

Ron Shamir

List of Publications by Year in Descending Order

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

280
papers

15,605
citations

61
h-index

119
g-index

324
ext. papers

18,256
ext. citations

6.2
avg, IF

6.73
L-index

#	Paper	IF	Citations
280	A machine learning model for predicting deterioration of COVID-19 inpatients.. <i>Scientific Reports</i> , 2022 , 12, 2630	4.9	4
279	2020 ISCB accomplishments by a Senior Scientist Award: Steven Salzberg. <i>Bioinformatics</i> , 2021 , 37, 3699-3700		
278	2020 ISCB Innovatory Award: Xiaole Shirley Liu. <i>Bioinformatics</i> , 2021 , 37, 3697-3698	7.2	
277	2020 Outstanding contributions to ISCB award: Judith Blake. <i>Bioinformatics</i> , 2021 , 37, 3701	7.2	
276	SCAPP: an algorithm for improved plasmid assembly in metagenomes. <i>Microbiome</i> , 2021 , 9, 144	16.6	5
275	2020 ISCB Overton Prize: Jian Peng. <i>Bioinformatics</i> , 2021 , 37, 1630-1631	7.2	
274	DOMINO: a network-based active module identification algorithm with reduced rate of false calls. <i>Molecular Systems Biology</i> , 2021 , 17, e9593	12.2	10
273	Classification of node-positive melanomas into prognostic subgroups using keratin, immune, and melanogenesis expression patterns. <i>Oncogene</i> , 2021 , 40, 1792-1805	9.2	4
272	Melanoma-Secreted Lysosomes Trigger Monocyte-Derived Dendritic Cell Apoptosis and Limit Cancer Immunotherapy. <i>Cancer Research</i> , 2020 , 80, 1942-1956	10.1	11
271	PRODIGY: personalized prioritization of driver genes. <i>Bioinformatics</i> , 2020 , 36, 1831-1839	7.2	8
270	Using the kinetics of C-reactive protein response to improve the differential diagnosis between acute bacterial and viral infections. <i>Infection</i> , 2020 , 48, 241-248	5.8	21
269	MONET: Multi-omic module discovery by omic selection. <i>PLoS Computational Biology</i> , 2020 , 16, e1008183		2
268	Bonnie Berger named ISCB 2019 ISCB Accomplishments by a Senior Scientist Award recipient. <i>Bioinformatics</i> , 2020 , 36, 5122-5123	7.2	
267	2019 ISCB Overton Prize: Christophe Dessimoz. <i>Bioinformatics</i> , 2020 , 36, 5124-5125	7.2	
266	2019 Outstanding Contributions to ISCB Awarded to Barb Bryant. <i>Bioinformatics</i> , 2020 , 36, 5126	7.2	
265	2019 ISCB Innovator Award Recognizes William Stafford Noble. <i>Bioinformatics</i> , 2020 , 36, 5127-5128	7.2	
264	Unravelling plasmidome distribution and interaction with its hosting microbiome. <i>Environmental Microbiology</i> , 2020 , 22, 32-44	5.2	7

263	PlasClass improves plasmid sequence classification. <i>PLoS Computational Biology</i> , 2020 , 16, e1007781	5	14
262	MONET: Multi-omic module discovery by omic selection 2020 , 16, e1008182		
261	MONET: Multi-omic module discovery by omic selection 2020 , 16, e1008182		
260	MONET: Multi-omic module discovery by omic selection 2020 , 16, e1008182		
259	MONET: Multi-omic module discovery by omic selection 2020 , 16, e1008182		
258	NEMO: cancer subtyping by integration of partial multi-omic data. <i>Bioinformatics</i> , 2019 , 35, 3348-3356	7.2	60
257	Genome Rearrangement Problems with Single and Multiple Gene Copies: A Review. <i>Computational Biology</i> , 2019 , 205-241	0.7	3
256	Personalized prediction of adverse heart and kidney events using baseline and longitudinal data from SPRINT and ACCORD. <i>PLoS ONE</i> , 2019 , 14, e0219728	3.7	3
255	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019 , 431, 2398-2406	6.5	13
254	Inaccuracy of the log-rank approximation in cancer data analysis. <i>Molecular Systems Biology</i> , 2019 , 15, e8754	12.2	6
253	PROMO: an interactive tool for analyzing clinically-labeled multi-omic cancer datasets. <i>BMC Bioinformatics</i> , 2019 , 20, 732	3.6	11
252	ADEPTUS: a discovery tool for disease prediction, enrichment and network analysis based on profiles from many diseases. <i>Bioinformatics</i> , 2018 , 34, 1959-1961	7.2	6
251	Faucet: streaming de novo assembly graph construction. <i>Bioinformatics</i> , 2018 , 34, 147-154	7.2	6
250	Sorting cancer karyotypes using double-cut-and-joins, duplications and deletions. <i>Bioinformatics</i> , 2018 ,	7.2	3
249	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. <i>Genome Biology</i> , 2018 , 19, 56	18.3	32
248	MorphDB: Prioritizing Genes for Specialized Metabolism Pathways and Gene Ontology Categories in Plants. <i>Frontiers in Plant Science</i> , 2018 , 9, 352	6.2	5
247	Computational analysis of mRNA expression profiling in the inner ear reveals candidate transcription factors associated with proliferation, differentiation, and deafness. <i>Human Genomics</i> , 2018 , 12, 30	6.8	8
246	2018 ISCB Innovator Award recognizes M. Madan Babu. <i>Bioinformatics</i> , 2018 , 34, 2336-2337	7.2	

245	2018 ISCB Overton Prize awarded to Cole Trapnell. <i>Bioinformatics</i> , 2018 , 34, 2330-2331	7.2	
244	2018 ISCB accomplishments by a senior scientist award. <i>PLoS Computational Biology</i> , 2018 , 14, e1006138		0
243	Message from the ISCB: 2018 Outstanding Contributions to ISCB Award: Russ Altman. <i>Bioinformatics</i> , 2018 , 34, 2334-2335	7.2	
242	2018 ISCB Overton Prize awarded to Cole Trapnell. <i>PLoS Computational Biology</i> , 2018 , 14, e1006163		5
241	2018 ISCB Innovator Award recognizes M. Madan Babu. <i>PLoS Computational Biology</i> , 2018 , 14, e1006164		5
240	2018 outstanding contributions to ISCB award: Russ Altman. <i>PLoS Computational Biology</i> , 2018 , 14, e1006140		5
239	Multi-omic and multi-view clustering algorithms: review and cancer benchmark. <i>Nucleic Acids Research</i> , 2018 , 46, 10546-10562	20.1	144
238	GePMI: A statistical model for personal intestinal microbiome identification. <i>Npj Biofilms and Microbiomes</i> , 2018 , 4, 20	8.2	4
237	Genomic meta-analysis of the interplay between 3D chromatin organization and gene expression programs under basal and stress conditions. <i>Epigenetics and Chromatin</i> , 2018 , 11, 49	5.8	4
236	Message from the ISCB: 2018 ISCB Accomplishments by a Senior Scientist Award. <i>Bioinformatics</i> , 2018 , 34, 2332-2333	7.2	
235	Utilizing somatic mutation data from numerous studies for cancer research: proof of concept and applications. <i>Oncogene</i> , 2017 , 36, 3375-3383	9.2	12
234	Transcription factor family-specific DNA shape readout revealed by quantitative specificity models. <i>Molecular Systems Biology</i> , 2017 , 13, 910	12.2	66
233	Tired and misconnected: A breakdown of brain modularity following sleep deprivation. <i>Human Brain Mapping</i> , 2017 , 38, 3300-3314	5.9	33
232	Reconstructing cancer karyotypes from short read data: the half empty and half full glass. <i>BMC Bioinformatics</i> , 2017 , 18, 488	3.6	4
231	Improving the performance of minimizers and winnowing schemes. <i>Bioinformatics</i> , 2017 , 33, i110-i117	7.2	27
230	A Linear-Time Algorithm for the Copy Number Transformation Problem. <i>Journal of Computational Biology</i> , 2017 , 24, 1179-1194	1.7	6
229	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , 2017 , 89, 1676-1683	3.5	59
228	Reduced changes in protein compared to mRNA levels across non-proliferating tissues. <i>BMC Genomics</i> , 2017 , 18, 305	4.5	43

227	Complexity and algorithms for copy-number evolution problems. <i>Algorithms for Molecular Biology</i> , 2017 , 12, 13	1.8	19
226	Sorting by Cuts, Joins, and Whole Chromosome Duplications. <i>Journal of Computational Biology</i> , 2017 , 24, 127-137	1.7	6
225	Tracing the Neural Carryover Effects of Interpersonal Anger on Resting-State fMRI in Men and Their Relation to Traumatic Stress Symptoms in a Subsample of Soldiers. <i>Frontiers in Behavioral Neuroscience</i> , 2017 , 11, 252	3.5	11
224	Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling the false discovery rate. <i>PLoS Computational Biology</i> , 2017 , 13, e1005700	5	7
223	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. <i>PLoS Computational Biology</i> , 2017 , 13, e1005777	5	22
222	Modeling protein-DNA binding via high-throughput in vitro technologies. <i>Briefings in Functional Genomics</i> , 2017 , 16, 171-180	4.9	12
221	Recycler: an algorithm for detecting plasmids from de novo assembly graphs. <i>Bioinformatics</i> , 2017 , 33, 475-482	7.2	62
220	SELMAP - SELEX affinity landscape MAPping of transcription factor binding sites using integrated microfluidics. <i>Scientific Reports</i> , 2016 , 6, 33351	4.9	11
219	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. <i>Nucleic Acids Research</i> , 2016 , 44, e51	20.1	14
218	Enhancer methylation dynamics contribute to cancer plasticity and patient mortality. <i>Genome Research</i> , 2016 , 26, 601-11	9.7	67
217	RichMind: A Tool for Improved Inference from Large-Scale Neuroimaging Results. <i>PLoS ONE</i> , 2016 , 11, e0159643	3.7	3
216	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. <i>Frontiers in Genetics</i> , 2016 , 7, 172	4.5	11
215	Expression and methylation patterns partition luminal-A breast tumors into distinct prognostic subgroups. <i>Breast Cancer Research</i> , 2016 , 18, 74	8.3	41
214	A large-scale perspective on stress-induced alterations in resting-state networks. <i>Scientific Reports</i> , 2016 , 6, 21503	4.9	39
213	Evidence of TAF1 dysfunction in peripheral models of X-linked dystonia-parkinsonism. <i>Cellular and Molecular Life Sciences</i> , 2016 , 73, 3205-15	10.3	28
212	Copy-Number Evolution Problems: Complexity and Algorithms. <i>Lecture Notes in Computer Science</i> , 2016 , 137-149	0.9	12
211	Compact Universal k-mer Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2016 , 257-268	0.9	17
210	MicroRNAs are essential for differentiation of the retinal pigmented epithelium and maturation of adjacent photoreceptors. <i>Development (Cambridge)</i> , 2015 , 142, 2487-98	6.6	42

209	Element: a computational tool for detecting core promoter elements. <i>Transcription</i> , 2015 , 6, 41-50	4.8	42
208	Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets. <i>Nucleic Acids Research</i> , 2015 , 43, 7779-89	20.1	20
207	A hierarchical Bayesian model for flexible module discovery in three-way time-series data. <i>Bioinformatics</i> , 2015 , 31, i17-26	7.2	8
206	The MORPH-R web server and software tool for predicting missing genes in biological pathways. <i>Physiologia Plantarum</i> , 2015 , 155, 12-20	4.6	1
205	Sorting by Cuts, Joins and Whole Chromosome Duplications. <i>Lecture Notes in Computer Science</i> , 2015 , 396-409	0.9	3
204	Functional gene groups are concentrated within chromosomes, among chromosomes and in the nuclear space of the human genome. <i>Nucleic Acids Research</i> , 2014 , 42, 9854-61	20.1	63
203	Drosophila TRF2 is a preferential core promoter regulator. <i>Genes and Development</i> , 2014 , 28, 2163-74	12.6	36
202	Fast lossless compression via cascading Bloom filters. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 9, S7	3.6	18
201	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , 2014 , 14, 329	5.3	17
200	A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and CHIP data. <i>Nucleic Acids Research</i> , 2014 , 42, e63	20.1	68
199	Examination of exhaustive cloning attempts reveals that <i>C. elegans</i> piRNAs, transposons, and repeat sequences are efficiently cloned in yeast, but not in bacteria. <i>Frontiers in Genetics</i> , 2014 , 5, 275	4.5	1
198	Constructing module maps for integrated analysis of heterogeneous biological networks. <i>Nucleic Acids Research</i> , 2014 , 42, 4208-19	20.1	23
197	Parallel profiling of the transcriptome, cistrome, and epigenome in the cellular response to ionizing radiation. <i>Science Signaling</i> , 2014 , 7, rs3	8.8	45
196	Transcription factor/microRNA axis blocks melanoma invasion program by miR-211 targeting NUA1. <i>Journal of Investigative Dermatology</i> , 2014 , 134, 441-451	4.3	82
195	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013 , 31, 126-34	44.5	268
194	Systematic inference of highways of horizontal gene transfer in prokaryotes. <i>Bioinformatics</i> , 2013 , 29, 571-9	7.2	19
193	Environmental stresses disrupt telomere length homeostasis. <i>PLoS Genetics</i> , 2013 , 9, e1003721	6	70
192	Dissection of regulatory networks that are altered in disease via differential co-expression. <i>PLoS Computational Biology</i> , 2013 , 9, e1002955	5	104

191	Design of shortest double-stranded DNA sequences covering all k-mers with applications to protein-binding microarrays and synthetic enhancers. <i>Bioinformatics</i> , 2013 , 29, i71-9	7.2	11
190	RAP: accurate and fast motif finding based on protein-binding microarray data. <i>Journal of Computational Biology</i> , 2013 , 20, 375-82	1.7	13
189	MGMR: leveraging RNA-Seq population data to optimize expression estimation. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 6, S2	3.6	3
188	Constructing logical models of gene regulatory networks by integrating transcription factor-DNA interactions with expression data: an entropy-based approach. <i>Journal of Computational Biology</i> , 2012 , 19, 30-41	1.7	23
187	Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , 2012 , 9, 796-804	21.6	1097
186	Network-induced classification kernels for gene expression profile analysis. <i>Journal of Computational Biology</i> , 2012 , 19, 694-709	1.7	25
185	The MORPH algorithm: ranking candidate genes for membership in Arabidopsis and tomato pathways. <i>Plant Cell</i> , 2012 , 24, 4389-406	11.6	19
184	A novel candidate cis-regulatory motif pair in the promoters of germline and oogenesis genes in <i>C. elegans</i> . <i>Genome Research</i> , 2012 , 22, 76-83	9.7	3
183	Transcriptional and proteomic analysis of the <i>Aspergillus fumigatus</i> PrtT protease-deficient mutant. <i>PLoS ONE</i> , 2012 , 7, e33604	3.7	17
182	Assessment of algorithms for inferring positional weight matrix motifs of transcription factor binding sites using protein binding microarray data. <i>PLoS ONE</i> , 2012 , 7, e46145	3.7	20
181	Using Computational Biology Methods to Improve Post-silicon Microprocessor Testing. <i>Lecture Notes in Computer Science</i> , 2012 , 261-262	0.9	
180	Transcriptional modulation induced by ionizing radiation: p53 remains a central player. <i>Molecular Oncology</i> , 2011 , 5, 336-48	7.9	74
179	Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy. <i>Genome Biology</i> , 2011 , 12, R61	18.3	42
178	Dynamic changes in the copy number of pluripotency and cell proliferation genes in human ESCs and iPSCs during reprogramming and time in culture. <i>Cell Stem Cell</i> , 2011 , 8, 106-18	18	700
177	PrtT-regulated proteins secreted by <i>Aspergillus fumigatus</i> activate MAPK signaling in exposed A549 lung cells leading to necrotic cell death. <i>PLoS ONE</i> , 2011 , 6, e17509	3.7	25
176	An . <i>Journal of Discrete Algorithms</i> , 2011 , 9, 344-357		6
175	Detecting highways of horizontal gene transfer. <i>Journal of Computational Biology</i> , 2011 , 18, 1087-114	1.7	12
174	A Note on the Fixed Parameter Tractability of the Gene-Duplication Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 848-50	3	16

173	Preface: 2nd Satellite Meeting on Bioinformatics Education, Research in Computational Molecular Biology (RECOMB-BE 2010). <i>Journal of Computational Biology</i> , 2011 , 18, 865	1.7	
172	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , 2011 , 39, D793-9	20.1	59
171	Integration of transcriptomics, proteomics, and microRNA analyses reveals novel microRNA regulation of targets in the mammalian inner ear. <i>PLoS ONE</i> , 2011 , 6, e18195	3.7	67
170	A point mutation in translation initiation factor eIF2B leads to function--and time-specific changes in brain gene expression. <i>PLoS ONE</i> , 2011 , 6, e26992	3.7	11
169	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 901-8	17.6	79
168	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , 2010 , 5, 303-22	18.8	165
167	Towards computational prediction of microRNA function and activity. <i>Nucleic Acids Research</i> , 2010 , 38, e160	20.1	75
166	Understanding gene sequence variation in the context of transcription regulation in yeast. <i>PLoS Genetics</i> , 2010 , 6, e1000800	6	9
165	Topology-free querying of protein interaction networks. <i>Journal of Computational Biology</i> , 2010 , 17, 237-52	1.7	80
164	Different sets of QTLs influence fitness variation in yeast. <i>Molecular Systems Biology</i> , 2010 , 6, 346	12.2	21
163	A faster algorithm for simultaneous alignment and folding of RNA. <i>Journal of Computational Biology</i> , 2010 , 17, 1051-65	1.7	6
162	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. <i>BMC Systems Biology</i> , 2010 , 4, 15	3.5	14
161	Ras inhibits endoplasmic reticulum stress in human cancer cells with amplified Myc. <i>International Journal of Cancer</i> , 2010 , 126, 2268-81	7.5	17
160	DEGAS: de novo discovery of dysregulated pathways in human diseases. <i>PLoS ONE</i> , 2010 , 5, e13367	3.7	94
159	Detecting Highways of Horizontal Gene Transfer. <i>Lecture Notes in Computer Science</i> , 2010 , 109-120	0.9	3
158	Discovering Transcriptional Modules by Combined Analysis of Expression Profiles and Regulatory Sequences. <i>Lecture Notes in Computer Science</i> , 2010 , 578-579	0.9	
157	Assessing the quality of whole genome alignments in bacteria. <i>Advances in Bioinformatics</i> , 2009 , 749027	5.5	3
156	Sorting cancer karyotypes by elementary operations. <i>Journal of Computational Biology</i> , 2009 , 16, 1445-60	7	8

155	TORQUE: topology-free querying of protein interaction networks. <i>Nucleic Acids Research</i> , 2009 , 37, W106-111	4.1	23
154	Identifying functional modules using expression profiles and confidence-scored protein interactions. <i>Bioinformatics</i> , 2009 , 25, 1158-64	7.2	93
153	Allegro: analyzing expression and sequence in concert to discover regulatory programs. <i>Nucleic Acids Research</i> , 2009 , 37, 1566-79	20.1	36
152	Faster pattern matching with character classes using prime number encoding. <i>Journal of Computer and System Sciences</i> , 2009 , 75, 155-162	1	12
151	Matching with don't-cares and a small number of mismatches. <i>Information Processing Letters</i> , 2009 , 109, 273-277	0.8	3
150	Towards accurate imputation of quantitative genetic interactions. <i>Genome Biology</i> , 2009 , 10, R140	18.3	19
149	Computing has changed biology--biology education must catch up. <i>Science</i> , 2009 , 325, 541-2	33.3	61
148	SlimPLS: a method for feature selection in gene expression-based disease classification. <i>PLoS ONE</i> , 2009 , 4, e6416	3.7	34
147	Topology-Free Querying of Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2009 , 74-89	0.9	13
146	Modelling and analysis of gene regulatory networks. <i>Nature Reviews Molecular Cell Biology</i> , 2008 , 9, 770-807	4.7	718
145	SPIKE--a database, visualization and analysis tool of cellular signaling pathways. <i>BMC Bioinformatics</i> , 2008 , 9, 110	3.6	48
144	MetaReg: a platform for modeling, analysis and visualization of biological systems using large-scale experimental data. <i>Genome Biology</i> , 2008 , 9, R1	18.3	15
143	Regulatory networks define phenotypic classes of human stem cell lines. <i>Nature</i> , 2008 , 455, 401-5	50.4	283
142	Computational problems in perfect phylogeny haplotyping: typing without calling the allele. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008 , 5, 101-9	3	6
141	Evolution and selection in yeast promoters: analyzing the combined effect of diverse transcription factor binding sites. <i>PLoS Computational Biology</i> , 2008 , 4, e7	5	19
140	Transcription factor and microRNA motif discovery: the Amadeus platform and a compendium of metazoan target sets. <i>Genome Research</i> , 2008 , 18, 1180-9	9.7	146
139	Sorting genomes with centromeres by translocations. <i>Journal of Computational Biology</i> , 2008 , 15, 793-812	12.7	17
138	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , 2008 , 4, 209	12.2	59

137	Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence. <i>Stem Cells</i> , 2008 , 26, 1506-16	5.8	184
136	DETECTING PATHWAYS TRANSCRIPTIONALLY CORRELATED WITH CLINICAL PARAMETERS 2008 ,		2
135	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles 2008 , 347-359		34
134	A Faster Algorithm for RNA Co-folding. <i>Lecture Notes in Computer Science</i> , 2008 , 174-185	0.9	17
133	Sorting Cancer Karyotypes by Elementary Operations. <i>Lecture Notes in Computer Science</i> , 2008 , 211-225	0.9	1
132	Detecting pathways transcriptionally correlated with clinical parameters. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008 , 7, 249-58		5
131	Degenerate primer design: theoretical analysis and the HYDEN program. <i>Methods in Molecular Biology</i> , 2007 , 402, 221-44	1.4	12
130	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007 , 3, 88	12.2	743
129	Pediatric onset Crohn's colitis is characterized by genotype-dependent age-related susceptibility. <i>Inflammatory Bowel Diseases</i> , 2007 , 13, 1509-15	4.5	51
128	Improved algorithms for the random cluster graph model. <i>Random Structures and Algorithms</i> , 2007 , 31, 418-449	0.8	4
127	A genome-wide analysis in <i>Saccharomyces cerevisiae</i> demonstrates the influence of chromatin modifiers on transcription. <i>Nature Genetics</i> , 2007 , 39, 303-9	36.3	59
126	Identification of functional modules using network topology and high-throughput data. <i>BMC Systems Biology</i> , 2007 , 1, 8	3.5	229
125	GEVALT: an integrated software tool for genotype analysis. <i>BMC Bioinformatics</i> , 2007 , 8, 36	3.6	36
124	Functional genomic delineation of TLR-induced transcriptional networks. <i>BMC Genomics</i> , 2007 , 8, 394	4.5	24
123	Refinement and expansion of signaling pathways: the osmotic response network in yeast. <i>Genome Research</i> , 2007 , 17, 358-67	9.7	44
122	Risk factors for perianal Crohn's disease: the role of genotype, phenotype, and ethnicity. <i>American Journal of Gastroenterology</i> , 2007 , 102, 1702-8	0.7	18
121	Gene expression signature of human cancer cell lines treated with the ras inhibitor salirasib (S-farnesylthiosalicylic acid). <i>Cancer Research</i> , 2007 , 67, 3320-8	10.1	43
120	Sorting by reciprocal translocations via reversals theory. <i>Journal of Computational Biology</i> , 2007 , 14, 408-22		7

119	A randomization test for controlling population stratification in whole-genome association studies. <i>American Journal of Human Genetics</i> , 2007 , 81, 895-905	11	42
118	Rearrangements in Genomes with Centromeres Part I: Translocations. <i>Lecture Notes in Computer Science</i> , 2007 , 339-353	0.9	1
117	Assessing the number of ancestral alternatively spliced exons in the human genome. <i>BMC Genomics</i> , 2006 , 7, 273	4.5	16
116	E2F1 identified by promoter and biochemical analysis as a central target of glioblastoma cell-cycle arrest in response to Ras inhibition. <i>International Journal of Cancer</i> , 2006 , 119, 527-38	7.5	24
115	A probabilistic methodology for integrating knowledge and experiments on biological networks. <i>Journal of Computational Biology</i> , 2006 , 13, 165-81	1.7	50
114	ATM haplotypes and breast cancer risk in Jewish high-risk women. <i>British Journal of Cancer</i> , 2006 , 94, 1537-43	8.7	25
113	Quantification of protein half-lives in the budding yeast proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13004-9	11.5	535
112	A fast method for computing high-significance disease association in large population-based studies. <i>American Journal of Human Genetics</i> , 2006 , 79, 481-92	11	36
111	Reconstructing Chain Functions in Genetic Networks. <i>SIAM Journal on Discrete Mathematics</i> , 2006 , 20, 727-740	0.7	0
110	A simpler and faster 1.5-approximation algorithm for sorting by transpositions. <i>Information and Computation</i> , 2006 , 204, 275-290	0.8	39
109	A specific RAD51 haplotype increases breast cancer risk in Jewish non-Ashkenazi high-risk women. <i>European Journal of Cancer</i> , 2006 , 42, 1129-34	7.5	3
108	Parallel induction of ATM-dependent pro- and antiapoptotic signals in response to ionizing radiation in murine lymphoid tissue. <i>Oncogene</i> , 2006 , 25, 1584-92	9.2	62
107	An $O(n^{3/2}\sqrt{\log(n)})$ Algorithm for Sorting by Reciprocal Translocations. <i>Lecture Notes in Computer Science</i> , 2006 , 258-269	0.9	11
106	Sorting by Translocations Via Reversals Theory. <i>Lecture Notes in Computer Science</i> , 2006 , 87-98	0.9	6
105	Deciphering transcriptional regulatory elements that encode specific cell cycle phasing by comparative genomics analysis. <i>Cell Cycle</i> , 2005 , 4, 1788-97	4.7	39
104	Integrative analysis of genome-wide experiments in the context of a large high-throughput data compendium. <i>Molecular Systems Biology</i> , 2005 , 1, 2005.0002	12.2	39
103	Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data. <i>Journal of Computational Biology</i> , 2005 , 12, 835-46	1.7	120
102	A global view of pleiotropy and phenotypically derived gene function in yeast. <i>Molecular Systems Biology</i> , 2005 , 1, 2005.0001	12.2	232

101	The degenerate primer design problem: theory and applications. <i>Journal of Computational Biology</i> , 2005 , 12, 431-56	1.7	49
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