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	Robust Mendelian randomization in the presence of residual population stratification, batch effects and horizontal pleiotropy. Nature Communications, 2022, 13, 1093.	5.8	10
2	Genomic epidemiology of the Los Angeles COVID-19 outbreak and the early history of the B.1.43 strain in the USA. BMC Genomics, 2022, 23, 260.	1.2	0
3	Bruins-in-Genomics: Evaluation of the impact of a UCLA undergraduate summer program in computational biology on participating students. PLoS ONE, 2022, 17, e0268861.	1.1	0
4	A comprehensive benchmarking of WGS-based deletion structural variant callers. Briefings in Bioinformatics, 2022, 23, .	3.2	9
5	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
6	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
7	MARS: leveraging allelic heterogeneity to increase power of association testing. Genome Biology, 2021, 22, 128.	3.8	2
8	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
9	Identifying causal variants by fine mapping across multiple studies. PLoS Genetics, 2021, 17, e1009733.	1.5	34
10	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. PLoS ONE, 2020, 15, e0239474.	1.1	53
11	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
12	Metalign: efficient alignment-based metagenomic profiling via containment min hash. Genome Biology, 2020, 21, 242.	3.8	29
13	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	3.8	26
14	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. Nature Communications, 2020, 11, 3126.	5.8	44
15	A Unifying Framework for Imputing Summary Statistics in Genome-Wide Association Studies. Journal of Computational Biology, 2020, 27, 418-428.	0.8	2
16	Genome-wide analysis highlights contribution of immune system pathways to the genetic architecture of asthma. Nature Communications, 2020, 11, 1776.	5.8	119
17	Improving the usability and comprehensiveness of microbial databases. BMC Biology, 2020, 18, 37.	1.7	15
18	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0

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19	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0
20	A linear mixed model approach to gene expression-tumor aneuploidy association studies. Scientific Reports, 2019, 9, 11944.	1.6	0
21	Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology. Nature Communications, 2019, 10, 3417.	5.8	92
22	Challenges and recommendations to improve the installability and archival stability of omics computational tools. PLoS Biology, 2019, 17, e3000333.	2.6	54
23	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
24	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. BMC Genomics, 2019, 20, 423.	1.2	22
25	Improving the usability and archival stability of bioinformatics software. Genome Biology, 2019, 20, 47.	3.8	62
26	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
27	Systematic benchmarking of omics computational tools. Nature Communications, 2019, 10, 1393.	5.8	111
28	A GWAS approach identifies Dapp1 as a determinant of air pollution-induced airway hyperreactivity. PLoS Genetics, 2019, 15, e1008528.	1.5	9
29	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. PLoS Genetics, 2019, 15, e1008481.	1.5	20
30	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
31	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. Journal of Computational Biology, 2019, 26, 1203-1213.	0.8	0
32	Involving undergraduates in genomics research to narrow the educationâ€“research gap. Nature Biotechnology, 2018, 36, 369-371.	9.4	2
33	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	0.6	17
34	Population structure in genetic studies: Confounding factors and mixed models. PLoS Genetics, 2018, 14, e1007309.	1.5	164
35	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
36	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

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37	Finding associated variants in genome-wide association studies on multiple traits. Bioinformatics, 2018, 34, i467-i474.	1.8	10
38	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	9.4	154
39	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. BMC Genomics, 2018, 19, 476.	1.2	35
40	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
41	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. Genetics, 2018, 209, 685-698.	1.2	5
42	Simultaneous Modeling of Disease Status and Clinical Phenotypes To Increase Power in Genome-Wide Association Studies. Genetics, 2017, 205, 1041-1047.	1.2	1
43	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. Nature Methods, 2017, 14, 218-219.	9.0	33
44	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90
45	Widespread Allelic Heterogeneity in Complex Traits. American Journal of Human Genetics, 2017, 100, 789-802.	2.6	74
46	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
47	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	9.4	57
48	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	6.0	260
49	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. Trends in Biotechnology, 2017, 35, 901-903.	4.9	22
50	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
51	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. Lecture Notes in Computer Science, 2017, , 303-317.	1.0	1
52	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. G3: Genes, Genomes, Genetics, 2016, 6, 1793-1798.	0.8	30
53	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
54	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

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55	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
56	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. Genetics, 2016, 204, 1379-1390.	1.2	26
57	Using genomic annotations increases statistical power to detect eGenes. Bioinformatics, 2016, 32, i156-i163.	1.8	14
58	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	1.4	42
59	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
60	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
61	Colocalization of GWAS and eQTL Signals Detects Target Genes. American Journal of Human Genetics, 2016, 99, 1245-1260.	2.6	569
62	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. Genetics, 2016, 204, 1057-1064.	1.2	17
63	Chromosome conformation elucidates regulatory relationships in developing human brain. Nature, 2016, 538, 523-527.	13.7	507
64	Fast and Accurate Construction of Confidence Intervals for Heritability. American Journal of Human Genetics, 2016, 98, 1181-1192.	2.6	31
65	Multiple testing correction in linear mixed models. Genome Biology, 2016, 17, 62.	3.8	72
66	Imputing Phenotypes for Genome-wide Association Studies. American Journal of Human Genetics, 2016, 99, 89-103.	2.6	40
67	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. Nature Methods, 2016, 13, 443-445.	9.0	205
68	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. ELife, 2016, 5, .	2.8	35
69	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
70	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
71	A Spatial Haplotype Copying Model with Applications to Genotype Imputation. Journal of Computational Biology, 2015, 22, 451-462.	0.8	0
72	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	2.6	25

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73	Geneâ€“Gene Interactions Detection Using a Two-stage Model. Journal of Computational Biology, 2015, 22, 563-576.	0.8	5
74	Identification of causal genes for complex traits. Bioinformatics, 2015, 31, i206-i213.	1.8	72
75	The Genetic Landscape of Hematopoietic Stem Cell Frequency in Mice. Stem Cell Reports, 2015, 5, 125-138.	2.3	21
76	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
77	Efficient Multiple-Trait Association and Estimation of Genetic Correlation Using the Matrix-Variate Linear Mixed Model. Genetics, 2015, 200, 59-68.	1.2	64
78	Genetic and environmental control of host-gut microbiota interactions. Genome Research, 2015, 25, 1558-1569.	2.4	288
79	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
80	Discovering genes involved in disease and the mystery of missing heritability. Communications of the ACM, 2015, 58, 80-87.	3.3	23
81	Genetic Architecture of Atherosclerosis in Mice: A Systems Genetics Analysis of Common Inbred Strains. PLoS Genetics, 2015, 11, e1005711.	1.5	124
82	Microbiome/Metabolic Syndrome/Diabetes and CVD. FASEB Journal, 2015, 29, 222.3.	0.2	0
83	Privacy preserving protocol for detecting genetic relatives using rare variants. Bioinformatics, 2014, 30, i204-i211.	1.8	10
84	Accurate viral population assembly from ultra-deep sequencing data. Bioinformatics, 2014, 30, i329-i337.	1.8	48
85	Meta-Analysis Identifies Gene-by-Environment Interactions as Demonstrated in a Study of 4,965 Mice. PLoS Genetics, 2014, 10, e1004022.	1.5	46
86	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
87	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
88	Spatial Localization of Recent Ancestors for Admixed Individuals. G3: Genes, Genomes, Genetics, 2014, 4, 2505-2518.	0.8	19
89	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
90	Identifying Causal Variants at Loci with Multiple Signals of Association. Genetics, 2014, 198, 497-508.	1.2	400

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91	Allele-specific expression and eQTL analysis in mouse adipose tissue. BMC Genomics, 2014, 15, 471.	1.2	57
92	Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies. Genome Biology, 2014, 15, r61.	13.9	32
93	Fast pairwise IBD association testing in genome-wide association studies. Bioinformatics, 2014, 30, 206-213.	1.8	5
94	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	1.2	36
95	A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation. Lecture Notes in Computer Science, 2014, , 371-384.	1.0	1
96	Gene-Gene Interactions Detection Using a Two-Stage Model. Lecture Notes in Computer Science, 2014, , 340-355.	1.0	0
97	Genome reassembly with high-throughput sequencing data. BMC Genomics, 2013, 14, S8.	1.2	3
98	Genome-wide association mapping of blood cell traits in mice. Mammalian Genome, 2013, 24, 105-118.	1.0	34
99	Leveraging reads that span multiple single nucleotide polymorphisms for haplotype inference from sequencing data. Bioinformatics, 2013, 29, 2245-2252.	1.8	23
100	Hap-seqX: Expedite algorithm for haplotype phasing with imputation using sequence data. Gene, 2013, 518, 2-6.	1.0	10
101	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
102	Mixed models can correct for population structure for genomic regions under selection. Nature Reviews Genetics, 2013, 14, 300-300.	7.7	29
103	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
104	Limited RNA Editing in Exons of Mouse Liver and Adipose. Genetics, 2013, 193, 1107-1115.	1.2	24
105	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
106	Rare Variant Association Testing Under Low-Coverage Sequencing. Genetics, 2013, 194, 769-779.	1.2	13
107	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. PLoS Genetics, 2013, 9, e1003491.	1.5	109
108	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

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109	CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping. Journal of Computational Biology, 2013, 20, 224-236.	0.8	22
110	Efficiently Identifying Significant Associations in Genome-wide Association Studies. Journal of Computational Biology, 2013, 20, 817-830.	0.8	4
111	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. Journal of Computational Biology, 2013, 20, 80-92.	0.8	18
112	Efficiently Identifying Significant Associations in Genome-Wide Association Studies. Lecture Notes in Computer Science, 2013, , 118-131.	1.0	1
113	Interpreting Meta-Analyses of Genome-Wide Association Studies. PLoS Genetics, 2012, 8, e1002555.	1.5	171
114	Systems Genetic Analysis of Osteoblast-Lineage Cells. PLoS Genetics, 2012, 8, e1003150.	1.5	48
115	â€œGood Enough Solutionsâ€•and the Genetics of Complex Diseases. Circulation Research, 2012, 111, 493-504.	2.0	94
116	High-Resolution Association Mapping of Atherosclerosis Loci in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 1790-1798.	1.1	12
117	Incorporating prior information into association studies. Bioinformatics, 2012, 28, i147-i153.	1.8	33
118	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
119	Efficient genotyping of individuals using overlapping pool sequencing and imputation. , 2012, , .		5
120	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
121	Improved linear mixed models for genome-wide association studies. Nature Methods, 2012, 9, 525-526.	9.0	292
122	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
123	Genome-wide association studies in mice. Nature Reviews Genetics, 2012, 13, 807-817.	7.7	172
124	CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping. Lecture Notes in Computer Science, 2012, , 326-340.	1.0	2
125	Mapping Genetic Variants Associated with Beta-Adrenergic Responses in Inbred Mice. PLoS ONE, 2012, 7, e41032.	1.1	8
126	A model-based approach for analysis of spatial structure in genetic data. Nature Genetics, 2012, 44, 725-731.	9.4	147

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127	Genomeâ€Wide Association Mapping With Longitudinal Data. Genetic Epidemiology, 2012, 36, 463-471.	0.6	43
128	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. Lecture Notes in Computer Science, 2012, , 64-78.	1.0	4
129	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
130	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
131	Gene networks associated with conditional fear in mice identified using a systems genetics approach. BMC Systems Biology, 2011, 5, 43.	3.0	71
132	Genotyping common and rare variation using overlapping pool sequencing. BMC Bioinformatics, 2011, 12, S2.	1.2	5
133	Assembly of non-unique insertion content using next-generation sequencing. BMC Bioinformatics, 2011, 12, S3.	1.2	11
134	Postassociation cleaning using linkage disequilibrium information. Genetic Epidemiology, 2011, 35, 1-10.	0.6	20
135	Using HLA binding prediction algorithms for epitope mapping in HIV vaccine clinical trials. , 2011, , .		1
136	Increasing Power of Groupwise Association Test with Likelihood Ratio Test. Journal of Computational Biology, 2011, 18, 1611-1624.	0.8	14
137	Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. Bioinformatics, 2011, 27, i288-i294.	1.8	21
138	Comparative Analysis of Proteome and Transcriptome Variation in Mouse. PLoS Genetics, 2011, 7, e1001393.	1.5	548
139	Efficient algorithms for tandem copy number variation reconstruction in repeat-rich regions. Bioinformatics, 2011, 27, 1513-1520.	1.8	26
140	An Optimal Weighted Aggregated Association Test for Identification of Rare Variants Involved in Common Diseases. Genetics, 2011, 188, 181-188.	1.2	43
141	Increasing Power of Genome-Wide Association Studies by Collecting Additional Single-Nucleotide Polymorphisms. Genetics, 2011, 188, 449-460.	1.2	21
142	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
143	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	1.5	85
144	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

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145	In silico QTL mapping of basal liver iron levels in inbred mouse strains. Physiological Genomics, 2011, 43, 136-147.	1.0	16
146	Detection and reconstruction of tandemly organized de novo copy number variations. BMC Bioinformatics, 2010, 11, S12.	1.2	8
147	Multi-marker tagging single nucleotide polymorphism selection using estimation of distribution algorithms. Artificial Intelligence in Medicine, 2010, 50, 193-201.	3.8	11
148	Imputation aware metaâ€analysis of genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 537-542.	0.6	22
149	Variance component model to account for sample structure in genome-wide association studies. Nature Genetics, 2010, 42, 348-354.	9.4	2,287
150	A high-resolution association mapping panel for the dissection of complex traits in mice. Genome Research, 2010, 20, 281-290.	2.4	299
151	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. Genetics, 2010, 185, 1081-1095.	1.2	95
152	EMINIM: An Adaptive and Memory-Efficient Algorithm for Genotype Imputation. Journal of Computational Biology, 2010, 17, 547-560.	0.8	16
153	Optimal algorithms for haplotype assembly from whole-genome sequence data. Bioinformatics, 2010, 26, i183-i190.	1.8	106
154	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
155	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
156	Genome-wide case/control studies in hypertension: only the â€˜tip of the icebergâ€™. Journal of Hypertension, 2010, 28, 1115-1123.	0.3	26
157	Linkage Effects and Analysis of Finite Sample Errors in the HapMap. Human Heredity, 2009, 68, 73-86.	0.4	6
158	Identification of Novel Genes That Mediate Innate Immunity Using Inbred Mice. Genetics, 2009, 183, 1535-1544.	1.2	55
159	Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers. PLoS Genetics, 2009, 5, e1000456.	1.5	157
160	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. PLoS Computational Biology, 2009, 5, e1000311.	1.5	28
161	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
162	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

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163	An Adaptive and Memory Efficient Algorithm for Genotype Imputation. Lecture Notes in Computer Science, 2009, , 482-495.	1.0	2
164	Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping. BMC Genetics, 2008, 9, 14.	2.7	31
165	Efficient Association Study Design Via Powerâ€Optimized Tag SNP Selection. Annals of Human Genetics, 2008, 72, 834-847.	0.3	19
166	Efficient Control of Population Structure in Model Organism Association Mapping. Genetics, 2008, 178, 1709-1723.	1.2	1,752
167	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
168	High-Resolution Mapping of Gene Expression Using Association in an Outbred Mouse Stock. PLoS Genetics, 2008, 4, e1000149.	1.5	53
169	Accurate Discovery of Expression Quantitative Trait Loci Under Confounding From Spurious and Genuine Regulatory Hotspots. Genetics, 2008, 180, 1909-1925.	1.2	136
170	Efficient Genome Wide Tagging by Reduction to SAT. Lecture Notes in Computer Science, 2008, , 135-147.	1.0	3
171	INCORPORATING HOMOLOGUES INTO SEQUENCE EMBEDDINGS FOR PROTEIN ANALYSIS. Journal of Bioinformatics and Computational Biology, 2007, 05, 717-738.	0.3	3
172	Catecholamine Releaseâ€“Inhibitory Peptide Catestatin (Chromogranin A 352â€“372). Circulation, 2007, 115, 2271-2281.	1.6	105
173	Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. Bioinformatics, 2007, 23, e84-e90.	1.8	11
174	Further evidence for association of GRK3 to bipolar disorder suggests a second disease mutation. Psychiatric Genetics, 2007, 17, 315-322.	0.6	21
175	Leveraging the HapMap Correlation Structure in Association Studies. American Journal of Human Genetics, 2007, 80, 683-691.	2.6	56
176	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. Nature, 2007, 448, 1050-1053.	13.7	406
177	Identification of Deletion Polymorphisms from Haplotypes. , 2007, , 354-365.		7
178	Reconstructing the Phylogeny of Mobile Elements. , 2007, , 196-210.		0
179	A Comparison of Phasing Algorithms for Trios and Unrelated Individuals. American Journal of Human Genetics, 2006, 78, 437-450.	2.6	308
180	Discrete profile comparison using information bottleneck. BMC Bioinformatics, 2006, 7, S8.	1.2	2

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181	Polymorphisms and Haplotypes of the Regulator of G Protein Signaling-2 Gene in Normotensives and Hypertensives. Hypertension, 2006, 47, 415-420.	1.3	68
182	A NOTE ON PHASING LONG GENOMIC REGIONS USING LOCAL HAPLOTYPE PREDICTIONS. Journal of Bioinformatics and Computational Biology, 2006, 04, 639-647.	0.3	6
183	Assessing computational tools for the discovery of transcription factor binding sites. Nature Biotechnology, 2005, 23, 137-144.	9.4	1,121
184	Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs. Lecture Notes in Computer Science, 2005, , 65-78.	1.0	9
185	Inference and analysis of haplotypes from combined genotyping studies deposited in dbSNP. Genome Research, 2005, 15, 1594-1600.	2.4	17
186	Searching Genomes for Noncoding RNA Using FastR. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 366-379.	1.9	48
187	Whole-Genome Patterns of Common DNA Variation in Three Human Populations. Science, 2005, 307, 1072-1079.	6.0	1,074
188	Haplotype reconstruction from genotype data using Imperfect Phylogeny. Bioinformatics, 2004, 20, 1842-1849.	1.8	185
189	Whole-genome analysis of Alu repeat elements reveals complex evolutionary history. Genome Research, 2004, 14, 2245-2252.	2.4	184
190	Mismatch string kernels for discriminative protein classification. Bioinformatics, 2004, 20, 467-476.	1.8	485
191	Dealing with large diagonals in kernel matrices. Annals of the Institute of Statistical Mathematics, 2003, 55, 391-408.	0.5	23
192	Protein Family Classification Using Sparse Markov Transducers. Journal of Computational Biology, 2003, 10, 187-213.	0.8	25
193	EFFICIENT RECONSTRUCTION OF HAPLOTYPE STRUCTURE VIA PERFECT PHYLOGENY. Journal of Bioinformatics and Computational Biology, 2003, 01, 1-20.	0.3	100
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