative trait loci in MCI and AD: A study of the ADNI cohort. *NeuroImage*, **2010**, 53, 1051-63	7.9	266
562	Epistasis and its implications for personal genetics. *American Journal of Human Genetics*, **2009**, 85, 309-20	11	262
561	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. *Genetic Epidemiology*, **2007**, 31, 306-15	2.6	261
560	Traversing the conceptual divide between biological and statistical epistasis: systems biology and a more modern synthesis. *BioEssays*, **2005**, 27, 637-46	4.1	258
559	Epigenomic enhancer profiling defines a signature of colon cancer. *Science*, **2012**, 336, 736-9	33.3	255
558	Gut microbial colonisation in premature neonates predicts neonatal sepsis. *Archives of Disease in Childhood: Fetal and Neonatal Edition*, **2012**, 97, F456-62	4.7	224
557	Serial analysis of the gut and respiratory microbiome in cystic fibrosis in infancy: interaction between intestinal and respiratory tracts and impact of nutritional exposures. *MBio*, **2012**, 3,	7.8	217
556	Computational analysis of gene-gene interactions using multifactor dimensionality reduction. *Expert Review of Molecular Diagnostics*, **2004**, 4, 795-803	3.8	213
555	Genetics, statistics and human disease: analytical retooling for complexity. *Trends in Genetics*, **2004**, 20, 640-7	8.5	205
554	Pathway analysis of genomic data: concepts, methods, and prospects for future development. *Trends in Genetics*, **2012**, 28, 323-32	8.5	203
553	Proteomic-based prognosis of brain tumor patients using direct-tissue matrix-assisted laser desorption ionization mass spectrometry. *Cancer Research*, **2005**, 65, 7674-81	10.1	200
552	Failure to replicate a genetic association may provide important clues about genetic architecture. *PLoS ONE*, **2009**, 4, e5639	3.7	198
551	Amplification and over-expression of the EGFR and erbB-2 genes in human esophageal adenocarcinomas. *International Journal of Cancer*, **1993**, 54, 213-9	7.5	193
550	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. *Nature Genetics*, **2013**, 45, 690-6	36.3	192
549	Cutting edge: molecular portrait of human autoimmune disease. *Journal of Immunology*, **2002**, 169, 5-9	5.3	180
548	Association of Cesarean Delivery and Formula Supplementation With the Intestinal Microbiome of 6-Week-Old Infants. *JAMA Pediatrics*, **2016**, 170, 212-9	8.3	170
547	Machine learning for detecting gene-gene interactions: a review. *Applied Bioinformatics*, **2006**, 5, 77-88		163
546	Multifactor-dimensionality reduction shows a two-locus interaction associated with Type 2 diabetes mellitus. *Diabetologia*, **2004**, 47, 549-554	10.3	161

545	Analysis of the RELN gene as a genetic risk factor for autism. *Molecular Psychiatry*, **2005**, 10, 563-71	15.1	154
544	Evaluation of a Tree-based Pipeline Optimization Tool for Automating Data Science **2016**,		149
543	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. *American Journal of Human Genetics*, **2013**, 93, 545-54	11	145
542	Concordance of multiple analytical approaches demonstrates a complex relationship between DNA repair gene SNPs, smoking and bladder cancer susceptibility. *Carcinogenesis*, **2006**, 27, 1030-7	4.6	144
541	Optimization of neural network architecture using genetic programming improves detection and modeling of gene-gene interactions in studies of human diseases. *BMC Bioinformatics*, **2003**, 4, 28	3.6	142
540	Multilocus analysis of hypertension: a hierarchical approach. *Human Heredity*, **2004**, 57, 28-38	1.1	139
539	Learning Classifier Systems: A Complete Introduction, Review, and Roadmap. *Journal of Artificial Evolution and Applications*, **2009**, 2009, 1-25		131
538	GAMETES: a fast, direct algorithm for generating pure, strict, epistatic models with random architectures. *BioData Mining*, **2012**, 5, 16	4.3	127
537	Shadows of complexity: what biological networks reveal about epistasis and pleiotropy. *BioEssays*, **2009**, 31, 220-7	4.1	117
536	Drinking-water arsenic exposure modulates gene expression in human lymphocytes from a U.S. population. *Environmental Health Perspectives*, **2008**, 116, 524-31	8.4	114
535	STUDENTJAMA. The challenges of whole-genome approaches to common diseases. *JAMA - Journal of the American Medical Association*, **2004**, 291, 1642-3	27.4	114
534	Pathways-based analyses of whole-genome association study data in bipolar disorder reveal genes mediating ion channel activity and synaptic neurotransmission. *Human Genetics*, **2009**, 125, 63-79	6.3	113
533	A gene expression signature for recent onset rheumatoid arthritis in peripheral blood mononuclear cells. *Annals of the Rheumatic Diseases*, **2004**, 63, 1387-92	2.4	112
532	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. *Brain Imaging and Behavior*, **2014**, 8, 183-207	4.1	111
531	Evidence for epistasis between SLC6A4 and ITGB3 in autism etiology and in the determination of platelet serotonin levels. *Human Genetics*, **2007**, 121, 243-56	6.3	111
530	Big data bioinformatics. *Journal of Cellular Physiology*, **2014**, 229, 1896-900	7	109
529	An application of conditional logistic regression and multifactor dimensionality reduction for detecting gene-gene interactions on risk of myocardial infarction: the importance of model validation. *BMC Bioinformatics*, **2004**, 5, 49	3.6	108
528	Integrative functional genomics identifies an enhancer looping to the SOX9 gene disrupted by the 17q24.3 prostate cancer risk locus. *Genome Research*, **2012**, 22, 1437-46	9.7	107

527	Automating Biomedical Data Science Through Tree-Based Pipeline Optimization. *Lecture Notes in Computer Science*, **2016**, 123-137	0.9	107
526	Recurrent tissue-specific mtDNA mutations are common in humans. *PLoS Genetics*, **2013**, 9, e1003929	6	105
525	Spatially uniform relieff (SURF) for computationally-efficient filtering of gene-gene interactions. *BioData Mining*, **2009**, 2, 5	4.3	105
524	A novel method to identify gene-gene effects in nuclear families: the MDR-PDT. *Genetic Epidemiology*, **2006**, 30, 111-23	2.6	101
523	Tuning ReliefF for Genome-Wide Genetic Analysis **2007**, 166-175		99
522	Scaling tree-based automated machine learning to biomedical big data with a feature set selector. *Bioinformatics*, **2020**, 36, 250-256	7.2	99
521	Single-nucleotide polymorphisms for diagnosis of salt-sensitive hypertension. *Clinical Chemistry*, **2006**, 52, 352-60	5.5	98
520	Relative impact of CYP3A genotype and concomitant medication on the severity of atorvastatin-induced muscle damage. *Pharmacogenetics and Genomics*, **2005**, 15, 415-21	1.9	98
519	PMLB: a large benchmark suite for machine learning evaluation and comparison. *BioData Mining*, **2017**, 10, 36	4.3	95
518	Acceleration of cardiovascular disease by a dysfunctional prostacyclin receptor mutation: potential implications for cyclooxygenase-2 inhibition. *Circulation Research*, **2008**, 102, 986-93	15.7	95
517	A gene expression fingerprint of C. elegans embryonic motor neurons. *BMC Genomics*, **2005**, 6, 42	4.5	95
516	Combinatorial pharmacogenetics. *Nature Reviews Drug Discovery*, **2005**, 4, 911-8	64.1	94
515	DNA repair polymorphisms modify bladder cancer risk: a multi-factor analytic strategy. *Human Heredity*, **2008**, 65, 105-18	1.1	93
514	Renin-angiotensin system gene polymorphisms and coronary artery disease in a large angiographic cohort: detection of high order gene-gene interaction. *Atherosclerosis*, **2007**, 195, 172-80	3.1	92
513	Characterizing genetic interactions in human disease association studies using statistical epistasis networks. *BMC Bioinformatics*, **2011**, 12, 364	3.6	90
512	A training-testing approach to the molecular classification of resected non-small cell lung cancer. *Clinical Cancer Research*, **2003**, 9, 4695-704	12.9	89
511	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. *Journal of Pediatrics*, **2015**, 167, 138-47.e1-3	3.6	88
510	Admixture mapping in lupus identifies multiple functional variants within IFIH1 associated with apoptosis, inflammation, and autoantibody production. *PLoS Genetics*, **2013**, 9, e1003222	6	87

509	Why epistasis is important for tackling complex human disease genetics. *Genome Medicine*, **2014**, 6, 124	14.4	86
508	Benchmarking relief-based feature selection methods for bioinformatics data mining. *Journal of Biomedical Informatics*, **2018**, 85, 168-188	10.2	82
507	Symbolic discriminant analysis of microarray data in autoimmune disease. *Genetic Epidemiology*, **2002**, 23, 57-69	2.6	75
506	The interaction of four genes in the inflammation pathway significantly predicts prostate cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2005**, 14, 2563-8	4	74
505	Exploiting the proteome to improve the genome-wide genetic analysis of epistasis in common human diseases. *Human Genetics*, **2008**, 124, 19-29	6.3	73
504	Bladder cancer SNP panel predicts susceptibility and survival. *Human Genetics*, **2009**, 125, 527-39	6.3	72
503	A computationally efficient hypothesis testing method for epistasis analysis using multifactor dimensionality reduction. *Genetic Epidemiology*, **2009**, 33, 87-94	2.6	70
502	The use of animal models in the study of complex disease: all else is never equal or why do so many human studies fail to replicate animal findings?. *BioEssays*, **2004**, 26, 170-9	4.1	69
501	E-cadherin expression in primary and metastatic thoracic neoplasms and in Barrett's oesophagus. *British Journal of Cancer*, **1995**, 71, 166-72	8.7	69
500	Structured sparse canonical correlation analysis for brain imaging genetics: an improved GraphNet method. *Bioinformatics*, **2016**, 32, 1544-51	7.2	66
499	Elevated male European and female African contributions to the genomes of African American individuals. *Human Genetics*, **2007**, 120, 713-22	6.3	66
498	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
497	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. *Blood*, **2012**, 120, 4873-81	2.2	65
496	Single nucleotide polymorphisms in ANKK1 and the dopamine D2 receptor gene affect cognitive outcome shortly after traumatic brain injury: a replication and extension study. *Brain Injury*, **2008**, 22, 705-14	2.1	64
495	Integrated analysis of genetic and proteomic data identifies biomarkers associated with adverse events following smallpox vaccination. *Genes and Immunity*, **2009**, 10, 112-9	4.4	63
494	COMT Val158Met Genotype and Individual Differences in Executive Function in Healthy Adults. *Journal of the International Neuropsychological Society*, **2011**, 17, 174-80	3.1	63
493	MnSOD polymorphism and breast cancer in a population-based case-control study. *Cancer Letters*, **2003**, 199, 27-33	9.9	63
492	A Simple and Computationally Efficient Approach to Multifactor Dimensionality Reduction Analysis of Gene-Gene Interactions for Quantitative Traits. *PLoS ONE*, **2013**, 8, e66545	3.7	63

491	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. *Npj Digital Medicine*, **2020**, 3, 109	15.7	61
490	The premature infant gut microbiome during the first 6 weeks of life differs based on gestational maturity at birth. *Pediatric Research*, **2018**, 84, 71-79	3.2	61
489	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. *Bioinformatics*, **2010**, 26, 694-5	7.2	60
488	Obesity is mediated by differential aryl hydrocarbon receptor signaling in mice fed a Western diet. *Environmental Health Perspectives*, **2012**, 120, 1252-9	8.4	60
487	Polymorphisms in the brain-derived neurotrophic factor gene influence memory and processing speed one month after brain injury. *Journal of Neurotrauma*, **2012**, 29, 1111-8	5.4	60
486	TPOT: A Tree-Based Pipeline Optimization Tool for Automating Machine Learning. *The Springer Series on Challenges in Machine Learning*, **2019**, 151-160	7.3	59
485	Genetic basis for adverse events after smallpox vaccination. *Journal of Infectious Diseases*, **2008**, 198, 16-22	7	59
484	ExSTraCS 2.0: Description and Evaluation of a Scalable Learning Classifier System. *Evolutionary Intelligence*, **2015**, 8, 89-116	1.7	57
483	beta2-Adrenergic receptor genotype and preterm delivery. *American Journal of Obstetrics and Gynecology*, **2002**, 187, 1294-8	6.4	57
482	Ideal discrimination of discrete clinical endpoints using multilocus genotypes. *In Silico Biology*, **2004** , 4, 183-94	2	56
481	An information-gain approach to detecting three-way epistatic interactions in genetic association studies. *Journal of the American Medical Informatics Association: JAMIA*, **2013**, 20, 630-6	8.6	55
480	Characterizing and Managing Missing Structured Data in Electronic Health Records: Data Analysis. *JMIR Medical Informatics*, **2018**, 6, e11	3.6	55
479	MISSING DATA IMPUTATION IN THE ELECTRONIC HEALTH RECORD USING DEEPLY LEARNED AUTOENCODERS. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2017**, 22, 207-218	1.3	54
478	Association of homozygous wild-type glutathione S-transferase M1 genotype with increased breast cancer risk. *Cancer Research*, **2004**, 64, 1233-6	10.1	54
477	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. *American Journal of Human Genetics*, **2016**, 98, 514-524	11	53
476	Data-driven advice for applying machine learning to bioinformatics problems **2018**,		52
475	Longitudinal assessment of cognitive changes associated with adjuvant treatment for breast cancer: the impact of APOE and smoking. *Psycho-Oncology*, **2014**, 23, 1382-90	3.9	52
474	A robust multifactor dimensionality reduction method for detecting gene-gene interactions with application to the genetic analysis of bladder cancer susceptibility. *Annals of Human Genetics*, **2011**, 75, 20-8	2.2	52

473	Intestinal differentiation and p53 gene alterations in Barrett's esophagus and esophageal adenocarcinoma. *International Journal of Cancer*, **1994**, 56, 487-93	7.5	51
472	Genetic Programming Neural Networks: A Powerful Bioinformatics Tool for Human Genetics. *Applied Soft Computing Journal*, **2007**, 7, 471-479	7.5	50
471	Gene expression signatures for autoimmune disease in peripheral blood mononuclear cells. *Arthritis Research*, **2004**, 6, 120-8		50
470	Multiple Plasma Biomarkers for Risk Stratification in Patients With Heart Failure and Preserved Ejection Fraction. *Journal of the American College of Cardiology*, **2020**, 75, 1281-1295	15.1	49
469	A Pilot Characterization of the Human Chronobiome. *Scientific Reports*, **2017**, 7, 17141	4.9	48
468	Effect of cardiopulmonary bypass on urea cycle intermediates and nitric oxide levels after congenital heart surgery. *Journal of Pediatrics*, **2003**, 142, 26-30	3.6	48
467	Data-driven advice for applying machine learning to bioinformatics problems. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2018**, 23, 192-203	1.3	47
466	A novel survival multifactor dimensionality reduction method for detecting gene-gene interactions with application to bladder cancer prognosis. *Human Genetics*, **2011**, 129, 101-10	6.3	46
465	Routine Discovery of Complex Genetic Models using Genetic Algorithms. *Applied Soft Computing Journal*, **2004**, 4, 79-86	7.5	46
464	Detecting, characterizing, and interpreting nonlinear gene-gene interactions using multifactor dimensionality reduction. *Advances in Genetics*, **2010**, 72, 101-16	3.3	45
463	Gene-gene interactions in folate and adenosine biosynthesis pathways affect methotrexate efficacy and tolerability in rheumatoid arthritis. *Pharmacogenetics and Genomics*, **2009**, 19, 935-44	1.9	45
462	Transcriptional profiling in coronary artery disease: indications for novel markers of coronary collateralization. *Circulation*, **2006**, 114, 1811-20	16.7	45
461	Symbolic modeling of epistasis. *Human Heredity*, **2007**, 63, 120-33	1.1	45
460	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. *Transplantation*, **2015**, 99, 2401-12	1.8	44
459	Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. *Genetic Epidemiology*, **2011**, 35, 706-21	2.6	44
458	Integrated analysis of genetic, genomic and proteomic data. *Expert Review of Proteomics*, **2004**, 1, 67-75	4.2	43
457	Sucrase-isomaltase gene expression in Barrett's esophagus and adenocarcinoma. *Gastroenterology*, **1993**, 105, 837-44	13.3	43
456	Role of genetic heterogeneity and epistasis in bladder cancer susceptibility and outcome: a learning classifier system approach. *Journal of the American Medical Informatics Association: JAMIA*, **2013**, 20, 603-12	8.6	42

455	Detecting pathway-based gene-gene and gene-environment interactions in pancreatic cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 1470-9	4	42
454	Transcriptome-guided amyloid imaging genetic analysis via a novel structured sparse learning algorithm. *Bioinformatics*, **2014**, 30, i564-71	7.2	41
453	Examination of polymorphic glutathione S-transferase (GST) genes, tobacco smoking and prostate cancer risk among men of African descent: a case-control study. *BMC Cancer*, **2009**, 9, 397	4.8	41
452	Effect of genetic variants, especially CYP2C9 and VKORC1, on the pharmacology of warfarin. *Seminars in Thrombosis and Hemostasis*, **2012**, 38, 893-904	5.3	39
451	Cytokine expression patterns associated with systemic adverse events following smallpox immunization. *Journal of Infectious Diseases*, **2006**, 194, 444-53	7	39
450	Exploiting Expert Knowledge in Genetic Programming for Genome-Wide Genetic Analysis. *Lecture Notes in Computer Science*, **2006**, 969-977	0.9	39
449	Problems with genome-wide association studies. *Science*, **2007**, 316, 1840-2	33.3	38
448	Adapting bioinformatics curricula for big data. *Briefings in Bioinformatics*, **2016**, 17, 43-50	13.4	37
447	Detecting gene-gene interactions using a permutation-based random forest method. *BioData Mining*, **2016**, 9, 14	4.3	37
446	Alterations of K-ras, p53, and erbB-2/neu in human lung adenocarcinomas. *Journal of Thoracic and Cardiovascular Surgery*, **1994**, 107, 590-595	1.5	37
445	Fetal exposures and perinatal influences on the stool microbiota of premature infants. *Journal of Maternal-Fetal and Neonatal Medicine*, **2016**, 29, 99-105	2	36
444	Interaction among variant vascular endothelial growth factor (VEGF) and its receptor in relation to prostate cancer risk. *Prostate*, **2010**, 70, 341-52	4.2	36
443	Gender-specific correlations of plasminogen activator inhibitor-1 and tissue plasminogen activator levels with cardiovascular disease-related traits. *Journal of Thrombosis and Haemostasis*, **2007**, 5, 313-20	15.4	36
442	Evaporative cooling feature selection for genotypic data involving interactions. *Bioinformatics*, **2007**, 23, 2113-20	7.2	36
441	Optimization of gene set annotations via entropy minimization over variable clusters (EMVC). *Bioinformatics*, **2014**, 30, 1698-706	7.2	35
440	An Analysis Pipeline with Statistical and Visualization-Guided Knowledge Discovery for Michigan-Style Learning Classifier Systems. *IEEE Computational Intelligence Magazine*, **2012**, 7, 35-45	5.6	35
439	Systems genetics for drug target discovery. *Trends in Pharmacological Sciences*, **2011**, 32, 623-30	13.2	35
438	Role for protein-protein interaction databases in human genetics. *Expert Review of Proteomics*, **2009**, 6, 647-59	4.2	35

437	ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. *Pharmacogenetics and Genomics*, **2007**, 17, 127-36	1.9	34
436	Petri net modeling of high-order genetic systems using grammatical evolution. *BioSystems*, **2003**, 72, 177-86	1.9	34
435	A dietary-wide association study (DWAS) of environmental metal exposure in US children and adults. *PLoS ONE*, **2014**, 9, e104768	3.7	33
434	Genome-wide association study for circulating tissue plasminogen activator levels and functional follow-up implicates endothelial STXBP5 and STX2. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 1093-101	9.4	33
433	A role for CETP TaqIB polymorphism in determining susceptibility to atrial fibrillation: a nested case control study. *BMC Medical Genetics*, **2006**, 7, 39	2.1	33
432	Where are we now? **2018**,		33
431	Electronic health records and polygenic risk scores for predicting disease risk. *Nature Reviews Genetics*, **2020**, 21, 493-502	30.1	32
430	SLC39A2 and FSIP1 polymorphisms as potential modifiers of arsenic-related bladder cancer. *Human Genetics*, **2012**, 131, 453-61	6.3	32
429	Distinct patterns of DNA methylation in conventional adenomas involving the right and left colon. *Modern Pathology*, **2014**, 27, 145-55	9.8	32
428	Investigating the parameter space of evolutionary algorithms. *BioData Mining*, **2018**, 11, 2	4.3	31
427	The ENCODE project and perspectives on pathways. *Genetic Epidemiology*, **2014**, 38, 275-80	2.6	31
426	ViSEN: methodology and software for visualization of statistical epistasis networks. *Genetic Epidemiology*, **2013**, 37, 283-5	2.6	31
425	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. *Briefings in Bioinformatics*, **2012**, 13, 420-9	13.4	31
424	Layers of epistasis: genome-wide regulatory networks and network approaches to genome-wide association studies. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2011**, 3, 513-26	6.6	31
423	Enabling personal genomics with an explicit test of epistasis. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2010**, 327-36	1.3	31
422	Diabetic nephropathy is associated with gene expression levels of oxidative phosphorylation and related pathways. *Diabetes*, **2006**, 55, 1826-31	0.9	31
421	Bioinformatics challenges in genome-wide association studies (GWAS). *Methods in Molecular Biology*, **2014**, 1168, 63-81	1.4	31
420	Epistasis analysis using multifactor dimensionality reduction. *Methods in Molecular Biology*, **2015**, 1253, 301-14	1.4	30

419	Multifactor dimensionality reduction reveals a three-locus epistatic interaction associated with susceptibility to pulmonary tuberculosis. *BioData Mining*, **2013**, 6, 4	4.3	30
418	Expression of tumor suppressive microRNA-34a is associated with a reduced risk of bladder cancer recurrence. *International Journal of Cancer*, **2015**, 137, 1158-66	7.5	30
417	Ability of epistatic interactions of cytokine single-nucleotide polymorphisms to predict susceptibility to disease subsets in systemic sclerosis patients. *Arthritis and Rheumatism*, **2008**, 59, 974-83		30
416	Identification of a two-loci epistatic interaction associated with susceptibility to rheumatoid arthritis through reverse engineering and multifactor dimensionality reduction. *Genomics*, **2007**, 90, 6-13	4.3	30
415	Connecting the dots between genes, biochemistry, and disease susceptibility: systems biology modeling in human genetics. *Molecular Genetics and Metabolism*, **2005**, 84, 104-11	3.7	30
414	Gene expression profiles in human autoimmune disease. *Current Pharmaceutical Design*, **2003**, 9, 1905-17	3.3	30
413	Cardiovascular Disease Risk Factors in Ghana during the Rural-to-Urban Transition: A Cross-Sectional Study. *PLoS ONE*, **2016**, 11, e0162753	3.7	30
412	Robustness, evolvability, and the logic of genetic regulation. *Artificial Life*, **2014**, 20, 111-26	1.4	29
411	Analysis of gene-gene interactions. *Current Protocols in Human Genetics*, **2011**, Chapter 1, Unit1.14	3.2	29
410	Accelerating epistasis analysis in human genetics with consumer graphics hardware. *BMC Research Notes*, **2009**, 2, 149	2.3	29
409	Gene expression differences in skin fibroblasts in identical twins discordant for type 1 diabetes. *Diabetes*, **2012**, 61, 739-44	0.9	29
408	A novel structure-aware sparse learning algorithm for brain imaging genetics. *Lecture Notes in Computer Science*, **2014**, 17, 329-36	0.9	29
407	Ion channels and schizophrenia: a gene set-based analytic approach to GWAS data for biological hypothesis testing. *Human Genetics*, **2012**, 131, 373-91	6.3	28
406	STatistical Inference Relief (STIR) feature selection. *Bioinformatics*, **2019**, 35, 1358-1365	7.2	28
405	CLCNKB-T481S and essential hypertension in a Ghanaian population. *Journal of Hypertension*, **2009**, 27, 298-304	1.9	27
404	Epistatic effects of polymorphisms in genes from the renin-angiotensin, bradykinin, and fibrinolytic systems on plasma t-PA and PAI-1 levels. *Genomics*, **2007**, 89, 362-9	4.3	27
403	Ant Colony Optimization for Genome-Wide Genetic Analysis. *Lecture Notes in Computer Science*, **2008**, 37-47	0.9	27
402	Learning from electronic health records across multiple sites: A communication-efficient and privacy-preserving distributed algorithm. *Journal of the American Medical Informatics Association: JAMIA*, **2020**, 27, 376-385	8.6	27

401	The application of michigan-style learning classifiersystems to address genetic heterogeneity and epistasisin association studies **2010**,		26
400	Microarray analysis of cytoplasmic versus whole cell RNA reveals a considerable number of missed and false positive mRNAs. *Rna*, **2009**, 15, 1917-28	5.8	26
399	Feature Selection using a Random Forests Classifier for the Integrated Analysis of Multiple Data Types **2006**,		26
398	The gender-specific role of polymorphisms from the fibrinolytic, renin-angiotensin, and bradykinin systems in determining plasma t-PA and PAI-1 levels. *Thrombosis and Haemostasis*, **2006**, 96, 471-477	7	26
397	Genome-Wide Analysis of Epistasis Using Multifactor Dimensionality Reduction **2007**, 17-30		26
396	Multidimensional genetic programming for multiclass classification. *Swarm and Evolutionary Computation*, **2019**, 44, 260-272	9.8	26
395	Predicting the difficulty of pure, strict, epistatic models: metrics for simulated model selection. *BioData Mining*, **2012**, 5, 15	4.3	25
394	Personalized medicine: genetic variation and loss of physiologic complexity are associated with mortality in 644 trauma patients. *Annals of Surgery*, **2009**, 250, 524-30	7.8	25
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