Jason H Moore

List of Publications by Year
in descending order

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626	33,850	5558	5519
papers	citations	82 h-index	163 g-index

668	668	668	37942
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multifactor-Dimensionality Reduction Reveals High-Order Interactions among Estrogen-Metabolism Genes in Sporadic Breast Cancer. American Journal of Human Genetics, 2001, 69, 138-147.	2.6	1,745
2	Missing heritability and strategies for finding the underlying causes of complex disease. Nature Reviews Genetics, 2010, 11, 446-450.	7.7	1,511
3	The Genetic Structure and History of Africans and African Americans. Science, 2009, 324, 1035-1044.	6.0	1,267
4	Multifactor dimensionality reduction software for detecting gene-gene and gene-environment interactions. Bioinformatics, 2003, 19, 376-382.	1.8	1,067
5	Chapter 11: Genome-Wide Association Studies. PLoS Computational Biology, 2012, 8, e1002822.	1.5	950
6	Relief-based feature selection: Introduction and review. Journal of Biomedical Informatics, 2018, 85, 189-203.	2.5	723
7	Characterization of MicroRNA Expression Levels and Their Biological Correlates in Human Cancer Cell Lines. Cancer Research, 2007, 67, 2456-2468.	0.4	669
8	The Ubiquitous Nature of Epistasis in Determining Susceptibility to Common Human Diseases. Human Heredity, 2003, 56, 73-82.	0.4	662
9	Proteomic patterns of tumour subsets in non-small-cell lung cancer. Lancet, The, 2003, 362, 433-439.	6.3	597
10	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, 252-261.	0.8	576
11	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, 150-157.	0.6	515
12	Bioinformatics challenges for genome-wide association studies. Bioinformatics, 2010, 26, 445-455.	1.8	477
13	A High-Density Admixture Map for Disease Gene Discovery in African Americans. American Journal of Human Genetics, 2004, 74, 1001-1013.	2.6	416
14	Alzheimer's Disease Neuroimaging Initiative biomarkers as quantitative phenotypes: Genetics core aims, progress, and plans. Alzheimer's and Dementia, 2010, 6, 265-273.	0.4	378
15	New strategies for identifying gene-gene interactions in hypertension. Annals of Medicine, 2002, 34, 88-95.	1.5	377
16	Breast cancer riskâ€“associated SNPs modulate the affinity of chromatin for FOXA1 and alter gene expression. Nature Genetics, 2012, 44, 1191-1198.	9.4	357
17	Renin-Angiotensin System Gene Polymorphisms and Atrial Fibrillation. Circulation, 2004, 109, 1640-1646.	1.6	343
18	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, 1051-1063.	2.1	340

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19	A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. Genetic Epidemiology, 2007, 31, 306-315.	0.6	337
20	Epistasis and Its Implications for Personal Genetics. American Journal of Human Genetics, 2009, 85, 309-320.	2.6	326
21	Epigenomic Enhancer Profiling Defines a Signature of Colon Cancer. Science, 2012, 336, 736-739.	6.0	304
22	Traversing the conceptual divide between biological and statistical epistasis: systems biology and a more modern synthesis. BioEssays, 2005, 27, 637-646.	1.2	301
23	Evaluation of a Tree-based Pipeline Optimization Tool for Automating Data Science. , 2016, , .		290
24	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, .	1.8	281
25	Gut microbial colonisation in premature neonates predicts neonatal sepsis. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2012, 97, F456-F462.	1.4	273
26	Scaling tree-based automated machine learning to biomedical big data with a feature set selector. Bioinformatics, 2020, 36, 250-256.	1.8	245
27	Association of Cesarean Delivery and Formula Supplementation With the Intestinal Microbiome of 6-Week-Old Infants. JAMA Pediatrics, 2016, 170, 212.	3.3	238
28	Pathway analysis of genomic data: concepts, methods, and prospects for future development. Trends in Genetics, 2012, 28, 323-332.	2.9	237
29	Computational analysis of gene-gene interactions using multifactor dimensionality reduction. Expert Review of Molecular Diagnostics, 2004, 4, 795-803.	1.5	235
30	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
31	Genetics, statistics and human disease: analytical retooling for complexity. Trends in Genetics, 2004, 20, 640-647.	2.9	230
32	Failure to Replicate a Genetic Association May Provide Important Clues About Genetic Architecture. PLoS ONE, 2009, 4, e5639.	1.1	227
33	A global view of epistasis. Nature Genetics, 2005, 37, 13-14.	9.4	221
34	Proteomic-Based Prognosis of Brain Tumor Patients Using Direct-Tissue Matrix-Assisted Laser Desorption Ionization Mass Spectrometry. Cancer Research, 2005, 65, 7674-7681.	0.4	221
35	Amplification and over-expression of theEGFR anderbB-2 genes in human esophageal adenocarcinomas. International Journal of Cancer, 1993, 54, 213-219.	2.3	209
36	Machine Learning for Detecting Gene-Gene Interactions. Applied Bioinformatics, 2006, 5, 77-88.	1.7	209

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37	Cutting Edge: Molecular Portrait of Human Autoimmune Disease. Journal of Immunology, 2002, 169, 5-9.	0.4	193
38	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.	1.2	190
39	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, 545-554.	2.6	189
40	PMLB: a large benchmark suite for machine learning evaluation and comparison. BioData Mining, 2017, 10, 36.	2.2	188
41	GAMETES: a fast, direct algorithm for generating pure, strict, epistatic models with random architectures. BioData Mining, 2012, 5, 16.	2.2	184
42	Multifactor-dimensionality reduction shows a two-locus interaction associated with Type 2 diabetes mellitus. Diabetologia, 2004, 47, 549-554.	2.9	183
43	Analysis of the RELN gene as a genetic risk factor for autism. Molecular Psychiatry, 2005, 10, 563-571.	4.1	181
44	Learning Classifier Systems: A Complete Introduction, Review, and Roadmap. Journal of Artificial Evolution and Applications, 2009, 2009, 1-25.	1.8	173
45	Automating Biomedical Data Science Through Tree-Based Pipeline Optimization. Lecture Notes in Computer Science, 2016, , 123-137.	1.0	170
46	Shadows of complexity: what biological networks reveal about epistasis and pleiotropy. BioEssays, 2009, 31, 220-227.	1.2	162
47	Concordance of multiple analytical approaches demonstrates a complex relationship between DNA repair gene SNPs, smoking and bladder cancer susceptibility. Carcinogenesis, 2006, 27, 1030-1037.	1.3	161
48	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. Brain Imaging and Behavior, 2014, 8, 183-207.	1.1	161
49	Big Data Bioinformatics. Journal of Cellular Physiology, 2014, 229, 1896-1900.	2.0	161
50	Benchmarking relief-based feature selection methods for bioinformatics data mining. Journal of Biomedical Informatics, 2018, 85, 168-188.	2.5	156
51	TPOT: A Tree-Based Pipeline Optimization Tool for Automating Machine Learning. The Springer Series on Challenges in Machine Learning, 2019, , 151-160.	10.4	149
52	Multilocus Analysis of Hypertension: A Hierarchical Approach. Human Heredity, 2004, 57, 28-38.	0.4	146
53	Evidence for epistasis between SLC6A4 and ITGB3 in autism etiology and in the determination of platelet serotonin levels. Human Genetics, 2007, 121, 243-256.	1.8	135
54	The Challenges of Whole-Genome Approaches to Common Diseases. JAMA - Journal of the American Medical Association, 2004, 291, 1642-1643.	3.8	133

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55	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. Journal of Pediatrics, 2015, 167, 138-147.e3.	0.9	131
56	Recurrent Tissue-Specific mtDNA Mutations Are Common in Humans. PLoS Genetics, 2013, 9, e1003929.	1.5	130
57	Why epistasis is important for tackling complex human disease genetics. Genome Medicine, 2014, 6, 124.	3.6	130
58	Drinking-Water Arsenic Exposure Modulates Gene Expression in Human Lymphocytes from a U.S. Population. Environmental Health Perspectives, 2008, 116, 524-531.	2.8	129
59	Spatially Uniform ReliefF (SURF) for computationally-efficient filtering of gene-gene interactions. BioData Mining, 2009, 2, 5.	2.2	129
60	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. Npj Digital Medicine, 2020, 3, 109.	5.7	128
61	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.	1.2	127
62	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.	1.8	126
63	A gene expression signature for recent onset rheumatoid arthritis in peripheral blood mononuclear cells. Annals of the Rheumatic Diseases, 2004, 63, 1387-1392.	0.5	124
64	Data-driven advice for applying machine learning to bioinformatics problems. , 2018, , .		118
65	Relative impact of CYP3A genotype and concomitant medication on the severity of atorvastatin-induced muscle damage. Pharmacogenetics and Genomics, 2005, 15, 415-421.	0.7	117
66	Tuning ReliefF for Genome-Wide Genetic Analysis. , 2007, , 166-175.		117
67	A gene expression fingerprint of C. elegans embryonic motor neurons. BMC Genomics, 2005, 6, 42.	1.2	116
68	Multiple Plasma Biomarkers for RiskÂStratification in Patients With HeartÂFailureÂand Preserved Ejection Fraction. Journal of the American College of Cardiology, 2020, 75, 1281-1295.	1.2	116
69	Integrative functional genomics identifies an enhancer looping to the SOX9 gene disrupted by the 17q24.3 prostate cancer risk locus. Genome Research, 2012, 22, 1437-1446.	2.4	115
70	A novel method to identify geneâ€“gene effects in nuclear families: the MDR-PDT. Genetic Epidemiology, 2006, 30, 111-123.	0.6	112
71	Acceleration of Cardiovascular Disease by a Dysfunctional Prostacyclin Receptor Mutation. Circulation Research, 2008, 102, 986-993.	2.0	112
72	Reninâ€“angiotensin system gene polymorphisms and coronary artery disease in a large angiographic cohort: Detection of high order geneâ€“gene interaction. Atherosclerosis, 2007, 195, 172-180.	0.4	107

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73	Admixture Mapping in Lupus Identifies Multiple Functional Variants within IFIH1 Associated with Apoptosis, Inflammation, and Autoantibody Production. PLoS Genetics, 2013, 9, e1003222.	1.5	107
74	Combinatorial Pharmacogenetics. Nature Reviews Drug Discovery, 2005, 4, 911-918.	21.5	106
75	Characterizing genetic interactions in human disease association studies using statistical epistasis networks. BMC Bioinformatics, 2011, 12, 364.	1.2	106
76	Characterizing and Managing Missing Structured Data in Electronic Health Records: Data Analysis. JMIR Medical Informatics, 2018, 6, e11.	1.3	104
77	Single-Nucleotide Polymorphisms for Diagnosis of Salt-Sensitive Hypertension. Clinical Chemistry, 2006, 52, 352-360.	1.5	103
78	A training-testing approach to the molecular classification of resected non-small cell lung cancer. Clinical Cancer Research, 2003, 9, 4695-704.	3.2	102
79	DNA Repair Polymorphisms Modify Bladder Cancer Risk: A Multi-factor Analytic Strategy. Human Heredity, 2008, 65, 105-118.	0.4	101
80	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.	1.1	101
81	Structured sparse canonical correlation analysis for brain imaging genetics: an improved GraphNet method. Bioinformatics, 2016, 32, 1544-1551.	1.8	96
82	The Interaction of Four Genes in the Inflammation Pathway Significantly Predicts Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2563-2568.	1.1	91
83	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	0.6	90
84	MISSING DATA IMPUTATION IN THE ELECTRONIC HEALTH RECORD USING DEEPLY LEARNED AUTOENCODERS. , 2017, 22, 207-218.		89
85	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
86	ExSTraCS 2.0: description and evaluation of a scalable learning classifier system. Evolutionary Intelligence, 2015, 8, 89-116.	2.3	88
87	Bladder cancer SNP panel predicts susceptibility and survival. Human Genetics, 2009, 125, 527-539.	1.8	85
88	Symbolic discriminant analysis of microarray data in autoimmune disease. Genetic Epidemiology, 2002, 23, 57-69.	0.6	84
89	Elevated male European and female African contributions to the genomes of African American individuals. Human Genetics, 2006, 120, 713-722.	1.8	84
90	Exploiting the proteome to improve the genome-wide genetic analysis of epistasis in common human diseases. Human Genetics, 2008, 124, 19-29.	1.8	83

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91	Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 2020, 9, .	3.3	83
92	A Simple and Computationally Efficient Approach to Multifactor Dimensionality Reduction Analysis of Gene-Gene Interactions for Quantitative Traits. PLoS ONE, 2013, 8, e66545.	1.1	82
93	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, 170-179.	1.2	81
94	A computationally efficient hypothesis testing method for epistasis analysis using multifactor dimensionality reduction. Genetic Epidemiology, 2009, 33, 87-94.	0.6	80
95	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. American Journal of Human Genetics, 2016, 98, 514-524.	2.6	78
96	Electronic health records and polygenic risk scores for predicting disease risk. Nature Reviews Genetics, 2020, 21, 493-502.	7.7	78
97	Integrated analysis of genetic and proteomic data identifies biomarkers associated with adverse events following smallpox vaccination. Genes and Immunity, 2009, 10, 112-119.	2.2	77
98	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. Bioinformatics, 2010, 26, 694-695.	1.8	76
99	E-cadherin expression in primary and metastatic thoracic neoplasms and in Barrett's oesophagus. British Journal of Cancer, 1995, 71, 166-172.	2.9	75
100	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, 705-714.	0.6	75
101	Obesity Is Mediated by Differential Aryl Hydrocarbon Receptor Signaling in Mice Fed a Western Diet. Environmental Health Perspectives, 2012, 120, 1252-1259.	2.8	74
102	Polymorphisms in the Brain-Derived Neurotrophic Factor Gene Influence Memory and Processing Speed One Month after Brain Injury. Journal of Neurotrauma, 2012, 29, 1111-1118.	1.7	72
103	Where are we now?. , 2018, , .		72
104	COMT Val158Met Genotype and Individual Differences in Executive Function in Healthy Adults. Journal of the International Neuropsychological Society, 2011, 17, 174-180.	1.2	70
105	A Pilot Characterization of the Human Chronobiome. Scientific Reports, 2017, 7, 17141.	1.6	70
106	An information-gain approach to detecting three-way epistatic interactions in genetic association studies. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 630-636.	2.2	69
107	Longitudinal assessment of cognitive changes associated with adjuvant treatment for breast cancer: the impact of APOE and smoking. Psycho-Oncology, 2014, 23, 1382-1390.	1.0	69
108	MnSOD polymorphism and breast cancer in a population-based caseâ€“control study. Cancer Letters, 2003, 199, 27-33.	3.2	68

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109	Genetic Basis for Adverse Events after Smallpox Vaccination. Journal of Infectious Diseases, 2008, 198, 16-22.	1.9	67
110	Optimization of gene set annotations via entropy minimization over variable clusters (EMVC). Bioinformatics, 2014, 30, 1698-1706.	1.8	65
111	Ideal discrimination of discrete clinical endpoints using multilocus genotypes. In Silico Biology, 2004, 4, 183-94.	0.4	63
112	Î²2-Adrenergic receptor genotype and preterm delivery. American Journal of Obstetrics and Gynecology, 2002, 187, 1294-1298.	0.7	62
113	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, 20-28.	0.3	62
114	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.	2.2	61
115	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. Journal of Medical Internet Research, 2021, 23, e22219.	2.1	61
116	Genetic programming neural networks: A powerful bioinformatics tool for human genetics. Applied Soft Computing Journal, 2007, 7, 471-479.	4.1	60
117	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. Transplantation, 2015, 99, 2401-2412.	0.5	60
118	Effect of cardiopulmonary bypass on urea cycle intermediates and nitric oxide levels after congenital heart surgery. Journal of Pediatrics, 2003, 142, 26-30.	0.9	59
119	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, 603-612.	2.2	59
120	Gene expression signatures for autoimmune disease in peripheral blood mononuclear cells. Arthritis Research, 2004, 6, 120.	2.0	58
121	Association of Homozygous Wild-Type Glutathione S-Transferase M1 Genotype with Increased Breast Cancer Risk. Cancer Research, 2004, 64, 1233-1236.	0.4	57
122	A novel survival multifactor dimensionality reduction method for detecting geneâ€“gene interactions with application to bladder cancer prognosis. Human Genetics, 2011, 129, 101-110.	1.8	57
123	Transcriptome-guided amyloid imaging genetic analysis via a novel structured sparse learning algorithm. Bioinformatics, 2014, 30, i564-i571.	1.8	57
124	Feature Selection using a Random Forests Classifier for the Integrated Analysis of Multiple Data Types. , 2006, , .		55
125	Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. Genetic Epidemiology, 2011, 35, 706-721.	0.6	54
126	Use of electronic health records to support a public health response to the COVID-19 pandemic in the United States: a perspective from 15 academic medical centers. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 393-401.	2.2	54

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127	Effect of Genetic Variants, Especially CYP2C9 and VKORC1, on the Pharmacology of Warfarin. Seminars in Thrombosis and Hemostasis, 2012, 38, 893-904.	1.5	53
128	Data-driven advice for applying machine learning to bioinformatics problems. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 192-203.	0.7	53
129	Intestinal differentiation andp53 gene alterations in barrett's esophagus and esophageal adenocarcinoma. International Journal of Cancer, 1994, 56, 487-493.	2.3	52
130	Detecting, Characterizing, and Interpreting Nonlinear Geneâ€“Gene Interactions Using Multifactor Dimensionality Reduction. Advances in Genetics, 2010, 72, 101-116.	0.8	52
131	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes. Nature Metabolism, 2022, 4, 284-299.	5.1	52
132	Integrated analysis of genetic, genomic and proteomic data. Expert Review of Proteomics, 2004, 1, 67-75.	1.3	51
133	Routine discovery of complex genetic models using genetic algorithms. Applied Soft Computing Journal, 2004, 4, 79-86.	4.1	51
134	Transcriptional Profiling in Coronary Artery Disease. Circulation, 2006, 114, 1811-1820.	1.6	51
135	Symbolic Modeling of Epistasis. Human Heredity, 2007, 63, 120-133.	0.4	51
136	Geneâ€“gene interactions in folate and adenosine biosynthesis pathways affect methotrexate efficacy and tolerability in rheumatoid arthritis. Pharmacogenetics and Genomics, 2009, 19, 935-944.	0.7	51
137	Detecting gene-gene interactions using a permutation-based random forest method. BioData Mining, 2016, 9, 14.	2.2	51
138	Investigating the parameter space of evolutionary algorithms. BioData Mining, 2018, 11, 2.	2.2	51
139	An analysis pipeline with statistical and visualization-guided knowledge discovery for Michigan-style learning classifier systems. IEEE Computational Intelligence Magazine, 2012, 7, 35-45.	3.4	50
140	The ENCODE Project and Perspectives on Pathways. Genetic Epidemiology, 2014, 38, 275-280.	0.6	47
141	STatistical Inference Relief (STIR) feature selection. Bioinformatics, 2019, 35, 1358-1365.	1.8	47
142	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.	1.1	46
143	Learning from local to global: An efficient distributed algorithm for modeling time-to-event data. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1028-1036.	2.2	46
144	Detecting Pathway-Based Gene-Gene and Gene-Environment Interactions in Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1470-1479.	1.1	45

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145	Role for proteinâ€“protein interaction databases in human genetics. Expert Review of Proteomics, 2009, 6, 647-659.	1.3	45
146	Sucrase-isomaltase gene expression in Barrett's esophagus and adenocarcinoma. Gastroenterology, 1993, 105, 837-844.	0.6	44
147	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, 313-320.	1.9	44
148	Systems genetics for drug target discovery. Trends in Pharmacological Sciences, 2011, 32, 623-630.	4.0	44
149	Adapting bioinformatics curricula for big data. Briefings in Bioinformatics, 2016, 17, 43-50.	3.2	44
150	Alterations of K-ras, p53, and erbB-2/neu in human lung adenocarcinomas. Journal of Thoracic and Cardiovascular Surgery, 1994, 107, 590-595.	0.4	43
151	Cytokine Expression Patterns Associated with Systemic Adverse Events following Smallpox Immunization. Journal of Infectious Diseases, 2006, 194, 444-453.	1.9	43
152	A Dietary-Wide Association Study (DWAS) of Environmental Metal Exposure in US Children and Adults. PLoS ONE, 2014, 9, e104768.	1.1	43
153	Robustness, Evolvability, and the Logic of Genetic Regulation. Artificial Life, 2014, 20, 111-126.	1.0	43
154	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, 1093-1101.	1.1	43
155	A Probabilistic and Multi-Objective Analysis of Lexicase Selection and Îµ-Lexicase Selection. Evolutionary Computation, 2019, 27, 377-402.	2.3	43
156	Diabetic Nephropathy Is Associated With Gene Expression Levels of Oxidative Phosphorylation and Related Pathways. Diabetes, 2006, 55, 1826-1831.	0.3	42
157	Interaction among variant vascular endothelial growth factor (VEGF) and its receptor in relation to prostate cancer risk. Prostate, 2010, 70, 341-352.	1.2	42
158	Fetal exposures and perinatal influences on the stool microbiota of premature infants. Journal of Maternal-Fetal and Neonatal Medicine, 2016, 29, 99-105.	0.7	42
159	Model selection for metabolomics: predicting diagnosis of coronary artery disease using automated machine learning. Bioinformatics, 2020, 36, 1772-1778.	1.8	42
160	Cardiovascular Disease Risk Factors in Ghana during the Rural-to-Urban Transition: A Cross-Sectional Study. PLoS ONE, 2016, 11, e0162753.	1.1	41
161	Distinct patterns of DNA methylation in conventional adenomas involving the right and left colon. Modern Pathology, 2014, 27, 145-155.	2.9	40
162	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	5.8	40

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163	Bioinformatics Challenges in Genome-Wide Association Studies (GWAS). Methods in Molecular Biology, 2014, 1168, 63-81.	0.4	40
164	Petri net modeling of high-order genetic systems using grammatical evolution. BioSystems, 2003, 72, 177-186.	0.9	39
165	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	39
166	Evaporative cooling feature selection for genotypic data involving interactions. Bioinformatics, 2007, 23, 2113-2120.	1.8	39
167	Analysis of Geneâ€Gene Interactions. Current Protocols in Human Genetics, 2011, 70, Unit1.14.	3.5	39
168	Vi<scp>SEN</scp>: Methodology and Software for Visualization of Statistical Epistasis Networks. Genetic Epidemiology, 2013, 37, 283-285.	0.6	39
169	Problems with genome-wide association studies. Science, 2007, 316, 1840-2.	6.0	39
170	Ant Colony Optimization for Genome-Wide Genetic Analysis. Lecture Notes in Computer Science, 2008, , 37-47.	1.0	38
171	The application of michigan-style learning classifiersystems to address genetic heterogeneity and epistasisin association studies. , 2010, , .		37
172	Validation of an internationally derived patient severity phenotype to support COVID-19 analytics from electronic health record data. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1411-1420.	2.2	37
173	Accelerating epistasis analysis in human genetics with consumer graphics hardware. BMC Research Notes, 2009, 2, 149.	0.6	36
174	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. Briefings in Bioinformatics, 2012, 13, 420-429.	3.2	36
175	Expression of tumor suppressive micro<scp>RNA</scp>â€34a is associated with a reduced risk of bladder cancer recurrence. International Journal of Cancer, 2015, 137, 1158-1166.	2.3	36
176	Multidimensional genetic programming for multiclass classification. Swarm and Evolutionary Computation, 2019, 44, 260-272.	4.5	36
177	A Novel Structure-Aware Sparse Learning Algorithm for Brain Imaging Genetics. Lecture Notes in Computer Science, 2014, 17, 329-336.	1.0	36
178	ABCB1 and GST polymorphisms associated with TP53 status in breast cancer. Pharmacogenetics and Genomics, 2007, 17, 127-136.	0.7	35
179	Ability of epistatic interactions of cytokine singleâ€nucleotide polymorphisms to predict susceptibility to disease subsets in systemic sclerosis patients. Arthritis and Rheumatism, 2008, 59, 974-983.	6.7	35
180	ENABLING PERSONAL GENOMICS WITH AN EXPLICIT TEST OF EPISTASIS. , 2009, , 327-336.		35

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181	Layers of epistasis: genomeâ€wide regulatory networks and network approaches to genomeâ€wide association studies. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 513-526.	6.6	35
182	Epistasis Analysis Using Multifactor Dimensionality Reduction. Methods in Molecular Biology, 2015, 1253, 301-314.	0.4	35
183	Gene Expression Profiles in Human Autoimmune Disease. Current Pharmaceutical Design, 2003, 9, 1905-1917.	0.9	34
184	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.	1.3	34
185	SLC39A2 and FSIP1 polymorphisms as potential modifiers of arsenic-related bladder cancer. Human Genetics, 2012, 131, 453-461.	1.8	34
186	Multifactor dimensionality reduction reveals a three-locus epistatic interaction associated with susceptibility to pulmonary tuberculosis. BioData Mining, 2013, 6, 4.	2.2	34
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