Eleazar Eskin

List of Publications by Year in Descending Order

214 papers	15,660 citations	51 h-index	123 g-index
228 ext. papers	19,435 ext. citations	8.8 avg, IF	6.37 L-index

#	Paper	IF	Citations
214	Robust Mendelian randomization in the presence of residual population stratification, batch effects and horizontal pleiotropy.. *Nature Communications*, **2022**, 13, 1093	17.4	0
213	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	4.5	
212	Bruins-in-Genomics: Evaluation of the impact of a UCLA undergraduate summer program in computational biology on participating students. *PLoS ONE*, **2022**, 17, e0268861	3.7	
211	Swab-Seq: A high-throughput platform for massively scaled up SARS-CoV-2 testing **2021**,		28
210	MARS: leveraging allelic heterogeneity to increase power of association testing. *Genome Biology*, **2021**, 22, 128	18.3	1
209	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	19	14
208	Genetic determinants of ammonia-induced acute lung injury in mice. *American Journal of Physiology - Lung Cellular and Molecular Physiology*, **2021**, 320, L41-L62	5.8	2
207	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. *American Journal of Human Genetics*, **2021**, 108, 36-48	11	2
206	Identifying causal variants by fine mapping across multiple studies. *PLoS Genetics*, **2021**, 17, e1009733	6	3
205	Benchmarking of computational error-correction methods for next-generation sequencing data. *Genome Biology*, **2020**, 21, 71	18.3	11
204	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. *Nature Communications*, **2020**, 11, 3126	17.4	12
203	A Unifying Framework for Imputing Summary Statistics in Genome-Wide Association Studies. *Journal of Computational Biology*, **2020**, 27, 418-428	1.7	1
202	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. *PLoS ONE*, **2020**, 15, e0239474	3.7	29
201	The impact of sex on gene expression across human tissues. *Science*, **2020**, 369,	33.3	100
200	Metalign: efficient alignment-based metagenomic profiling via containment min hash. *Genome Biology*, **2020**, 21, 242	18.3	11
199	Genome-wide analysis highlights contribution of immune system pathways to the genetic architecture of asthma. *Nature Communications*, **2020**, 11, 1776	17.4	33
198	Improving the usability and comprehensiveness of microbial databases. *BMC Biology*, **2020**, 18, 37	7.3	5

197	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity **2020**, 15, e0239474		
196	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity **2020**, 15, e0239474		
195	Profiling allele-specific gene expression in brains from individuals with autism spectrum disorder reveals preferential minor allele usage. *Nature Neuroscience*, **2019**, 22, 1521-1532	25.5	17
194	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. *BMC Genomics*, **2019**, 20, 423	4.5	7
193	How bioinformatics and open data can boost basic science in countries and universities with limited resources. *Nature Biotechnology*, **2019**, 37, 324-326	44.5	11
192	Systematic benchmarking of omics computational tools. *Nature Communications*, **2019**, 10, 1393	17.4	62
191	A linear mixed model approach to gene expression-tumor aneuploidy association studies. *Scientific Reports*, **2019**, 9, 11944	4.9	
190	Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology. *Nature Communications*, **2019**, 10, 3417	17.4	34
189	Challenges and recommendations to improve the installability and archival stability of omics computational tools. *PLoS Biology*, **2019**, 17, e3000333	9.7	23
188	A GWAS approach identifies Dapp1 as a determinant of air pollution-induced airway hyperreactivity. *PLoS Genetics*, **2019**, 15, e1008528	6	4
187	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. *PLoS Genetics*, **2019**, 15, e1008481	6	8
186	Word and Sentence Embedding Tools to Measure Semantic Similarity of Gene Ontology Terms by Their Definitions. *Journal of Computational Biology*, **2019**, 26, 38-52	1.7	12
185	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. *Journal of Computational Biology*, **2019**, 26, 1203-1213	1.7	
184	Involving undergraduates in genomics research to narrow the education-research gap. *Nature Biotechnology*, **2018**, 36, 369-371	44.5	2
183	An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. *BMC Genomics*, **2018**, 19, 476	4.5	20
182	ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. *Genome Biology*, **2018**, 19, 36	18.3	26
181	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. *Genetics*, **2018**, 209, 685-698	4	4
180	An ancestry-based approach for detecting interactions. *Genetic Epidemiology*, **2018**, 42, 49-63	2.6	11

179	Population structure in genetic studies: Confounding factors and mixed models. *PLoS Genetics*, **2018**, 14, e1007309	6	62
178	BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference. *Genome Biology*, **2018**, 19, 141	18.3	23
177	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. *Nature Genetics*, **2018**, 50, 956-967	36.3	239
176	Finding associated variants in genome-wide association studies on multiple traits. *Bioinformatics*, **2018**, 34, i467-i474	7.2	2
175	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. *Nature Genetics*, **2018**, 50, 1041-1047	36.3	67
174	Simultaneous Modeling of Disease Status and Clinical Phenotypes To Increase Power in Genome-Wide Association Studies. *Genetics*, **2017**, 205, 1041-1047	4	1
173	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. *Nature Methods*, **2017**, 14, 218-219	21.6	27
172	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. *Molecular Biology and Evolution*, **2017**, 34, 1307-1318	8.3	50
171	Widespread Allelic Heterogeneity in Complex Traits. *American Journal of Human Genetics*, **2017**, 100, 789-802	11	49
170	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	1.7	10
169	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. *Nature Genetics*, **2017**, 49, 1714-1721	36.3	43
168	Loci associated with skin pigmentation identified in African populations. *Science*, **2017**, 358,	33.3	179
167	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. *Trends in Biotechnology*, **2017**, 35, 901-903	15.1	13
166	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	7.2	15
165	Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies. *Lecture Notes in Computer Science*, **2017**, 303-317	0.9	1
164	The Genetic Architecture of Noise-Induced Hearing Loss: Evidence for a Gene-by-Environment Interaction. *G3: Genes, Genomes, Genetics*, **2016**, 6, 3219-3228	3.2	20
163	Colocalization of GWAS and eQTL Signals Detects Target Genes. *American Journal of Human Genetics*, **2016**, 99, 1245-1260	11	311
162	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. *Genetics*, **2016**, 204, 1057-1064	4	14

161	Chromosome conformation elucidates regulatory relationships in developing human brain. *Nature*, **2016**, 538, 523-527	50.4	334
160	Fast and Accurate Construction of Confidence Intervals for Heritability. *American Journal of Human Genetics*, **2016**, 98, 1181-1192	11	18
159	Multiple testing correction in linear mixed models. *Genome Biology*, **2016**, 17, 62	18.3	44
158	Imputing Phenotypes for Genome-wide Association Studies. *American Journal of Human Genetics*, **2016**, 99, 89-103	11	18
157	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. *Nature Methods*, **2016**, 13, 443-5	21.6	154
156	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. *ELife*, **2016**, 5,	8.9	26
155	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. *G3: Genes, Genomes, Genetics*, **2016**, 6, 1793-8	3.2	21
154	Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder. *PLoS Genetics*, **2016**, 12, e1006046	6	4
153	Accounting for Population Structure in Gene-by-Environment Interactions in Genome-Wide Association Studies Using Mixed Models. *PLoS Genetics*, **2016**, 12, e1005849	6	35
152	The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, Anopheles arabiensis. *PLoS Genetics*, **2016**, 12, e1006303	6	55
151	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. *Genetics*, **2016**, 204, 1379-1390	4	14
150	Using genomic annotations increases statistical power to detect eGenes. *Bioinformatics*, **2016**, 32, i156-i163	7.3	10
149	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. *Human Molecular Genetics*, **2016**, 25, 1857-66	5.6	28
148	The Hybrid Mouse Diversity Panel: a resource for systems genetics analyses of metabolic and cardiovascular traits. *Journal of Lipid Research*, **2016**, 57, 925-42	6.3	86
147	Gene-Gene Interactions Detection Using a Two-stage Model. *Journal of Computational Biology*, **2015**, 22, 563-76	1.7	5
146	Identification of causal genes for complex traits. *Bioinformatics*, **2015**, 31, i206-13	7.2	51
145	The Genetic Landscape of Hematopoietic Stem Cell Frequency in Mice. *Stem Cell Reports*, **2015**, 5, 125-38	8	18
144	Genome-wide association study identifies nox3 as a critical gene for susceptibility to noise-induced hearing loss. *PLoS Genetics*, **2015**, 11, e1005094	6	41

143	Efficient multiple-trait association and estimation of genetic correlation using the matrix-variate linear mixed model. *Genetics*, **2015**, 200, 59-68	4	39
142	Genetic and environmental control of host-gut microbiota interactions. *Genome Research*, **2015**, 25, 1558-69	9.7	199
141	The Genetic Architecture of Hearing Impairment in Mice: Evidence for Frequency-Specific Genetic Determinants. *G3: Genes, Genomes, Genetics*, **2015**, 5, 2329-39	3.2	13
140	High-Density Genotypes of Inbred Mouse Strains: Improved Power and Precision of Association Mapping. *G3: Genes, Genomes, Genetics*, **2015**, 5, 2021-6	3.2	25
139	A spatial haplotype copying model with applications to genotype imputation. *Journal of Computational Biology*, **2015**, 22, 451-62	1.7	
138	Accurate and fast multiple-testing correction in eQTL studies. *American Journal of Human Genetics*, **2015**, 96, 857-68	11	18
137	Discovering genes involved in disease and the mystery of missing heritability. *Communications of the ACM*, **2015**, 58, 80-87	2.5	14
136	Genetic Architecture of Atherosclerosis in Mice: A Systems Genetics Analysis of Common Inbred Strains. *PLoS Genetics*, **2015**, 11, e1005711	6	83
135	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. *Lecture Notes in Computer Science*, **2015**, 136-153	0.9	1
134	Microbiome/Metabolic Syndrome/Diabetes and CVD. *FASEB Journal*, **2015**, 29, 222.3	0.9	
133	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, 335-52	3.3	24
132	Identifying causal variants at loci with multiple signals of association. *Genetics*, **2014**, 198, 497-508	4	266
131	Allele-specific expression and eQTL analysis in mouse adipose tissue. *BMC Genomics*, **2014**, 15, 471	4.5	39
130	Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies. *Genome Biology*, **2014**, 15, r61	18.3	25
129	Fast pairwise IBD association testing in genome-wide association studies. *Bioinformatics*, **2014**, 30, 206-12	7.2	5
128	Genetic implication of a novel thiamine transporter in human hypertension. *Journal of the American College of Cardiology*, **2014**, 63, 1542-55	15.1	27
127	Privacy preserving protocol for detecting genetic relatives using rare variants. *Bioinformatics*, **2014**, 30, i204-11	7.2	7
126	Accurate viral population assembly from ultra-deep sequencing data. *Bioinformatics*, **2014**, 30, i329-37	7.2	42

125	Meta-analysis identifies gene-by-environment interactions as demonstrated in a study of 4,965 mice. *PLoS Genetics*, **2014**, 10, e1004022	6	34
124	Integrating functional data to prioritize causal variants in statistical fine-mapping studies. *PLoS Genetics*, **2014**, 10, e1004722	6	305
123	Diversity, differentiation, and linkage disequilibrium: prospects for association mapping in the malaria vector Anopheles arabiensis. *G3: Genes, Genomes, Genetics*, **2014**, 4, 121-31	3.2	27
122	Spatial localization of recent ancestors for admixed individuals. *G3: Genes, Genomes, Genetics*, **2014**, 4, 2505-18	3.2	14
121	A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation. *Lecture Notes in Computer Science*, **2014**, 371-384	0.9	1
120	Gene-Gene Interactions Detection Using a Two-Stage Model. *Lecture Notes in Computer Science*, **2014**, 340-355	0.9	
119	Genome reassembly with high-throughput sequencing data. *BMC Genomics*, **2013**, 14 Suppl 1, S8	4.5	2
118	Genome-wide association mapping of blood cell traits in mice. *Mammalian Genome*, **2013**, 24, 105-18	3.2	32
117	Leveraging reads that span multiple single nucleotide polymorphisms for haplotype inference from sequencing data. *Bioinformatics*, **2013**, 29, 2245-52	7.2	20
116	Hap-seqX: expedite algorithm for haplotype phasing with imputation using sequence data. *Gene*, **2013**, 518, 2-6	3.8	8
115	Improving the accuracy and efficiency of partitioning heritability into the contributions of genomic regions. *American Journal of Human Genetics*, **2013**, 92, 558-64	11	18
114	Mixed models can correct for population structure for genomic regions under selection. *Nature Reviews Genetics*, **2013**, 14, 300	30.1	18
113	Genetic control of obesity and gut microbiota composition in response to high-fat, high-sucrose diet in mice. *Cell Metabolism*, **2013**, 17, 141-52	24.6	383
112	Limited RNA editing in exons of mouse liver and adipose. *Genetics*, **2013**, 193, 1107-15	4	22
111	Functional genomic assessment of phosgene-induced acute lung injury in mice. *American Journal of Respiratory Cell and Molecular Biology*, **2013**, 49, 368-83	5.7	15
110	Rare variant association testing under low-coverage sequencing. *Genetics*, **2013**, 194, 769-79	4	10
109	Effectively identifying eQTLs from multiple tissues by combining mixed model and meta-analytic approaches. *PLoS Genetics*, **2013**, 9, e1003491	6	78
108	Analysis of allele-specific expression in mouse liver by RNA-Seq: a comparison with Cis-eQTL identified using genetic linkage. *Genetics*, **2013**, 195, 1157-66	4	34

107	CNVeM: copy number variation detection using uncertainty of read mapping. *Journal of Computational Biology*, **2013**, 20, 224-36	1.7	18
106	Efficiently identifying significant associations in genome-wide association studies. *Journal of Computational Biology*, **2013**, 20, 817-30	1.7	3
105	Hap-seq: an optimal algorithm for haplotype phasing with imputation using sequencing data. *Journal of Computational Biology*, **2013**, 20, 80-92	1.7	14
104	Efficiently Identifying Significant Associations in Genome-Wide Association Studies. *Lecture Notes in Computer Science*, **2013**, 118-131	0.9	1
103	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. *Mammalian Genome*, **2012**, 23, 680-92	3.2	101
102	Improved linear mixed models for genome-wide association studies. *Nature Methods*, **2012**, 9, 525-6	21.6	228
101	Increasing association mapping power and resolution in mouse genetic studies through the use of meta-analysis for structured populations. *Genetics*, **2012**, 191, 959-67	4	11
100	Genome-wide association studies in mice. *Nature Reviews Genetics*, **2012**, 13, 807-17	30.1	141
99	CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping. *Lecture Notes in Computer Science*, **2012**, 326-340	0.9	2
98	Mapping genetic variants associated with beta-adrenergic responses in inbred mice. *PLoS ONE*, **2012**, 7, e41032	3.7	8
97	A model-based approach for analysis of spatial structure in genetic data. *Nature Genetics*, **2012**, 44, 725-31	36.3	114
96	Genome-wide association mapping with longitudinal data. *Genetic Epidemiology*, **2012**, 36, 463-71	2.6	35
95	Interpreting meta-analyses of genome-wide association studies. *PLoS Genetics*, **2012**, 8, e1002555	6	109
94	Systems genetic analysis of osteoblast-lineage cells. *PLoS Genetics*, **2012**, 8, e1003150	6	40
93	"Good enough solutions" and the genetics of complex diseases. *Circulation Research*, **2012**, 111, 493-504	15.7	68
92	High-resolution association mapping of atherosclerosis loci in mice. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2012**, 32, 1790-8	9.4	12
91	Incorporating prior information into association studies. *Bioinformatics*, **2012**, 28, i147-53	7.2	27
90	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, 430-40		5

89	Efficient genotyping of individuals using overlapping pool sequencing and imputation **2012**,		3
88	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. *Lecture Notes in Computer Science*, **2012**, 64-78	0.9	4
87	Mouse genomic variation and its effect on phenotypes and gene regulation. *Nature*, **2011**, 477, 289-94	50.4	1087
86	Random-effects model aimed at discovering associations in meta-analysis of genome-wide association studies. *American Journal of Human Genetics*, **2011**, 88, 586-98	11	351
85	Gene networks associated with conditional fear in mice identified using a systems genetics approach. *BMC Systems Biology*, **2011**, 5, 43	3.5	64
84	Genotyping common and rare variation using overlapping pool sequencing. *BMC Bioinformatics*, **2011**, 12 Suppl 6, S2	3.6	3
83	Assembly of non-unique insertion content using next-generation sequencing. *BMC Bioinformatics*, **2011**, 12 Suppl 6, S3	3.6	9
82	Postassociation cleaning using linkage disequilibrium information. *Genetic Epidemiology*, **2011**, 35, 1-10	2.6	18
81	Using HLA binding prediction algorithms for epitope mapping in HIV vaccine clinical trials **2011**,		1
80	Increasing power of groupwise association test with likelihood ratio test. *Journal of Computational Biology*, **2011**, 18, 1611-24	1.7	12
79	Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. *Bioinformatics*, **2011**, 27, i288-94	7.2	14
78	Comparative analysis of proteome and transcriptome variation in mouse. *PLoS Genetics*, **2011**, 7, e1001393		417
77	Efficient algorithms for tandem copy number variation reconstruction in repeat-rich regions. *Bioinformatics*, **2011**, 27, 1513-20	7.2	19
76	An optimal weighted aggregated association test for identification of rare variants involved in common diseases. *Genetics*, **2011**, 188, 181-8	4	37
75	Increasing power of genome-wide association studies by collecting additional single-nucleotide polymorphisms. *Genetics*, **2011**, 188, 449-60	4	20
74	Increased power of mixed models facilitates association mapping of 10 loci for metabolic traits in an isolated population. *Human Molecular Genetics*, **2011**, 20, 827-39	5.6	22
73	Identification and functional validation of the novel antimalarial resistance locus PF10_0355 in Plasmodium falciparum. *PLoS Genetics*, **2011**, 7, e1001383	6	71
72	Mouse genome-wide association and systems genetics identify Asxl2 as a regulator of bone mineral density and osteoclastogenesis. *PLoS Genetics*, **2011**, 7, e1002038	6	95

71	In silico QTL mapping of basal liver iron levels in inbred mouse strains. *Physiological Genomics*, **2011**, 43, 136-47	3.6	13
70	Increasing Power of Groupwise Association Test with Likelihood Ratio Test. *Lecture Notes in Computer Science*, **2011**, 452-467	0.9	2
69	Variance component model to account for sample structure in genome-wide association studies. *Nature Genetics*, **2010**, 42, 348-54	36.3	1624
68	A high-resolution association mapping panel for the dissection of complex traits in mice. *Genome Research*, **2010**, 20, 281-90	9.7	246
67	Fine mapping in 94 inbred mouse strains using a high-density haplotype resource. *Genetics*, **2010**, 185, 1081-95	4	82
66	EMINIM: an adaptive and memory-efficient algorithm for genotype imputation. *Journal of Computational Biology*, **2010**, 17, 547-60	1.7	12
65	Optimal algorithms for haplotype assembly from whole-genome sequence data. *Bioinformatics*, **2010**, 26, i183-90	7.2	91
64	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. *NeuroImage*, **2010**, 51, 542-54	7.9	119
63	Detecting the presence and absence of causal relationships between expression of yeast genes with very few samples. *Journal of Computational Biology*, **2010**, 17, 533-46	1.7	5
62	Detection and reconstruction of tandemly organized de novo copy number variations. *BMC Bioinformatics*, **2010**, 11 Suppl 11, S12	3.6	8
61	Multi-marker tagging single nucleotide polymorphism selection using estimation of distribution algorithms. *Artificial Intelligence in Medicine*, **2010**, 50, 193-201	7.4	9
60	Imputation aware meta-analysis of genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 537-42	2.6	17
59	Genome-wide case/control studies in hypertension: only the 'tip of the iceberg' *Journal of Hypertension*, **2010**, 28, 1115-23	1.9	23
58	Linkage effects and analysis of finite sample errors in the HapMap. *Human Heredity*, **2009**, 68, 73-86	1.1	5
57	Identification of novel genes that mediate innate immunity using inbred mice. *Genetics*, **2009**, 183, 1535-44	4	51
56	Rapid and accurate multiple testing correction and power estimation for millions of correlated markers. *PLoS Genetics*, **2009**, 5, e1000456	6	132
55	Using network component analysis to dissect regulatory networks mediated by transcription factors in yeast. *PLoS Computational Biology*, **2009**, 5, e1000311	5	26
54	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, 419-28	4.7	8

53	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	0.9	2
52	An Adaptive and Memory Efficient Algorithm for Genotype Imputation. *Lecture Notes in Computer Science*, **2009**, 482-495	0.9	2
51	Efficient association study design via power-optimized tag SNP selection. *Annals of Human Genetics* , **2008**, 72, 834-47	2.2	19
50	Efficient control of population structure in model organism association mapping. *Genetics*, **2008**, 178, 1709-23	4	1244
49	Increasing power in association studies by using linkage disequilibrium structure and molecular function as prior information. *Genome Research*, **2008**, 18, 653-60	9.7	42
48	High-resolution mapping of gene expression using association in an outbred mouse stock. *PLoS Genetics*, **2008**, 4, e1000149	6	48
47	Accurate discovery of expression quantitative trait loci under confounding from spurious and genuine regulatory hotspots. *Genetics*, **2008**, 180, 1909-25	4	107
46	Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping. *BMC Genetics*, **2008** , 9, 14	2.6	30
45	Efficient Genome Wide Tagging by Reduction to SAT. *Lecture Notes in Computer Science*, **2008**, 135-147	0.9	3
44	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. *Nature*, **2007**, 448, 1050-3	50.4	352
43	Incorporating homologues into sequence embeddings for protein analysis. *Journal of Bioinformatics and Computational Biology*, **2007**, 5, 717-38	1	3
42	Catecholamine release-inhibitory peptide catestatin (chromogranin A(352-372)): naturally occurring amino acid variant Gly364Ser causes profound changes in human autonomic activity and alters risk for hypertension. *Circulation*, **2007**, 115, 2271-81	16.7	91
41	Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. *Bioinformatics*, **2007**, 23, e84-90	7.2	10
40	Further evidence for association of GRK3 to bipolar disorder suggests a second disease mutation. *Psychiatric Genetics*, **2007**, 17, 315-22	2.9	18
39	Leveraging the HapMap correlation structure in association studies. *American Journal of Human Genetics*, **2007**, 80, 683-91	11	53
38	Reconstructing the Phylogeny of Mobile Elements **2007**, 196-210		
37	Identification of Deletion Polymorphisms from Haplotypes **2007**, 354-365		7
36	Discrete profile comparison using information bottleneck. *BMC Bioinformatics*, **2006**, 7 Suppl 1, S8	3.6	1

35	Polymorphisms and haplotypes of the regulator of G protein signaling-2 gene in normotensives and hypertensives. *Hypertension*, **2006**, 47, 415-20	8.5	62
34	A note on phasing long genomic regions using local haplotype predictions. *Journal of Bioinformatics and Computational Biology*, **2006**, 4, 639-47	1	6
33	A comparison of phasing algorithms for trios and unrelated individuals. *American Journal of Human Genetics*, **2006**, 78, 437-50	11	267
32	Searching genomes for noncoding RNA using FastR. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2005**, 2, 366-79	3	37
31	Whole-genome patterns of common DNA variation in three human populations. *Science*, **2005**, 307, 1072-9	33.3	972
30	Assessing computational tools for the discovery of transcription factor binding sites. *Nature Biotechnology*, **2005**, 23, 137-44	44.5	950
29	Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs. *Lecture Notes in Computer Science*, **2005**, 65-78	0.9	8
28	Inference and analysis of haplotypes from combined genotyping studies deposited in dbSNP. *Genome Research*, **2005**, 15, 1594-600	9.7	13
27	Haplotype reconstruction from genotype data using Imperfect Phylogeny. *Bioinformatics*, **2004**, 20, 1842-9	7.2	169
26	Whole-genome analysis of Alu repeat elements reveals complex evolutionary history. *Genome Research*, **2004**, 14, 2245-52	9.7	146
25	Mismatch string kernels for discriminative protein classification. *Bioinformatics*, **2004**, 20, 467-76	7.2	377
24	Efficient reconstruction of haplotype structure via perfect phylogeny. *Journal of Bioinformatics and Computational Biology*, **2003**, 1, 1-20	1	82
23	Dealing with large diagonals in kernel matrices. *Annals of the Institute of Statistical Mathematics*, **2003**, 55, 391-408	1	15
22	Protein family classification using sparse markov transducers. *Journal of Computational Biology*, **2003**, 10, 187-213	1.7	16
21	. *Annals of the Institute of Statistical Mathematics*, **2003**, 55, 391-408	1	2
20	Genome-wide analysis of bacterial promoter regions. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2003**, 29-40	1.3	10
19	Detecting Malicious Software by Monitoring Anomalous Windows Registry Accesses. *Lecture Notes in Computer Science*, **2002**, 36-53	0.9	21
18	Finding composite regulatory patterns in DNA sequences. *Bioinformatics*, **2002**, 18 Suppl 1, S354-63	7.2	199

17	Using substitution matrices to estimate probability distributions for biological sequences. *Journal of Computational Biology*, **2002**, 9, 775-91	1.7	1
16	GENOME-WIDE ANALYSIS OF BACTERIAL PROMOTER REGIONS **2002**,		5
15	A Kernel Approach for Learning from almost Orthogonal Patterns. *Lecture Notes in Computer Science*, **2002**, 511-528	0.9	9
14	Adaptive Model Generation. *Advances in Information Security*, **2002**, 153-193	0.7	10
13	THE SPECTRUM KERNEL: A STRING KERNEL FOR SVM PROTEIN CLASSIFICATION **2001**,		69
12	Genetic programming applied to Othello. *SIGCSE Bulletin*, **1999**, 31, 242-246	0	3
11	The genetic basis of host choice and resting behavior in the major African malaria vector, Anopheles arabiensis		2
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