Eleazar Eskin

List of Publications by Year
in descending order

202	21,865	30047 54	12258 133
papers	citations	h-index	g-index

228	228	228	32310
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Variance component model to account for sample structure in genome-wide association studies. Nature Genetics, 2010, 42, 348-354.	9.4	2,287
2	Efficient Control of Population Structure in Model Organism Association Mapping. Genetics, 2008, 178, 1709-1723.	1.2	1,752
3	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
4	Assessing computational tools for the discovery of transcription factor binding sites. Nature Biotechnology, 2005, 23, 137-144.	9.4	1,121
5	Whole-Genome Patterns of Common DNA Variation in Three Human Populations. Science, 2005, 307, 1072-1079.	6.0	1,074
6	Colocalization of GWAS and eQTL Signals Detects Target Genes. American Journal of Human Genetics, 2016, 99, 1245-1260.	2.6	569
7	Comparative Analysis of Proteome and Transcriptome Variation in Mouse. PLoS Genetics, 2011, 7, e1001393.	1.5	548
8	Random-Effects Model Aimed at Discovering Associations in Meta-Analysis of Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 586-598.	2.6	515
9	Chromosome conformation elucidates regulatory relationships in developing human brain. Nature, 2016, 538, 523-527.	13.7	507
10	Mismatch string kernels for discriminative protein classification. Bioinformatics, 2004, 20, 467-476.	1.8	485
11	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
12	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. Cell Metabolism, 2013, 17, 141-152.	7.2	464
13	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. Nature, 2007, 448, 1050-1053.	13.7	406
14	Identifying Causal Variants at Loci with Multiple Signals of Association. Genetics, 2014, 198, 497-508.	1.2	400
15	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	9.4	389
16	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
17	THE SPECTRUM KERNEL: A STRING KERNEL FOR SVM PROTEIN CLASSIFICATION. , 2001, , .		321
18	A Comparison of Phasing Algorithms for Trios and Unrelated Individuals. American Journal of Human Genetics, 2006, 78, 437-450.	2.6	308

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19	A high-resolution association mapping panel for the dissection of complex traits in mice. Genome Research, 2010, 20, 281-290.	2.4	299
20	Improved linear mixed models for genome-wide association studies. Nature Methods, 2012, 9, 525-526.	9.0	292
21	Genetic and environmental control of host-gut microbiota interactions. Genome Research, 2015, 25, 1558-1569.	2.4	288
22	Finding composite regulatory patterns in DNA sequences. Bioinformatics, 2002, 18, S354-S363.	1.8	263
23	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	6.0	260
24	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. Nature Methods, 2016, 13, 443-445.	9.0	205
25	Haplotype reconstruction from genotype data using Imperfect Phylogeny. Bioinformatics, 2004, 20, 1842-1849.	1.8	185
26	Whole-genome analysis of Alu repeat elements reveals complex evolutionary history. Genome Research, 2004, 14, 2245-2252.	2.4	184
27	Genome-wide association studies in mice. Nature Reviews Genetics, 2012, 13, 807-817.	7.7	172
28	Interpreting Meta-Analyses of Genome-Wide Association Studies. PLoS Genetics, 2012, 8, e1002555.	1.5	171
29	Population structure in genetic studies: Confounding factors and mixed models. PLoS Genetics, 2018, 14, e1007309.	1.5	164
30	Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers. PLoS Genetics, 2009, 5, e1000456.	1.5	157
31	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	9.4	154
32	A model-based approach for analysis of spatial structure in genetic data. Nature Genetics, 2012, 44, 725-731.	9.4	147
33	The Hybrid Mouse Diversity Panel: a resource for systems genetics analyses of metabolic and cardiovascular traits. Journal of Lipid Research, 2016, 57, 925-942.	2.0	143
34	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. NeuroImage, 2010, 51, 542-554.	2.1	141
35	Accurate Discovery of Expression Quantitative Trait Loci Under Confounding From Spurious and Genuine Regulatory Hotspots. Genetics, 2008, 180, 1909-1925.	1.2	136
36	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. Mammalian Genome, 2012, 23, 680-692.	1.0	134

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37	Genetic Architecture of Atherosclerosis in Mice: A Systems Genetics Analysis of Common Inbred Strains. PLoS Genetics, 2015, 11, e1005711.	1.5	124
38	Genome-wide analysis highlights contribution of immune system pathways to the genetic architecture of asthma. Nature Communications, 2020, 11, 1776.	5.8	119
39	Systematic benchmarking of omics computational tools. Nature Communications, 2019, 10, 1393.	5.8	111
40	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. PLoS Genetics, 2013, 9, e1003491.	1.5	109
41	Mouse Genome-Wide Association and Systems Genetics Identify Asxl2 As a Regulator of Bone Mineral Density and Osteoclastogenesis. PLoS Genetics, 2011, 7, e1002038.	1.5	108
42	Optimal algorithms for haplotype assembly from whole-genome sequence data. Bioinformatics, 2010, 26, i183-i190.	1.8	106
43	Catecholamine Releaseâ€“Inhibitory Peptide Catestatin (Chromogranin A 352â€“372). Circulation, 2007, 115, 2271-2281.	1.6	105
44	EFFICIENT RECONSTRUCTION OF HAPLOTYPE STRUCTURE VIA PERFECT PHYLOGENY. Journal of Bioinformatics and Computational Biology, 2003, 01, 1-20.	0.3	100
45	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. Genetics, 2010, 185, 1081-1095.	1.2	95
46	â€œGood Enough Solutionsâ€•and the Genetics of Complex Diseases. Circulation Research, 2012, 111, 493-504.	2.0	94
47	Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology. Nature Communications, 2019, 10, 3417.	5.8	92
48	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90
49	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	1.5	85
50	The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, Anopheles arabiensis. PLoS Genetics, 2016, 12, e1006303.	1.5	76
51	Widespread Allelic Heterogeneity in Complex Traits. American Journal of Human Genetics, 2017, 100, 789-802.	2.6	74
52	Identification of causal genes for complex traits. Bioinformatics, 2015, 31, i206-i213.	1.8	72
53	Multiple testing correction in linear mixed models. Genome Biology, 2016, 17, 62.	3.8	72
54	Gene networks associated with conditional fear in mice identified using a systems genetics approach. BMC Systems Biology, 2011, 5, 43.	3.0	71

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55	Polymorphisms and Haplotypes of the Regulator of G Protein Signaling-2 Gene in Normotensives and Hypertensives. Hypertension, 2006, 47, 415-420.	1.3	68
56	Genome-Wide Association Study Identifies Nox3 as a Critical Gene for Susceptibility to Noise-Induced Hearing Loss. PLoS Genetics, 2015, 11, e1005094.	1.5	64
57	Efficient Multiple-Trait Association and Estimation of Genetic Correlation Using the Matrix-Variate Linear Mixed Model. Genetics, 2015, 200, 59-68.	1.2	64
58	Improving the usability and archival stability of bioinformatics software. Genome Biology, 2019, 20, 47.	3.8	62
59	Accounting for Population Structure in Gene-by-Environment Interactions in Genome-Wide Association Studies Using Mixed Models. PLoS Genetics, 2016, 12, e1005849.	1.5	61
60	Allele-specific expression and eQTL analysis in mouse adipose tissue. BMC Genomics, 2014, 15, 471.	1.2	57
61	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	9.4	57
62	Leveraging the HapMap Correlation Structure in Association Studies. American Journal of Human Genetics, 2007, 80, 683-691.	2.6	56
63	Identification of Novel Genes That Mediate Innate Immunity Using Inbred Mice. Genetics, 2009, 183, 1535-1544.	1.2	55
64	Challenges and recommendations to improve the installability and archival stability of omics computational tools. PLoS Biology, 2019, 17, e3000333.	2.6	54
65	High-Resolution Mapping of Gene Expression Using Association in an Outbred Mouse Stock. PLoS Genetics, 2008, 4, e1000149.	1.5	53
66	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. PLoS ONE, 2020, 15, e0239474.	1.1	53
67	Searching Genomes for Noncoding RNA Using FastR. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 366-379.	1.9	48
68	Increasing power in association studies by using linkage disequilibrium structure and molecular function as prior information. Genome Research, 2008, 18, 653-660.	2.4	48
69	Systems Genetic Analysis of Osteoblast-Lineage Cells. PLoS Genetics, 2012, 8, e1003150.	1.5	48
70	Accurate viral population assembly from ultra-deep sequencing data. Bioinformatics, 2014, 30, i329-i337.	1.8	48
71	Meta-Analysis Identifies Gene-by-Environment Interactions as Demonstrated in a Study of 4,965 Mice. PLoS Genetics, 2014, 10, e1004022.	1.5	46
72	Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples. Nature Biomedical Engineering, 2021, 5, 657-665.	11.6	46

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73	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. Nature Communications, 2020, 11, 3126.	5.8	44
74	An Optimal Weighted Aggregated Association Test for Identification of Rare Variants Involved in Common Diseases. Genetics, 2011, 188, 181-188.	1.2	43
75	Genomeâ€Wide Association Mapping With Longitudinal Data. Genetic Epidemiology, 2012, 36, 463-471.	0.6	43
76	Analysis of Allele-Specific Expression in Mouse Liver by RNA-Seq: A Comparison With Cis-eQTL Identified Using Genetic Linkage. Genetics, 2013, 195, 1157-1166.	1.2	43
77	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	1.4	42
78	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome Biology, 2018, 19, 36.	3.8	42
79	Imputing Phenotypes for Genome-wide Association Studies. American Journal of Human Genetics, 2016, 99, 89-103.	2.6	40
80	BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference. Genome Biology, 2018, 19, 141.	3.8	40
81	High-Density Genotypes of Inbred Mouse Strains: Improved Power and Precision of Association Mapping. G3: Genes, Genomes, Genetics, 2015, 5, 2021-2026.	0.8	37
82	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	1.2	36
83	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. BMC Genomics, 2018, 19, 476.	1.2	35
84	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. ELife, 2016, 5, .	2.8	35
85	Genome-wide association mapping of blood cell traits in mice. Mammalian Genome, 2013, 24, 105-118.	1.0	34
86	Identifying causal variants by fine mapping across multiple studies. PLoS Genetics, 2021, 17, e1009733.	1.5	34
87	Incorporating prior information into association studies. Bioinformatics, 2012, 28, i147-i153.	1.8	33
88	Diversity, Differentiation, and Linkage Disequilibrium: Prospects for Association Mapping in the Malaria VectorAnopheles arabiensis. G3: Genes, Genomes, Genetics, 2014, 4, 121-131.	0.8	33
89	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. Nature Methods, 2017, 14, 218-219.	9.0	33
90	Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies. Genome Biology, 2014, 15, r61.	13.9	32

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91	Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping. BMC Genetics, 2008, 9, 14.	2.7	31
92	Genome-Wide Association Study for Age-Related Hearing Loss (AHL) in the Mouse: A Meta-Analysis. JARO - Journal of the Association for Research in Otolaryngology, 2014, 15, 335-352.	0.9	31
93	Fast and Accurate Construction of Confidence Intervals for Heritability. American Journal of Human Genetics, 2016, 98, 1181-1192.	2.6	31
94	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. G3: Genes, Genomes, Genetics, 2016, 6, 1793-1798.	0.8	30
95	Mixed models can correct for population structure for genomic regions under selection. Nature Reviews Genetics, 2013, 14, 300-300.	7.7	29
96	Metalign: efficient alignment-based metagenomic profiling via containment min hash. Genome Biology, 2020, 21, 242.	3.8	29
97	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. PLoS Computational Biology, 2009, 5, e1000311.	1.5	28
98	Profiling allele-specific gene expression in brains from individuals with autism spectrum disorder reveals preferential minor allele usage. Nature Neuroscience, 2019, 22, 1521-1532.	7.1	28
99	Efficient algorithms for tandem copy number variation reconstruction in repeat-rich regions. Bioinformatics, 2011, 27, 1513-1520.	1.8	26
100	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. Genetics, 2016, 204, 1379-1390.	1.2	26
101	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	3.8	26
102	Genome-wide case/control studies in hypertension: only the â€˜tip of the icebergâ€™. Journal of Hypertension, 2010, 28, 1115-1123.	0.3	26
103	Protein Family Classification Using Sparse Markov Transducers. Journal of Computational Biology, 2003, 10, 187-213.	0.8	25
104	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	2.6	25
105	How bioinformatics and open data can boost basic science in countries and universities with limited resources. Nature Biotechnology, 2019, 37, 324-326.	9.4	25
106	A Kernel Approach for Learning from almost Orthogonal Patterns. Lecture Notes in Computer Science, 2002, , 511-528.	1.0	25
107	Increased power of mixed models facilitates association mapping of 10 loci for metabolic traits in an isolated population. Human Molecular Genetics, 2011, 20, 827-839.	1.4	24
108	Improving the Accuracy and Efficiency of Partitioning Heritability into the Contributions of Genomic Regions. American Journal of Human Genetics, 2013, 92, 558-564.	2.6	24

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109	Limited RNA Editing in Exons of Mouse Liver and Adipose. Genetics, 2013, 193, 1107-1115.	1.2	24
110	The Genetic Architecture of Noise-Induced Hearing Loss: Evidence for a Gene-by-Environment Interaction. G3: Genes, Genomes, Genetics, 2016, 6, 3219-3228.	0.8	24
111	Dealing with large diagonals in kernel matrices. Annals of the Institute of Statistical Mathematics, 2003, 55, 391-408.	0.5	23
112	Leveraging reads that span multiple single nucleotide polymorphisms for haplotype inference from sequencing data. Bioinformatics, 2013, 29, 2245-2252.	1.8	23
113	Discovering genes involved in disease and the mystery of missing heritability. Communications of the ACM, 2015, 58, 80-87.	3.3	23
114	Imputation aware metaâ€analysis of genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 537-542.	0.6	22
115	CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping. Journal of Computational Biology, 2013, 20, 224-236.	0.8	22
116	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. Trends in Biotechnology, 2017, 35, 901-903.	4.9	22
117	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. BMC Genomics, 2019, 20, 423.	1.2	22
118	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. American Journal of Human Genetics, 2021, 108, 36-48.	2.6	22
119	Further evidence for association of GRK3 to bipolar disorder suggests a second disease mutation. Psychiatric Genetics, 2007, 17, 315-322.	0.6	21
120	Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. Bioinformatics, 2011, 27, i288-i294.	1.8	21
121	Increasing Power of Genome-Wide Association Studies by Collecting Additional Single-Nucleotide Polymorphisms. Genetics, 2011, 188, 449-460.	1.2	21
122	The Genetic Landscape of Hematopoietic Stem Cell Frequency in Mice. Stem Cell Reports, 2015, 5, 125-138.	2.3	21
123	Applying meta-analysis to genotype-tissue expression data from multiple tissues to identify eQTLs and increase the number of eGenes. Bioinformatics, 2017, 33, i67-i74.	1.8	21
124	Postassociation cleaning using linkage disequilibrium information. Genetic Epidemiology, 2011, 35, 1-10.	0.6	20
125	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. PLoS Genetics, 2019, 15, e1008481.	1.5	20
126	Efficient Association Study Design Via Powerâ€Optimized Tag SNP Selection. Annals of Human Genetics, 2008, 72, 834-847.	0.3	19

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127	Spatial Localization of Recent Ancestors for Admixed Individuals. G3: Genes, Genomes, Genetics, 2014, 4, 2505-2518.	0.8	19
128	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. Journal of Computational Biology, 2013, 20, 80-92.	0.8	18
129	Inference and analysis of haplotypes from combined genotyping studies deposited in dbSNP. Genome Research, 2005, 15, 1594-1600.	2.4	17
130	Functional Genomic Assessment of Phosgene-Induced Acute Lung Injury in Mice. American Journal of Respiratory Cell and Molecular Biology, 2013, 49, 368-383.	1.4	17
131	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. Genetics, 2016, 204, 1057-1064.	1.2	17
132	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	0.6	17
133	EMINIM: An Adaptive and Memory-Efficient Algorithm for Genotype Imputation. Journal of Computational Biology, 2010, 17, 547-560.	0.8	16
134	In silico QTL mapping of basal liver iron levels in inbred mouse strains. Physiological Genomics, 2011, 43, 136-147.	1.0	16
135	The Genetic Architecture of Hearing Impairment in Mice: Evidence for Frequency-Specific Genetic Determinants. G3: Genes, Genomes, Genetics, 2015, 5, 2329-2339.	0.8	16
136	Word and Sentence Embedding Tools to Measure Semantic Similarity of Gene Ontology Terms by Their Definitions. Journal of Computational Biology, 2019, 26, 38-52.	0.8	16
137	Improving the usability and comprehensiveness of microbial databases. BMC Biology, 2020, 18, 37.	1.7	15
138	Increasing Power of Groupwise Association Test with Likelihood Ratio Test. Journal of Computational Biology, 2011, 18, 1611-1624.	0.8	14
139	Increasing Association Mapping Power and Resolution in Mouse Genetic Studies Through the Use of Meta-Analysis for Structured Populations. Genetics, 2012, 191, 959-967.	1.2	14
140	Using genomic annotations increases statistical power to detect eGenes. Bioinformatics, 2016, 32, i156-i163.	1.8	14
141	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. Journal of Computational Biology, 2017, 24, 558-570.	0.8	14
142	GENOME-WIDE ANALYSIS OF BACTERIAL PROMOTER REGIONS. , 2002, , .		14
143	Rare Variant Association Testing Under Low-Coverage Sequencing. Genetics, 2013, 194, 769-779.	1.2	13
144	High-Resolution Association Mapping of Atherosclerosis Loci in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 1790-1798.	1.1	12

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145	Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. Bioinformatics, 2007, 23, e84-e90.	1.8	11
146	Multi-marker tagging single nucleotide polymorphism selection using estimation of distribution algorithms. Artificial Intelligence in Medicine, 2010, 50, 193-201.	3.8	11
147	Assembly of non-unique insertion content using next-generation sequencing. BMC Bioinformatics, 2011, 12, S3.	1.2	11
148	Hap-seqX: Expedite algorithm for haplotype phasing with imputation using sequence data. Gene, 2013, 518, 2-6.	1.0	10
149	Privacy preserving protocol for detecting genetic relatives using rare variants. Bioinformatics, 2014, 30, i204-i211.	1.8	10
150	Finding associated variants in genome-wide association studies on multiple traits. Bioinformatics, 2018, 34, i467-i474.	1.8	10
151	Adaptive Model Generation. Advances in Information Security, 2002, , 153-193.	0.9	10
152	Genome-wide analysis of bacterial promoter regions. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2003, , 29-40.	0.7	10
153	Robust Mendelian randomization in the presence of residual population stratification, batch effects and horizontal pleiotropy. Nature Communications, 2022, 13, 1093.	5.8	10
154	Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs. Lecture Notes in Computer Science, 2005, , 65-78.	1.0	9
155	A GWAS approach identifies Dapp1 as a determinant of air pollution-induced airway hyperreactivity. PLoS Genetics, 2019, 15, e1008528.	1.5	9
156	A comprehensive benchmarking of WGS-based deletion structural variant callers. Briefings in Bioinformatics, 2022, 23, .	3.2	9
157	Natural Variation within the Neuronal Nicotinic Acetylcholine Receptor Cluster on Human Chromosome 15q24: Influence on Heritable Autonomic Traits in Twin Pairs. Journal of Pharmacology and Experimental Therapeutics, 2009, 331, 419-428.	1.3	8
158	Detection and reconstruction of tandemly organized de novo copy number variations. BMC Bioinformatics, 2010, 11, S12.	1.2	8
159	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. Journal of Computational Biology, 2010, 17, 533-546.	0.8	8
160	Mapping Genetic Variants Associated with Beta-Adrenergic Responses in Inbred Mice. PLoS ONE, 2012, 7, e41032.	1.1	8
161	Identification of Deletion Polymorphisms from Haplotypes. , 2007, , 354-365.		7
162	A NOTE ON PHASING LONG GENOMIC REGIONS USING LOCAL HAPLOTYPE PREDICTIONS. Journal of Bioinformatics and Computational Biology, 2006, 04, 639-647.	0.3	6

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163	Linkage Effects and Analysis of Finite Sample Errors in the HapMap. Human Heredity, 2009, 68, 73-86.	0.4	6
164	Integrated Computational and Experimental Analysis of the Neuroendocrine Transcriptome in Genetic Hypertension Identifies Novel Control Points for the Cardiometabolic Syndrome. Circulation: Cardiovascular Genetics, 2012, 5, 430-440.	5.1	6
165	Genotyping common and rare variation using overlapping pool sequencing. BMC Bioinformatics, 2011, 12, S2.	1.2	5
166	Efficient genotyping of individuals using overlapping pool sequencing and imputation. , 2012, , .		5
167	Fast pairwise IBD association testing in genome-wide association studies. Bioinformatics, 2014, 30, 206-213.	1.8	5
168	Geneâ€“Gene Interactions Detection Using a Two-stage Model. Journal of Computational Biology, 2015, 22, 563-576.	0.8	5
169	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. Genetics, 2018, 209, 685-698.	1.2	5
170	Genetic determinants of ammonia-induced acute lung injury in mice. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L41-L62.	1.3	5
171	Title is missing!. Annals of the Institute of Statistical Mathematics, 2003, 55, 391-408.	0.5	5
172	Genetic programming applied to Othello. SIGCSE Bulletin, 1999, 31, 242-246.	0.1	4
173	Efficiently Identifying Significant Associations in Genome-wide Association Studies. Journal of Computational Biology, 2013, 20, 817-830.	0.8	4
174	Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder. PLoS Genetics, 2016, 12, e1006046.	1.5	4
175	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. Lecture Notes in Computer Science, 2012, , 64-78.	1.0	4
176	INCORPORATING HOMOLOGUES INTO SEQUENCE EMBEDDINGS FOR PROTEIN ANALYSIS. Journal of Bioinformatics and Computational Biology, 2007, 05, 717-738.	0.3	3
177	Genome reassembly with high-throughput sequencing data. BMC Genomics, 2013, 14, S8.	1.2	3
178	Efficient Genome Wide Tagging by Reduction to SAT. Lecture Notes in Computer Science, 2008, , 135-147.	1.0	3
179	Discrete profile comparison using information bottleneck. BMC Bioinformatics, 2006, 7, S8.	1.2	2
180	CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping. Lecture Notes in Computer Science, 2012, , 326-340.	1.0	2

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181	Involving undergraduates in genomics research to narrow the educationâ€“research gap. Nature Biotechnology, 2018, 36, 369-371.	9.4	2
182	A Unifying Framework for Imputing Summary Statistics in Genome-Wide Association Studies. Journal of Computational Biology, 2020, 27, 418-428.	0.8	2
183	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	3.8	2
184	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. Lecture Notes in Computer Science, 2009, , 466-481.	1.0	2
185	An Adaptive and Memory Efficient Algorithm for Genotype Imputation. Lecture Notes in Computer Science, 2009, , 482-495.	1.0	2
186	Using Substitution Matrices to Estimate Probability Distributions for Biological Sequences. Journal of Computational Biology, 2002, 9, 775-791.	0.8	1
187	Using HLA binding prediction algorithms for epitope mapping in HIV vaccine clinical trials. , 2011, , .		1
188	Simultaneous Modeling of Disease Status and Clinical Phenotypes To Increase Power in Genome-Wide Association Studies. Genetics, 2017, 205, 1041-1047.	1.2	1
189	A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation. Lecture Notes in Computer Science, 2014, , 371-384.	1.0	1
190	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. Lecture Notes in Computer Science, 2015, , 136-153.	1.0	1
191	Efficiently Identifying Significant Associations in Genome-Wide Association Studies. Lecture Notes in Computer Science, 2013, , 118-131.	1.0	1
192	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. Lecture Notes in Computer Science, 2017, , 303-317.	1.0	1
193	A Spatial Haplotype Copying Model with Applications to Genotype Imputation. Journal of Computational Biology, 2015, 22, 451-462.	0.8	0
194	A linear mixed model approach to gene expression-tumor aneuploidy association studies. Scientific Reports, 2019, 9, 11944.	1.6	0
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