Vineet Bafna

List of Publications by Year
in descending order

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184 papers	51,304 citations	22099 59 h-index	4535 171 g-index
211 all docs	211 docs citations	211 times ranked	69930 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
4	The Diploid Genome Sequence of an Individual Human. PLoS Biology, 2007, 5, e254.	2.6	1,491
5	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
6	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	2.6	736
7	De novo somatic mutations in components of the PI3K-AKT3-mTOR pathway cause hemimegalencephaly. Nature Genetics, 2012, 44, 941-945.	9.4	628
8	InsPecT:Â Identification of Posttranslationally Modified Peptides from Tandem Mass Spectra. Analytical Chemistry, 2005, 77, 4626-4639.	3.2	546
9	Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. Nature, 2017, 543, 122-125.	13.7	530
10	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
11	The Dog Genome: Survey Sequencing and Comparative Analysis. Science, 2003, 301, 1898-1903.	6.0	482
12	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research, 2012, 22, 246-258.	2.4	476
13	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. Molecular and Cellular Proteomics, 2008, 7, 1389-1396.	2.5	472
14	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
15	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	13.7	343
16	Sorting by Transpositions. SIAM Journal on Discrete Mathematics, 1998, 11, 224-240.	0.4	330
17	Genome Rearrangements and Sorting by Reversals. SIAM Journal on Computing, 1996, 25, 272-289.	0.8	313
18	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. Genome Research, 2017, 27, 801-812.	2.4	285

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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	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
21	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
22	A 2-Approximation Algorithm for the Undirected Feedback Vertex Set Problem. SIAM Journal on Discrete Mathematics, 1999, 12, 289-297.	0.4	258
23	HapCUT: an efficient and accurate algorithm for the haplotype assembly problem. Bioinformatics, 2008, 24, i153-i159.	1.8	250
24	Identification of post-translational modifications by blind search of mass spectra. Nature Biotechnology, 2005, 23, 1562-1567.	9.4	247
25	Exome Sequencing Can Improve Diagnosis and Alter Patient Management. Science Translational Medicine, 2012, 4, 138ra78.	5.8	226
26	Extrachromosomal oncogene amplification in tumour pathogenesis and evolution. Nature Reviews Cancer, 2019, 19, 283-288.	12.8	219
27	Whole proteome analysis of post-translational modifications: Applications of mass-spectrometry for proteogenomic annotation. Genome Research, 2007, 17, 1362-1377.	2.4	175
28	SCOPE: a probabilistic model for scoring tandem mass spectra against a peptide database. Bioinformatics, 2001, 17, S13-S21.	1.8	165
29	Exploring the landscape of focal amplifications in cancer using AmpliconArchitect. Nature Communications, 2019, 10, 392.	5.8	164
30	Improving gene annotation using peptide mass spectrometry. Genome Research, 2007, 17, 231-239.	2.4	157
31	NAD metabolic dependency in cancer is shaped by gene amplification and enhancer remodelling. Nature, 2019, 569, 570-575.	13.7	153
32	Proteogenomics to discover the full coding content of genomes: A computational perspective. Journal of Proteomics, 2010, 73, 2124-2135.	1.2	145
33	Deconvolution and Database Search of Complex Tandem Mass Spectra of Intact Proteins. Molecular and Cellular Proteomics, 2010, 9, 2772-2782.	2.5	145
34	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. Journal of Proteome Research, 2005, 4, 1287-1295.	1.8	131
35	iDASH: integrating data for analysis, anonymization, and sharing. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 196-201.	2.2	130
36	Protein Identification Using Top-Down Spectra. Molecular and Cellular Proteomics, 2012, 11, M111.008524.	2.5	127

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37	ecDNA hubs drive cooperative intermolecular oncogene expression. Nature, 2021, 600, 731-736.	13.7	123
38	Haplotyping as Perfect Phylogeny: A Direct Approach. Journal of Computational Biology, 2003, 10, 323-340.	0.8	115
39	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
40	An MCMC algorithm for haplotype assembly from whole-genome sequence data. Genome Research, 2008, 18, 1336-1346.	2.4	114
41	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. Genome Research, 2004, 14, 1633-1640.	2.4	113
42	Proteogenomic Database Construction Driven from Large Scale RNA-seq Data. Journal of Proteome Research, 2014, 13, 21-28.	1.8	107
43	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
44	Learning Natural Selection from the Site Frequency Spectrum. Genetics, 2013, 195, 181-193.	1.2	105
45	A Polynomial-Time Approximation Scheme for Minimum Routing Cost Spanning Trees. SIAM Journal on Computing, 2000, 29, 761-778.	0.8	103
46	Comparative proteogenomics: Combining mass spectrometry and comparative genomics to analyze multiple genomes. Genome Research, 2008, 18, 1133-1142.	2.4	97
47	Using Genome Query Language to uncover genetic variation. Bioinformatics, 2014, 30, 1-8.	1.8	96
48	QNet: A Tool for Querying Protein Interaction Networks. Journal of Computational Biology, 2008, 15, 913-925.	0.8	86
49	A Covering Method for Detecting Genetic Associations between Rare Variants and Common Phenotypes. PLoS Computational Biology, 2010, 6, e1000954.	1.5	85
50	Expansion of the mycobacterial â€œPUPylomeâ€• Molecular BioSystems, 2010, 6, 376-385.	2.9	83
51	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
52	Inferring gene ontologies from pairwise similarity data. Bioinformatics, 2014, 30, i34-i42.	1.8	78
53	High-altitude adaptation in humans: from genomics to integrative physiology. Journal of Molecular Medicine, 2017, 95, 1269-1282.	1.7	76
54	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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55	A Survey of Computational Methods for Determining Haplotypes. Lecture Notes in Computer Science, 2004, , 26-47.	1.0	72
56	On the Approximability of Numerical Taxonomy (Fitting Distances by Tree Metrics). SIAM Journal on Computing, 1998, 28, 1073-1085.	0.8	71
57	Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. Genome Biology, 2014, 15, R36.	13.9	71
58	Compressing Genomic Sequence Fragments Using S<scp>lim</scp>G<scp>ene</scp>. Journal of Computational Biology, 2011, 18, 401-413.	0.8	70
59	Skmer: assembly-free and alignment-free sample identification using genome skims. Genome Biology, 2019, 20, 34.	3.8	70
60	Evidence for large inversion polymorphisms in the human genome from HapMap data. Genome Research, 2007, 17, 219-230.	2.4	67
61	Proteogenomic strategies for identification of aberrant cancer peptides using largeâ€scale nextâ€generation sequencing data. Proteomics, 2014, 14, 2719-2730.	1.3	62
62	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	13.7	60
63	Targeted genotyping of variable number tandem repeats with adVNTR. Genome Research, 2018, 28, 1709-1719.	2.4	59
64	Virmid: accurate detection of somatic mutations with sample impurity inference. Genome Biology, 2013, 14, R90.	13.9	58
65	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. Molecular Ecology, 2020, 29, 2521-2534.	2.0	58
66	Fast and Accurate Alignment of Multiple Protein Networks. Journal of Computational Biology, 2009, 16, 989-999.	0.8	57
67	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. Lecture Notes in Computer Science, 2002, , 29-43.	1.0	56
68	Identifying the favored mutation in a positive selective sweep. Nature Methods, 2018, 15, 279-282.	9.0	56
69	Robustness of Inference of Haplotype Block Structure. Journal of Computational Biology, 2003, 10, 13-19.	0.8	54
70	Sensitive gene fusion detection using ambiguously mapping RNA-Seq read pairs. Bioinformatics, 2011, 27, 1068-1075.	1.8	53
71	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
72	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. Molecular and Cellular Proteomics, 2014, 13, 3184-3198.	2.5	52

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73	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
74	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. Journal of Proteome Research, 2008, 7, 3373-3381.	1.8	51
75	Polynomial and APX-hard cases of the individual haplotyping problem. Theoretical Computer Science, 2005, 335, 109-125.	0.5	50
76	Accurate Annotation of Peptide Modifications through Unrestrictive Database Search. Journal of Proteome Research, 2008, 7, 170-181.	1.8	50
77	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
78	Nonoverlapping local alignments (weighted independent sets of axis-parallel rectangles). Discrete Applied Mathematics, 1996, 71, 41-53.	0.5	49
79	AmpliconReconstructor integrates NGS and optical mapping to resolve the complex structures of focal amplifications. Nature Communications, 2020, 11, 4374.	5.8	49
80	Searching Genomes for Noncoding RNA Using FastR. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 366-379.	1.9	48
81	Shotgun Protein Sequencing by Tandem Mass Spectra Assembly. Analytical Chemistry, 2004, 76, 7221-7233.	3.2	47
82	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
83	Variable number tandem repeats mediate the expression of proximal genes. Nature Communications, 2021, 12, 2075.	5.8	47
84	Template Proteogenomics: Sequencing Whole Proteins Using an Imperfect Database. Molecular and Cellular Proteomics, 2010, 9, 1260-1270.	2.5	46
85	Diversity, Productivity, and Stability of an Industrial Microbial Ecosystem. Applied and Environmental Microbiology, 2016, 82, 2494-2505.	1.4	46
86	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
87	Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. Nature Communications, 2020, 11, 550.	5.8	45
88	Computing similarity between RNA strings. Lecture Notes in Computer Science, 1995, , 1-16.	1.0	44
89	Extrachromosomal DNA: An Emerging Hallmark in Human Cancer. Annual Review of Pathology: Mechanisms of Disease, 2022, 17, 367-386.	9.6	44
90	A Decomposition Theory for Phylogenetic Networks and Incompatible Characters. Journal of Computational Biology, 2007, 14, 1247-1272.	0.8	43

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91	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
92	Accurate Mass Spectrometry Based Protein Quantification via Shared Peptides. Journal of Computational Biology, 2012, 19, 337-348.	0.8	40
93	Approximation algorithms for multiple sequence alignment. Theoretical Computer Science, 1997, 182, 233-244.	0.5	39
94	Wessim: a whole-exome sequencing simulator based on in silico exome capture. Bioinformatics, 2013, 29, 1076-1077.	1.8	38
95	The elusive evidence for chromothripsis. Nucleic Acids Research, 2014, 42, 8231-8242.	6.5	38
96	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
97	Orthologous repeats and mammalian phylogenetic inference. Genome Research, 2005, 15, 998-1006.	2.4	37
98	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
99	RAPID detection of geneâ€“gene interactions in genome-wide association studies. Bioinformatics, 2010, 26, 2856-2862.	1.8	35
100	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
101	Unrestrictive identification of post-translational modifications through peptide mass spectrometry. Nature Protocols, 2006, 1, 67-72.	5.5	33
102	Structural Alignment of Pseudoknotted RNA. Journal of Computational Biology, 2008, 15, 489-504.	0.8	32
103	<scp>Clear</scp>: Composition of Likelihoods for Evolve and Resequence Experiments. Genetics, 2017, 206, 1011-1023.	1.2	32
104	Fast and Accurate Alignment of Multiple Protein Networks. Lecture Notes in Computer Science, 2008, , 246-256.	1.0	32
105	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
106	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
107	A sequence-based filtering method for ncRNA identification and its application to searching for riboswitch elements. Bioinformatics, 2006, 22, e557-e565.	1.8	30
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	Automated Querying and Identification of Novel Peptides using MALDI Mass Spectrometric Imaging. Journal of Proteome Research, 2011, 10, 1915-1928.	1.8	30
110	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
111	EcSeg: Semantic Segmentation of Metaphase Images Containing Extrachromosomal DNA. IScience, 2019, 21, 428-435.	1.9	30
112	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
113	Extrachromosomal DNA (ecDNA) in cancer pathogenesis. Current Opinion in Genetics and Development, 2021, 66, 78-82.	1.5	29
114	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
115	A Note on Efficient Computation of Haplotypes via Perfect Phylogeny. Journal of Computational Biology, 2004, 11, 858-866.	0.8	28
116	QNet: A Tool for Querying Protein Interaction Networks. Lecture Notes in Computer Science, 2007, , 1-15.	1.0	28
117	Cerulean: A Hybrid Assembly Using High Throughput Short and Long Reads. Lecture Notes in Computer Science, 2013, , 349-363.	1.0	28
118	Consensus Folding of Unaligned RNA Sequences Revisited. Journal of Computational Biology, 2006, 13, 283-295.	0.8	27
119	The Genetic Basis of Chronic Mountain Sickness. Physiology, 2014, 29, 403-412.	1.6	27
120	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
121	ProteoStorm: An Ultrafast Metaproteomics Database Search Framework. Cell Systems, 2018, 7, 463-467.e6.	2.9	27
122	Plasticity of Extrachromosomal and IntrachromosomalBRAFAmplifications in Overcoming Targeted Therapy Dosage Challenges. Cancer Discovery, 2022, 12, 1046-1069.	7.7	27
123	Constant ratio approximations of the weighted feedback vertex set problem for undirected graphs. Lecture Notes in Computer Science, 1995, , 142-151.	1.0	26
124	The TGFÎ²1 Promoter SNP C-509T and Food Sensitization Promote Esophageal Remodeling in Pediatric Eosinophilic Esophagitis. PLoS ONE, 2015, 10, e0144651.	1.1	26
125	Sorting by Reversals: Genome Rearrangements in Plant Organelles and Evolutionary History of X Chromosome. Molecular Biology and Evolution, 0, , .	3.5	24
126	AMASS: Algorithm for MSI Analysis by Semi-supervised Segmentation. Journal of Proteome Research, 2011, 10, 4734-4743.	1.8	24

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127	Designing deep sequencing experiments: detecting structural variation and estimating transcript abundance. BMC Genomics, 2010, 11, 385.	1.2	23
128	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	0.6	22
129	Amplification and thrifty single-molecule sequencing of recurrent somatic structural variations. Genome Research, 2014, 24, 318-328.	2.4	21
130	Identification of post-translational modifications via blind search of mass-spectra. , 2005, , 157-66.		20
131	Extrachromosomal DNA in HPV-Mediated Oropharyngeal Cancer Drives Diverse Oncogene Transcription. Clinical Cancer Research, 2021, 27, 6772-6786.	3.2	20
132	Detecting non-adjoining correlations with signals in DNA. , 1998, , .		19
133	FastR: fast database search tool for non-coding RNA. , 2004, , 52-61.		19
134	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. PLoS Genetics, 2015, 11, e1005527.	1.5	19
135	Strobe sequence design for haplotype assembly. BMC Bioinformatics, 2011, 12, S24.	1.2	18
136	Combinatorics of the Breakage-Fusion-Bridge Mechanism. Journal of Computational Biology, 2012, 19, 662-678.	0.8	18
137	On the design of clone-based haplotyping. Genome Biology, 2013, 14, R100.	13.9	18
138	Optimization of primer design for the detection of variable genomic lesions in cancer. Bioinformatics, 2007, 23, 2807-2815.	1.8	17
139	Combinatorial Problems Arising in SNP and Haplotype Analysis. Lecture Notes in Computer Science, 2003, , 26-47.	1.0	17
140	Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. PLoS Computational Biology, 2021, 17, e1009449.	1.5	17
141	Practical 4â€²-Phosphopantetheine Active Site Discovery from Proteomic Samples. Journal of Proteome Research, 2011, 10, 320-329.	1.8	16
142	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
143	Extrachromosomal DNA in Cancer. Annual Review of Genomics and Human Genetics, 2022, 23, 29-52.	2.5	16
144	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

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145	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19. IScience, 2022, 25, 103760.	1.9	15
146	Inference about Recombination from Haplotype Data: Lower Bounds and Recombination Hotspots. Journal of Computational Biology, 2006, 13, 501-521.	0.8	14
147	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
148	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
149	CONSULT: accurate contamination removal using locality-sensitive hashing. NAR Genomics and Bioinformatics, 2021, 3, lqab071.	1.5	14
150	Integrating scientific cultures. Molecular Systems Biology, 2007, 3, 105.	3.2	13
151	Speeding up tandem mass spectral identification using indexes. Bioinformatics, 2012, 28, 1692-1697.	1.8	12
152	Abstractions for genomics. Communications of the ACM, 2013, 56, 83-93.	3.3	12
153	Improved Recombination Lower Bounds for Haplotype Data. Lecture Notes in Computer Science, 2005, , 569-584.	1.0	11
154	FaNDOM: Fast nested distance-based seeding of optical maps. Patterns, 2021, 2, 100248.	3.1	11
155	Ligand-Receptor Pairing Via Tree Comparison. Journal of Computational Biology, 2000, 7, 59-70.	0.8	10
156	Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Journal of Computational Biology, 2015, 22, 577-594.	0.8	10
157	On the Approximability of Reachability-Preserving Network Orientations. Internet Mathematics, 2011, 7, 209-232.	0.7	8
158	The Antibody Repertoire of Colorectal Cancer. Molecular and Cellular Proteomics, 2017, 16, 2111-2124.	2.5	8
159	Computing the Statistical Significance of Overlap between Genome Annotations with iStat. Cell Systems, 2019, 8, 523-529.e4.	2.9	8
160	Compressing Genomic Sequence Fragments Using SlimGene. Lecture Notes in Computer Science, 2010, , 310-324.	1.0	8
161	Reprever: resolving low-copy duplicated sequences using template driven assembly. Nucleic Acids Research, 2013, 41, e128-e128.	6.5	7
162	Shared Peptides in Mass Spectrometry Based Protein Quantification. Lecture Notes in Computer Science, 2009, , 356-371.	1.0	7

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163	Multiple mechanisms drive genomic adaptation to extreme O2 levels in Drosophila melanogaster. Nature Communications, 2021, 12, 997.	5.8	6
164	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
165	Structural Alignment of Pseudoknotted RNA. Lecture Notes in Computer Science, 2006, , 143-158.	1.0	5
166	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
167	Detecting tandem repeat variants in coding regions using code-adVNTR. IScience, 2022, 25, 104785.	1.9	5
168	Optimizing PCR Assays for DNA-Based Cancer Diagnostics. Journal of Computational Biology, 2010, 17, 369-381.	0.8	4
169	Tests of Selection in Pooled Case-Control Data: An Empirical Study. Frontiers in Genetics, 2011, 2, 83.	1.1	3
170	Evaluating genome architecture of a complex region via generalized bipartite matching. BMC Bioinformatics, 2013, 14, S13.	1.2	2
171	FastViFi: Fast and accurate detection of (Hybrid) Viral DNA and RNA. NAR Genomics and Bioinformatics, 2022, 4, lqac032.	1.5	2
172	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
173	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. Nucleic Acids Research, 2016, 44, e111-e111.	6.5	1
174	Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. Lecture Notes in Computer Science, 2014, , 400-417.	1.0	1
175	Learning Natural Selection from the Site Frequency Spectrum. Lecture Notes in Computer Science, 2013, , 230-233.	1.0	1
176	EXPLORING THE OCEAN'S MICROBES: SEQUENCING THE SEVEN SEAS. , 2006, , .		0
177	Deciphering the genetic basis of common diseases by integrated functional annotation of common and rare variants. Genome Biology, 2010, 11, .	3.8	0
178	Preface: Research in Computational Molecular Biology (RECOMB 2011). Journal of Computational Biology, 2011, 18, 1369-1369.	0.8	0
179	Principles of Systems Biology, No. 31. Cell Systems, 2018, 7, 133-135.	2.9	0
180	FaNDOM: Fast Nested Distance-Based Seeding of Optical Maps. SSRN Electronic Journal, 0, , .	0.4	0

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181	Heterozygous Tropomodulin 3 mice have improved lung vascularization after chronic hypoxia. Human Molecular Genetics, 2022, 31, 1130-1140.	1.4	0
182	Optimizing PCR Assays for DNA Based Cancer Diagnostics. Lecture Notes in Computer Science, 2009, , 220-235.	1.0	0
183	Parallel implementation of logic languages. Lecture Notes in Computer Science, 1990, , 154-165.	1.0	0
184	Abstract 16038: Heterozygous Endothelin Receptor Type B Knockout Confers Cardiac Resistance to Extreme Hypoxia in Mice. Circulation, 2015, 132, .	1.6	0