Vineet Bafna

List of Publications by Year
in descending order

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184 papers	51,304 citations	22132 59 h-index	4545 171 g-index
211 all docs	211 docs citations	211 times ranked	69930 citing authors

#	Article	IF	Citations
1	Heterozygous Tropomodulin 3 mice have improved lung vascularization after chronic hypoxia. Human Molecular Genetics, 2022, 31, 1130-1140.	1.4	0
2	Extrachromosomal DNA: An Emerging Hallmark in Human Cancer. Annual Review of Pathology: Mechanisms of Disease, 2022, 17, 367-386.	9.6	44
3	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19. IScience, 2022, 25, 103760.	1.9	15
4	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	13.7	60
5	Plasticity of Extrachromosomal and IntrachromosomalBRAFAmplifications in Overcoming Targeted Therapy Dosage Challenges. Cancer Discovery, 2022, 12, 1046-1069.	7.7	27
6	FastViFi: Fast and accurate detection of (Hybrid) Viral DNA and RNA. NAR Genomics and Bioinformatics, 2022, 4, lqac032.	1.5	2
7	Extrachromosomal DNA in Cancer. Annual Review of Genomics and Human Genetics, 2022, 23, 29-52.	2.5	16
8	ARID1B, a molecular suppressor of erythropoiesis, is essential for the prevention of Mongeâ€™s disease. Experimental and Molecular Medicine, 2022, 54, 777-787.	3.2	6
9	Detecting tandem repeat variants in coding regions using code-adVNTR. IScience, 2022, 25, 104785.	1.9	5
10	Extrachromosomal DNA (ecDNA) in cancer pathogenesis. Current Opinion in Genetics and Development, 2021, 66, 78-82.	1.5	29
11	Multiple mechanisms drive genomic adaptation to extreme O2 levels in Drosophila melanogaster. Nature Communications, 2021, 12, 997.	5.8	6
12	Variable number tandem repeats mediate the expression of proximal genes. Nature Communications, 2021, 12, 2075.	5.8	47
13	FaNDOM: Fast nested distance-based seeding of optical maps. Patterns, 2021, 2, 100248.	3.1	11
14	CONSULT: accurate contamination removal using locality-sensitive hashing. NAR Genomics and Bioinformatics, 2021, 3, lqab071.	1.5	14
15	Extrachromosomal DNA in HPV-Mediated Oropharyngeal Cancer Drives Diverse Oncogene Transcription. Clinical Cancer Research, 2021, 27, 6772-6786.	3.2	20
16	Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. PLoS Computational Biology, 2021, 17, e1009449.	1.5	17
17	ecDNA hubs drive cooperative intermolecular oncogene expression. Nature, 2021, 600, 731-736.	13.7	123
18	AmpliconReconstructor integrates NGS and optical mapping to resolve the complex structures of focal amplifications. Nature Communications, 2020, 11, 4374.	5.8	49

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19	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. Nature Genetics, 2020, 52, 891-897.	9.4	273
20	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. Molecular Ecology, 2020, 29, 2521-2534.	2.0	58
21	The impact of contaminants on the accuracy of genome skimming and the effectiveness of exclusion read filters. Molecular Ecology Resources, 2020, 20, 649-661.	2.2	16
22	Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. Nature Communications, 2020, 11, 550.	5.8	45
23	Computing the Statistical Significance of Overlap between Genome Annotations with iStat. Cell Systems, 2019, 8, 523-529.e4.	2.9	8
24	EcSeg: Semantic Segmentation of Metaphase Images Containing Extrachromosomal DNA. IScience, 2019, 21, 428-435.	1.9	30
25	Exploring the landscape of focal amplifications in cancer using AmpliconArchitect. Nature Communications, 2019, 10, 392.	5.8	164
26	NAD metabolic dependency in cancer is shaped by gene amplification and enhancer remodelling. Nature, 2019, 569, 570-575.	13.7	153
27	Proteogenomic Annotation of Chinese Hamsters Reveals Extensive Novel Translation Events and Endogenous Retroviral Elements. Journal of Proteome Research, 2019, 18, 2433-2445.	1.8	15
28	Extrachromosomal oncogene amplification in tumour pathogenesis and evolution. Nature Reviews Cancer, 2019, 19, 283-288.	12.8	219
29	Skmer: assembly-free and alignment-free sample identification using genome skims. Genome Biology, 2019, 20, 34.	3.8	70
30	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	13.7	343
31	Novel insight into the genetic basis of high-altitude pulmonary hypertension in Kyrgyz highlanders. European Journal of Human Genetics, 2019, 27, 150-159.	1.4	14
32	Identifying the favored mutation in a positive selective sweep. Nature Methods, 2018, 15, 279-282.	9.0	56
33	MHC class I loaded ligands from breast cancer cell lines: A potential HLA-I-typed antigen collection. Journal of Proteomics, 2018, 176, 13-23.	1.2	27
34	ViFi: accurate detection of viral integration and mRNA fusion reveals indiscriminate and unregulated transcription in proximal genomic regions in cervical cancer. Nucleic Acids Research, 2018, 46, 3309-3325.	6.5	47
35	ProteoStorm: An Ultrafast Metaproteomics Database Search Framework. Cell Systems, 2018, 7, 463-467.e6.	2.9	27
36	Targeted genotyping of variable number tandem repeats with adVNTR. Genome Research, 2018, 28, 1709-1719.	2.4	59

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37	Principles of Systems Biology, No. 31. Cell Systems, 2018, 7, 133-135.	2.9	0
38	Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. Nature, 2017, 543, 122-125.	13.7	530
39	<scp>Clear</scp>: Composition of Likelihoods for Evolve and Resequence Experiments. Genetics, 2017, 206, 1011-1023.	1.2	32
40	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. Genome Research, 2017, 27, 801-812.	2.4	285
41	Ultraaccurate genome sequencing and haplotyping of single human cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12512-12517.	3.3	41
42	High-altitude adaptation in humans: from genomics to integrative physiology. Journal of Molecular Medicine, 2017, 95, 1269-1282.	1.7	76
43	The Antibody Repertoire of Colorectal Cancer. Molecular and Cellular Proteomics, 2017, 16, 2111-2124.	2.5	8
44	New Insights into the Genetic Basis of Mongeâ€™s Disease and Adaptation to High-Altitude. Molecular Biology and Evolution, 2017, 34, 3154-3168.	3.5	31
45	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. Nucleic Acids Research, 2016, 44, e111-e111.	6.5	1
46	Senp1 drives hypoxia-induced polycythemia via GATA1 and Bcl-xL in subjects with Mongeâ€™s disease. Journal of Experimental Medicine, 2016, 213, 2729-2744.	4.2	29
47	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
48	Diversity, Productivity, and Stability of an Industrial Microbial Ecosystem. Applied and Environmental Microbiology, 2016, 82, 2494-2505.	1.4	46
49	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. PLoS Genetics, 2015, 11, e1005527.	1.5	19
50	Endothelin receptor B, a candidate gene from human studies at high altitude, improves cardiac tolerance to hypoxia in genetically engineered heterozygote mice. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10425-10430.	3.3	45
51	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. Journal of Proteome Research, 2015, 14, 3555-3567.	1.8	36
52	Haplotype Allele Frequency (HAF) Score: Predicting Carriers of Ongoing Selective Sweeps Without Knowledge of the Adaptive Allele. Lecture Notes in Computer Science, 2015, , 276-280.	1.0	1
53	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
54	Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Journal of Computational Biology, 2015, 22, 577-594.	0.8	10

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55	Next-Generation Sequencing of Plasmodium vivax Patient Samples Shows Evidence of Direct Evolution in Drug-Resistance Genes. ACS Infectious Diseases, 2015, 1, 367-379.	1.8	30
56	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	0.6	22
57	The TGFÎ²1 Promoter SNP C-509T and Food Sensitization Promote Esophageal Remodeling in Pediatric Eosinophilic Esophagitis. PLoS ONE, 2015, 10, e0144651.	1.1	26
58	Abstract 16038: Heterozygous Endothelin Receptor Type B Knockout Confers Cardiac Resistance to Extreme Hypoxia in Mice. Circulation, 2015, 132, .	1.6	0
59	The Genetic Basis of Chronic Mountain Sickness. Physiology, 2014, 29, 403-412.	1.6	27
60	Proteogenomic strategies for identification of aberrant cancer peptides using largeâ€scale nextâ€generation sequencing data. Proteomics, 2014, 14, 2719-2730.	1.3	62
61	Amplification and thrifty single-molecule sequencing of recurrent somatic structural variations. Genome Research, 2014, 24, 318-328.	2.4	21
62	The elusive evidence for chromothripsis. Nucleic Acids Research, 2014, 42, 8231-8242.	6.5	38
63	Inferring gene ontologies from pairwise similarity data. Bioinformatics, 2014, 30, i34-i42.	1.8	78
64	Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. Genome Biology, 2014, 15, R36.	13.9	71
65	Using Genome Query Language to uncover genetic variation. Bioinformatics, 2014, 30, 1-8.	1.8	96
66	An Automated Proteogenomic Method Uses Mass Spectrometry to Reveal Novel Genes in Zea mays. Molecular and Cellular Proteomics, 2014, 13, 157-167.	2.5	79
67	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. Molecular and Cellular Proteomics, 2014, 13, 3184-3198.	2.5	52
68	Proteogenomic Database Construction Driven from Large Scale RNA-seq Data. Journal of Proteome Research, 2014, 13, 21-28.	1.8	107
69	Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Lecture Notes in Computer Science, 2014, , 400-417.	1.0	1
70	Evaluating genome architecture of a complex region via generalized bipartite matching. BMC Bioinformatics, 2013, 14, S13.	1.2	2
71	Whole-Genome Sequencing Uncovers the Genetic Basis of Chronic Mountain Sickness in Andean Highlanders. American Journal of Human Genetics, 2013, 93, 452-462.	2.6	115
72	Learning Natural Selection from the Site Frequency Spectrum. Genetics, 2013, 195, 181-193.	1.2	105

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73	Virmid: accurate detection of somatic mutations with sample impurity inference. Genome Biology, 2013, 14, R90.	13.9	58
74	On the design of clone-based haplotyping. Genome Biology, 2013, 14, R100.	13.9	18
75	An algorithmic approach for breakage-fusion-bridge detection in tumor genomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5546-5551.	3.3	53
76	Reprever: resolving low-copy duplicated sequences using template driven assembly. Nucleic Acids Research, 2013, 41, e128-e128.	6.5	7
77	Wessim: a whole-exome sequencing simulator based on in silico exome capture. Bioinformatics, 2013, 29, 1076-1077.	1.8	38
78	Abstractions for genomics. Communications of the ACM, 2013, 56, 83-93.	3.3	12
79	Cerulean: A Hybrid Assembly Using High Throughput Short and Long Reads. Lecture Notes in Computer Science, 2013, , 349-363.	1.0	28
80	Learning Natural Selection from the Site Frequency Spectrum. Lecture Notes in Computer Science, 2013, , 230-233.	1.0	1
81	Protein Identification Using Top-Down Spectra. Molecular and Cellular Proteomics, 2012, 11, M111.008524.	2.5	127
82	Accurate Mass Spectrometry Based Protein Quantification via Shared Peptides. Journal of Computational Biology, 2012, 19, 337-348.	0.8	40
83	Combinatorics of the Breakage-Fusion-Bridge Mechanism. Journal of Computational Biology, 2012, 19, 662-678.	0.8	18
84	Speeding up tandem mass spectral identification using indexes. Bioinformatics, 2012, 28, 1692-1697.	1.8	12
85	Exome Sequencing Can Improve Diagnosis and Alter Patient Management. Science Translational Medicine, 2012, 4, 138ra78.	5.8	226
86	iDASH: integrating data for analysis, anonymization, and sharing. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 196-201.	2.2	130
87	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
88	De novo somatic mutations in components of the PI3K-AKT3-mTOR pathway cause hemimegalencephaly. Nature Genetics, 2012, 44, 941-945.	9.4	628
89	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research, 2012, 22, 246-258.	2.4	476
90	Sample Reproducibility of Genetic Association Using Different Multimarker TDTs in Genome-Wide Association Studies: Characterization and a New Approach. PLoS ONE, 2012, 7, e29613.	1.1	5

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91	TCLUST: A Fast Method for Clustering Genome-Scale Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 808-818.	1.9	14
92	On the Approximability of Reachability-Preserving Network Orientations. Internet Mathematics, 2011, 7, 209-232.	0.7	8
93	Practical 4â€²-Phosphopantetheine Active Site Discovery from Proteomic Samples. Journal of Proteome Research, 2011, 10, 320-329.	1.8	16
94	Automated Querying and Identification of Novel Peptides using MALDI Mass Spectrometric Imaging. Journal of Proteome Research, 2011, 10, 1915-1928.	1.8	30
95	AMASS: Algorithm for MSI Analysis by Semi-supervised Segmentation. Journal of Proteome Research, 2011, 10, 4734-4743.	1.8	24
96	Tests of Selection in Pooled Case-Control Data: An Empirical Study. Frontiers in Genetics, 2011, 2, 83.	1.1	3
97	Strobe sequence design for haplotype assembly. BMC Bioinformatics, 2011, 12, S24.	1.2	18
98	Resurrection of a clinical antibody: Template proteogenomic de novo proteomic sequencing and reverse engineering of an antiâ€lymphotoxinâ€î± antibody. Proteomics, 2011, 11, 395-405.	1.3	31
99	Preface: Research in Computational Molecular Biology (RECOMB 2011). Journal of Computational Biology, 2011, 18, 1369-1369.	0.8	0
100	Compressing Genomic Sequence Fragments Using S<scp>lim</scp>G<scp>ene</scp>. Journal of Computational Biology, 2011, 18, 401-413.	0.8	70
101	Experimental selection of hypoxia-tolerant Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2349-2354.	3.3	105
102	Sensitive gene fusion detection using ambiguously mapping RNA-Seq read pairs. Bioinformatics, 2011, 27, 1068-1075.	1.8	53
103	Designing deep sequencing experiments: detecting structural variation and estimating transcript abundance. BMC Genomics, 2010, 11, 385.	1.2	23
104	Construction of a medicinal leech transcriptome database and its application to the identification of leech homologs of neural and innate immune genes. BMC Genomics, 2010, 11, 407.	1.2	50
105	Proteogenomics to discover the full coding content of genomes: A computational perspective. Journal of Proteomics, 2010, 73, 2124-2135.	1.2	145
106	Deconvolution and Database Search of Complex Tandem Mass Spectra of Intact Proteins. Molecular and Cellular Proteomics, 2010, 9, 2772-2782.	2.5	145
107	Template Proteogenomics: Sequencing Whole Proteins Using an Imperfect Database. Molecular and Cellular Proteomics, 2010, 9, 1260-1270.	2.5	46
108	Protein-Protein Interaction Network Evaluation for Identifying Potential Drug Targets. Journal of Computational Biology, 2010, 17, 669-684.	0.8	30

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109	A Covering Method for Detecting Genetic Associations between Rare Variants and Common Phenotypes. PLoS Computational Biology, 2010, 6, e1000954.	1.5	85
110	RAPID detection of geneâ€“gene interactions in genome-wide association studies. Bioinformatics, 2010, 26, 2856-2862.	1.8	35
111	Population sequencing of two endocannabinoid metabolic genes identifies rare and common regulatory variants associated with extreme obesity and metabolite level. Genome Biology, 2010, 11, R118.	13.9	34
112	Deciphering the genetic basis of common diseases by integrated functional annotation of common and rare variants. Genome Biology, 2010, 11, .	3.8	0
113	Expansion of the mycobacterial â€œPUPylomeâ€• Molecular BioSystems, 2010, 6, 376-385.	2.9	83
114	Optimizing PCR Assays for DNA-Based Cancer Diagnostics. Journal of Computational Biology, 2010, 17, 369-381.	0.8	4
115	Compressing Genomic Sequence Fragments Using SlimGene. Lecture Notes in Computer Science, 2010, , 310-324.	1.0	8
116	Fast and Accurate Alignment of Multiple Protein Networks. Journal of Computational Biology, 2009, 16, 989-999.	0.8	57
117	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. Genome Research, 2009, 19, 1527-1541.	2.4	448
118	Shared Peptides in Mass Spectrometry Based Protein Quantification. Lecture Notes in Computer Science, 2009, , 356-371.	1.0	7
119	Optimizing PCR Assays for DNA Based Cancer Diagnostics. Lecture Notes in Computer Science, 2009, , 220-235.	1.0	0
120	Accurate Annotation of Peptide Modifications through Unrestrictive Database Search. Journal of Proteome Research, 2008, 7, 170-181.	1.8	50
121	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. Journal of Proteome Research, 2008, 7, 3373-3381.	1.8	51
122	HapCUT: an efficient and accurate algorithm for the haplotype assembly problem. Bioinformatics, 2008, 24, i153-i159.	1.8	250
123	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. Molecular and Cellular Proteomics, 2008, 7, 1389-1396.	2.5	472
124	QNet: A Tool for Querying Protein Interaction Networks. Journal of Computational Biology, 2008, 15, 913-925.	0.8	86
125	Discovery and revision of Arabidopsis genes by proteogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 21034-21038.	3.3	268
126	Evaluation of Paired-End Sequencing Strategies for Detection of Genome Rearrangements in Cancer. PLoS Computational Biology, 2008, 4, e1000051.	1.5	72

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127	Comparative proteogenomics: Combining mass spectrometry and comparative genomics to analyze multiple genomes. Genome Research, 2008, 18, 1133-1142.	2.4	97
128	An MCMC algorithm for haplotype assembly from whole-genome sequence data. Genome Research, 2008, 18, 1336-1346.	2.4	114
129	Structural Alignment of Pseudoknotted RNA. Journal of Computational Biology, 2008, 15, 489-504.	0.8	32
130	Fast and Accurate Alignment of Multiple Protein Networks. Lecture Notes in Computer Science, 2008, , 246-256.	1.0	32
131	An Algorithm for Orienting Graphs Based on Cause-Effect Pairs and Its Applications to Orienting Protein Networks. Lecture Notes in Computer Science, 2008, , 222-232.	1.0	29
132	Evidence for large inversion polymorphisms in the human genome from HapMap data. Genome Research, 2007, 17, 219-230.	2.4	67
133	The Diploid Genome Sequence of an Individual Human. PLoS Biology, 2007, 5, e254.	2.6	1,491
134	A Decomposition Theory for Phylogenetic Networks and Incompatible Characters. Journal of Computational Biology, 2007, 14, 1247-1272.	0.8	43
135	Optimization of primer design for the detection of variable genomic lesions in cancer. Bioinformatics, 2007, 23, 2807-2815.	1.8	17
136	Improving gene annotation using peptide mass spectrometry. Genome Research, 2007, 17, 231-239.	2.4	157
137	Integrating scientific cultures. Molecular Systems Biology, 2007, 3, 105.	3.2	13
138	Whole proteome analysis of post-translational modifications: Applications of mass-spectrometry for proteogenomic annotation. Genome Research, 2007, 17, 1362-1377.	2.4	175
139	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	2.6	736
140	QNet: A Tool for Querying Protein Interaction Networks. Lecture Notes in Computer Science, 2007, , 1-15.	1.0	28
141	Inference about Recombination from Haplotype Data: Lower Bounds and Recombination Hotspots. Journal of Computational Biology, 2006, 13, 501-521.	0.8	14
142	Age-Related Changes in Human Crystallins Determined from Comparative Analysis of Post-translational Modifications in Young and Aged Lens:â€‰ Does Deamidation Contribute to Crystallin Insolubility?. Journal of Proteome Research, 2006, 5, 2554-2566.	1.8	259
143	Unrestrictive identification of post-translational modifications through peptide mass spectrometry. Nature Protocols, 2006, 1, 67-72.	5.5	33
144	A sequence-based filtering method for ncRNA identification and its application to searching for riboswitch elements. Bioinformatics, 2006, 22, e557-e565.	1.8	30

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145	EXPLORING THE OCEAN'S MICROBES: SEQUENCING THE SEVEN SEAS. , 2006, , .		0
146	Structural Alignment of Pseudoknotted RNA. Lecture Notes in Computer Science, 2006, , 143-158.	1.0	5
147	Consensus Folding of Unaligned RNA Sequences Revisited. Journal of Computational Biology, 2006, 13, 283-295.	0.8	27
148	Identification of post-translational modifications by blind search of mass spectra. Nature Biotechnology, 2005, 23, 1562-1567.	9.4	247
149	Polynomial and APX-hard cases of the individual haplotyping problem. Theoretical Computer Science, 2005, 335, 109-125.	0.5	50
150	Improved Recombination Lower Bounds for Haplotype Data. Lecture Notes in Computer Science, 2005, , 569-584.	1.0	11
151	Orthologous repeats and mammalian phylogenetic inference. Genome Research, 2005, 15, 998-1006.	2.4	37
152	Searching Genomes for Noncoding RNA Using FastR. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 366-379.	1.9	48
153	Identification of post-translational modifications via blind search of mass-spectra. , 2005, , 157-66.		20
154	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. Journal of Proteome Research, 2005, 4, 1287-1295.	1.8	131
155	InsPecT:Â Identification of Posttranslationally Modified Peptides from Tandem Mass Spectra. Analytical Chemistry, 2005, 77, 4626-4639.	3.2	546
156	A Note on Efficient Computation of Haplotypes via Perfect Phylogeny. Journal of Computational Biology, 2004, 11, 858-866.	0.8	28
157	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. Genome Research, 2004, 14, 1633-1640.	2.4	113
158	FastR: fast database search tool for non-coding RNA. , 2004, , 52-61.		19
159	The number of recombination events in a sample history: conflict graph and lower bounds. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 78-90.	1.9	37
160	Shotgun Protein Sequencing by Tandem Mass Spectra Assembly. Analytical Chemistry, 2004, 76, 7221-7233.	3.2	47
161	A Survey of Computational Methods for Determining Haplotypes. Lecture Notes in Computer Science, 2004, , 26-47.	1.0	72
162	The Dog Genome: Survey Sequencing and Comparative Analysis. Science, 2003, 301, 1898-1903.	6.0	482

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163	Haplotyping as Perfect Phylogeny: A Direct Approach. Journal of Computational Biology, 2003, 10, 323-340.	0.8	115
164	Robustness of Inference of Haplotype Block Structure. Journal of Computational Biology, 2003, 10, 13-19.	0.8	54
165	Combinatorial Problems Arising in SNP and Haplotype Analysis. Lecture Notes in Computer Science, 2003, , 26-47.	1.0	17
166	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
167	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. Lecture Notes in Computer Science, 2002, , 29-43.	1.0	56
168	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
169	SCOPE: a probabilistic model for scoring tandem mass spectra against a peptide database. Bioinformatics, 2001, 17, S13-S21.	1.8	165
170	Ligand-Receptor Pairing Via Tree Comparison. Journal of Computational Biology, 2000, 7, 59-70.	0.8	10
171	A Polynomial-Time Approximation Scheme for Minimum Routing Cost Spanning Trees. SIAM Journal on Computing, 2000, 29, 761-778.	0.8	103
172	A 2-Approximation Algorithm for the Undirected Feedback Vertex Set Problem. SIAM Journal on Discrete Mathematics, 1999, 12, 289-297.	0.4	258
173	Sorting by Transpositions. SIAM Journal on Discrete Mathematics, 1998, 11, 224-240.	0.4	330
174	On the Approximability of Numerical Taxonomy (Fitting Distances by Tree Metrics). SIAM Journal on Computing, 1998, 28, 1073-1085.	0.8	71
175	Detecting non-adjoining correlations with signals in DNA. , 1998, , .		19
176	Human beta-defensin 2 is a salt-sensitive peptide antibiotic expressed in human lung.. Journal of Clinical Investigation, 1998, 102, 874-880.	3.9	513
177	Approximation algorithms for multiple sequence alignment. Theoretical Computer Science, 1997, 182, 233-244.	0.5	39
178	Genome Rearrangements and Sorting by Reversals. SIAM Journal on Computing, 1996, 25, 272-289.	0.8	313
179	Nonoverlapping local alignments (weighted independent sets of axis-parallel rectangles). Discrete Applied Mathematics, 1996, 71, 41-53.	0.5	49
180	Constant ratio approximations of the weighted feedback vertex set problem for undirected graphs. Lecture Notes in Computer Science, 1995, , 142-151.	1.0	26

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181	Computing similarity between RNA strings. Lecture Notes in Computer Science, 1995, , 1-16.	1.0	44
182	Parallel implementation of logic languages. Lecture Notes in Computer Science, 1990, , 154-165.	1.0	0
183	Sorting by Reversals: Genome Rearrangements in Plant Organelles and Evolutionary History of X Chromosome. Molecular Biology and Evolution, 0, , .	3.5	24
184	FaNDOM: Fast Nested Distance-Based Seeding of Optical Maps. SSRN Electronic Journal, 0, , .	0.4	0