Vineet Bafna

List of Publications by Citations

184 papers	38,431 citations	56 h-index	196 g-index
211 ext. papers	46,241 ext. citations	9.7 avg, IF	6.49 L-index

#	Paper	IF	Citations
184	The sequence of the human genome. *Science*, **2001**, 291, 1304-51	33.3	10609
183	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
182	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
181	The diploid genome sequence of an individual human. *PLoS Biology*, **2007**, 5, e254	9.7	1249
180	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. *PLoS Biology*, **2007**, 5, e16	9.7	638
179	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. *Cell*, **2016**, 166, 755-765	56.2	544
178	De novo somatic mutations in components of the PI3K-AKT3-mTOR pathway cause hemimegalencephaly. *Nature Genetics*, **2012**, 44, 941-5	36.3	505
177	InsPecT: identification of posttranslationally modified peptides from tandem mass spectra. *Analytical Chemistry*, **2005**, 77, 4626-39	7.8	502
176	Human beta-defensin 2 is a salt-sensitive peptide antibiotic expressed in human lung. *Journal of Clinical Investigation*, **1998**, 102, 874-80	15.9	449
175	The dog genome: survey sequencing and comparative analysis. *Science*, **2003**, 301, 1898-903	33.3	422
174	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. *Genome Research*, **2009**, 19, 1527-41	9.7	401
173	A multidimensional chromatography technology for in-depth phosphoproteome analysis. *Molecular and Cellular Proteomics*, **2008**, 7, 1389-96	7.6	392
172	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. *Genome Research*, **2012**, 22, 246-58	9.7	385
171	Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. *Nature*, **2017**, 543, 122-125	50.4	260
170	Sorting by Transpositions. *SIAM Journal on Discrete Mathematics*, **1998**, 11, 224-240	0.7	258
169	Genome Rearrangements and Sorting by Reversals. *SIAM Journal on Computing*, **1996**, 25, 272-289	1.1	252
168	Identification of post-translational modifications by blind search of mass spectra. *Nature Biotechnology*, **2005**, 23, 1562-7	44.5	231

167	Discovery and revision of Arabidopsis genes by proteogenomics. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 21034-8	11.5	226
166	Age-related changes in human crystallins determined from comparative analysis of post-translational modifications in young and aged lens: does deamidation contribute to crystallin insolubility?. *Journal of Proteome Research*, **2006**, 5, 2554-66	5.6	224
165	A 2-Approximation Algorithm for the Undirected Feedback Vertex Set Problem. *SIAM Journal on Discrete Mathematics*, **1999**, 12, 289-297	0.7	215
164	HapCUT: an efficient and accurate algorithm for the haplotype assembly problem. *Bioinformatics*, **2008**, 24, i153-9	7.2	198
163	Exome sequencing can improve diagnosis and alter patient management. *Science Translational Medicine*, **2012**, 4, 138ra78	17.5	191
162	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. *Genome Research*, **2017**, 27, 801-812	9.7	161
161	Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation. *Genome Research*, **2007**, 17, 1362-77	9.7	155
160	Improving gene annotation using peptide mass spectrometry. *Genome Research*, **2007**, 17, 231-9	9.7	144
159	SCOPE: a probabilistic model for scoring tandem mass spectra against a peptide database. *Bioinformatics*, **2001**, 17 Suppl 1, S13-21	7.2	134
158	Circular ecDNA promotes accessible chromatin and high oncogene expression. *Nature*, **2019**, 575, 699-703	50.4	134
157	Proteogenomics to discover the full coding content of genomes: a computational perspective. *Journal of Proteomics*, **2010**, 73, 2124-35	3.9	132
156	Deconvolution and database search of complex tandem mass spectra of intact proteins: a combinatorial approach. *Molecular and Cellular Proteomics*, **2010**, 9, 2772-82	7.6	130
155	iDASH: integrating data for analysis, anonymization, and sharing. *Journal of the American Medical Informatics Association: JAMIA*, **2012**, 19, 196-201	8.6	114
154	Protein identification using top-down. *Molecular and Cellular Proteomics*, **2012**, 11, M111.008524	7.6	112
153	Extrachromosomal oncogene amplification in tumour pathogenesis and evolution. *Nature Reviews Cancer*, **2019**, 19, 283-288	31.3	108
152	Peptide sequence tags for fast database search in mass-spectrometry. *Journal of Proteome Research*, **2005**, 4, 1287-95	5.6	103
151	Haplotyping as perfect phylogeny: a direct approach. *Journal of Computational Biology*, **2003**, 10, 323-40	1.7	91
150	Proteogenomic database construction driven from large scale RNA-seq data. *Journal of Proteome Research*, **2014**, 13, 21-8	5.6	90

149	Whole-genome sequencing uncovers the genetic basis of chronic mountain sickness in Andean highlanders. *American Journal of Human Genetics*, **2013**, 93, 452-62	11	90
148	Comparative proteogenomics: combining mass spectrometry and comparative genomics to analyze multiple genomes. *Genome Research*, **2008**, 18, 1133-42	9.7	90
147	An MCMC algorithm for haplotype assembly from whole-genome sequence data. *Genome Research*, **2008**, 18, 1336-46	9.7	88
146	Experimental selection of hypoxia-tolerant Drosophila melanogaster. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 2349-54	11.5	85
145	Optimal haplotype block-free selection of tagging SNPs for genome-wide association studies. *Genome Research*, **2004**, 14, 1633-40	9.7	84
144	Using Genome Query Language to uncover genetic variation. *Bioinformatics*, **2014**, 30, 1-8	7.2	82
143	NAD metabolic dependency in cancer is shaped by gene amplification and enhancer remodelling. *Nature*, **2019**, 569, 570-575	50.4	81
142	SNPs Problems, Complexity, and Algorithms. *Lecture Notes in Computer Science*, **2001**, 182-193	0.9	80
141	Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers. *Nature Genetics*, **2020**, 52, 891-897	36.3	79
140	Learning natural selection from the site frequency spectrum. *Genetics*, **2013**, 195, 181-93	4	78
139	Deciphering the genetic basis of common diseases by integrated functional annotation of common and rare variants. *Genome Biology*, **2010**, 11,	18.3	78
138	A Polynomial-Time Approximation Scheme for Minimum Routing Cost Spanning Trees. *SIAM Journal on Computing*, **2000**, 29, 761-778	1.1	78
137	Expansion of the mycobacterial "PUPylome". *Molecular BioSystems*, **2010**, 6, 376-85		75
136	A covering method for detecting genetic associations between rare variants and common phenotypes. *PLoS Computational Biology*, **2010**, 6, e1000954	5	73
135	QNet: a tool for querying protein interaction networks. *Journal of Computational Biology*, **2008**, 15, 913-25	1.7	71
134	An automated proteogenomic method uses mass spectrometry to reveal novel genes in Zea mays. *Molecular and Cellular Proteomics*, **2014**, 13, 157-67	7.6	69
133	Evaluation of paired-end sequencing strategies for detection of genome rearrangements in cancer. *PLoS Computational Biology*, **2008**, 4, e1000051	5	63
132	Exploring the landscape of focal amplifications in cancer using AmpliconArchitect. *Nature Communications*, **2019**, 10, 392	17.4	59

131	Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. *Genome Biology*, **2014**, 15, R36	18.3	59
130	Inferring gene ontologies from pairwise similarity data. *Bioinformatics*, **2014**, 30, i34-42	7.2	57
129	Compressing genomic sequence fragments using SlimGene. *Journal of Computational Biology*, **2011**, 18, 401-13	1.7	57
128	A Survey of Computational Methods for Determining Haplotypes. *Lecture Notes in Computer Science*, **2004**, 26-47	0.9	55
127	On the Approximability of Numerical Taxonomy (Fitting Distances by Tree Metrics). *SIAM Journal on Computing*, **1998**, 28, 1073-1085	1.1	52
126	Evidence for large inversion polymorphisms in the human genome from HapMap data. *Genome Research*, **2007**, 17, 219-30	9.7	51
125	Robustness of inference of haplotype block structure. *Journal of Computational Biology*, **2003**, 10, 13-9	1.7	51
124	Virmid: accurate detection of somatic mutations with sample impurity inference. *Genome Biology*, **2013**, 14, R90	18.3	50
123	Sensitive gene fusion detection using ambiguously mapping RNA-Seq read pairs. *Bioinformatics*, **2011**, 27, 1068-75	7.2	48
122	Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. *Proteomics*, **2014**, 14, 2719-30	4.8	47
121	Fast and accurate alignment of multiple protein networks. *Journal of Computational Biology*, **2009**, 16, 989-99	1.7	47
120	Accurate annotation of peptide modifications through unrestrictive database search. *Journal of Proteome Research*, **2008**, 7, 170-81	5.6	47
119	Phosphorylation-specific MS/MS scoring for rapid and accurate phosphoproteome analysis. *Journal of Proteome Research*, **2008**, 7, 3373-81	5.6	45
118	Nonoverlapping local alignments (weighted independent sets of axis-parallel rectangles). *Discrete Applied Mathematics*, **1996**, 71, 41-53	1	45
117	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	4.5	44
116	Shotgun protein sequencing by tandem mass spectra assembly. *Analytical Chemistry*, **2004**, 76, 7221-33	7.8	44
115	High-altitude adaptation in humans: from genomics to integrative physiology. *Journal of Molecular Medicine*, **2017**, 95, 1269-1282	5.5	43
114	Annotation of the zebrafish genome through an integrated transcriptomic and proteomic analysis. *Molecular and Cellular Proteomics*, **2014**, 13, 3184-98	7.6	40

113	Template proteogenomics: sequencing whole proteins using an imperfect database. *Molecular and Cellular Proteomics*, **2010**, 9, 1260-70	7.6	40
112	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, 5546-51	11.5	39
111	Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem. *Lecture Notes in Computer Science*, **2002**, 29-43	0.9	38
110	Skmer: assembly-free and alignment-free sample identification using genome skims. *Genome Biology*, **2019**, 20, 34	18.3	37
109	Searching genomes for noncoding RNA using FastR. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2005**, 2, 366-79	3	37
108	A decomposition theory for phylogenetic networks and incompatible characters. *Journal of Computational Biology*, **2007**, 14, 1247-72	1.7	36
107	Polynomial and APX-hard cases of the individual haplotyping problem. *Theoretical Computer Science* , **2005**, 335, 109-125	1.1	36
106	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, 10425-30	11.5	35
105	Diversity, Productivity, and Stability of an Industrial Microbial Ecosystem. *Applied and Environmental Microbiology*, **2016**, 82, 2494-2505	4.8	34
104	Identifying the favored mutation in a positive selective sweep. *Nature Methods*, **2018**, 15, 279-282	21.6	33
103	Haplotypes and informative SNP selection algorithms **2003**,		33
102	Unrestrictive identification of post-translational modifications through peptide mass spectrometry. *Nature Protocols*, **2006**, 1, 67-72	18.8	32
101	Orthologous repeats and mammalian phylogenetic inference. *Genome Research*, **2005**, 15, 998-1006	9.7	32
100	Accurate mass spectrometry based protein quantification via shared peptides. *Journal of Computational Biology*, **2012**, 19, 337-48	1.7	31
99	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	3	31
98	The elusive evidence for chromothripsis. *Nucleic Acids Research*, **2014**, 42, 8231-42	20.1	30
97	Computing similarity between RNA strings. *Lecture Notes in Computer Science*, **1995**, 1-16	0.9	30
96	Approximation algorithms for multiple sequence alignment. *Theoretical Computer Science*, **1997**, 182, 233-244	1.1	29

95	Automated querying and identification of novel peptides using MALDI mass spectrometric imaging. *Journal of Proteome Research*, **2011**, 10, 1915-28	5.6	28
94	RAPID detection of gene-gene interactions in genome-wide association studies. *Bioinformatics*, **2010**, 26, 2856-62	7.2	28
93	Fast and Accurate Alignment of Multiple Protein Networks **2008**, 246-256		28
92	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	11.5	27
91	Wessim: a whole-exome sequencing simulator based on in silico exome capture. *Bioinformatics*, **2013**, 29, 1076-7	7.2	26
90	QNet: A Tool for Querying Protein Interaction Networks. *Lecture Notes in Computer Science*, **2007**, 1-15	0.9	26
89	Targeted genotyping of variable number tandem repeats with adVNTR. *Genome Research*, **2018**, 28, 1709-1719	9.7	26
88	Resurrection of a clinical antibody: template proteogenomic de novo proteomic sequencing and reverse engineering of an anti-lymphotoxin- antibody. *Proteomics*, **2011**, 11, 395-405	4.8	25
87	A note on efficient computation of haplotypes via perfect phylogeny. *Journal of Computational Biology*, **2004**, 11, 858-66	1.7	25
86	Protein-protein interaction network evaluation for identifying potential drug targets. *Journal of Computational Biology*, **2010**, 17, 669-84	1.7	24
85	Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. *Nature Communications*, **2020**, 11, 550	17.4	23
84	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	20.1	23
83	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	18.3	23
82	A sequence-based filtering method for ncRNA identification and its application to searching for riboswitch elements. *Bioinformatics*, **2006**, 22, e557-65	7.2	23
81	Consensus folding of unaligned RNA sequences revisited. *Journal of Computational Biology*, **2006**, 13, 283-95	1.7	23
80	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	0.9	23
79	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. *Journal of Proteome Research*, **2015**, 14, 3555-67	5.6	22
78	Next-Generation Sequencing of Plasmodium vivax Patient Samples Shows Evidence of Direct Evolution in Drug-Resistance Genes. *ACS Infectious Diseases*, **2015**, 1, 367-79	5.5	22

77	Senp1 drives hypoxia-induced polycythemia via GATA1 and Bcl-xL in subjects with Monge's disease. *Journal of Experimental Medicine*, **2016**, 213, 2729-2744	16.6	22
76	AMASS: algorithm for MSI analysis by semi-supervised segmentation. *Journal of Proteome Research*, **2011**, 10, 4734-43	5.6	22
75	The genetic basis of chronic mountain sickness. *Physiology*, **2014**, 29, 403-12	9.8	21
74	Constant ratio approximations of the weighted feedback vertex set problem for undirected graphs. *Lecture Notes in Computer Science*, **1995**, 142-151	0.9	21
73	Cerulean: A Hybrid Assembly Using High Throughput Short and Long Reads. *Lecture Notes in Computer Science*, **2013**, 349-363	0.9	21
72	Designing deep sequencing experiments: detecting structural variation and estimating transcript abundance. *BMC Genomics*, **2010**, 11, 385	4.5	20
71	The TGFβ1 Promoter SNP C-509T and Food Sensitization Promote Esophageal Remodeling in Pediatric Eosinophilic Esophagitis. *PLoS ONE*, **2015**, 10, e0144651	3.7	20
70	New Insights into the Genetic Basis of Monge's Disease and Adaptation to High-Altitude. *Molecular Biology and Evolution*, **2017**, 34, 3154-3168	8.3	19
69	Structural alignment of pseudoknotted RNA. *Journal of Computational Biology*, **2008**, 15, 489-504	1.7	18
68	ecDNA hubs drive cooperative intermolecular oncogene expression. *Nature*, **2021**,	50.4	18
67	ProteoStorm: An Ultrafast Metaproteomics Database Search Framework. *Cell Systems*, **2018**, 7, 463-467.e6	6.6	18
66	Clear: Composition of Likelihoods for Evolve and Resequence Experiments. *Genetics*, **2017**, 206, 1011-1023	4	17
65	MHC class I loaded ligands from breast cancer cell lines: A potential HLA-I-typed antigen collection. *Journal of Proteomics*, **2018**, 176, 13-23	3.9	17
64	On the design of clone-based haplotyping. *Genome Biology*, **2013**, 14, R100	18.3	17
63	Optimization of primer design for the detection of variable genomic lesions in cancer. *Bioinformatics*, **2007**, 23, 2807-15	7.2	16
62	Genetic simulation tools for post-genome wide association studies of complex diseases. *Genetic Epidemiology*, **2015**, 39, 11-19	2.6	15
61	Amplification and thrifty single-molecule sequencing of recurrent somatic structural variations. *Genome Research*, **2014**, 24, 318-28	9.7	15
60	Strobe sequence design for haplotype assembly. *BMC Bioinformatics*, **2011**, 12 Suppl 1, S24	3.6	15

59	Practical 4Sphosphopantetheine active site discovery from proteomic samples. *Journal of Proteome Research*, **2011**, 10, 320-9	5.6	14
58	Combinatorics of the breakage-fusion-bridge mechanism. *Journal of Computational Biology*, **2012**, 19, 662-78	1.7	14
57	AmpliconReconstructor integrates NGS and optical mapping to resolve the complex structures of focal amplifications. *Nature Communications*, **2020**, 11, 4374	17.4	14
56	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. *PLoS Genetics*, **2015**, 11, e1005527	6	13
55	Identification of post-translational modifications via blind search of mass-spectra **2005**, 157-66		13
54	Inference about recombination from haplotype data: lower bounds and recombination hotspots. *Journal of Computational Biology*, **2006**, 13, 501-21	1.7	13
53	FastR: fast database search tool for non-coding RNA **2004**, 52-61		13
52	Proteogenomic Annotation of Chinese Hamsters Reveals Extensive Novel Translation Events and Endogenous Retroviral Elements. *Journal of Proteome Research*, **2019**, 18, 2433-2445	5.6	12
51	EcSeg: Semantic Segmentation of Metaphase Images Containing Extrachromosomal DNA. *IScience*, **2019**, 21, 428-435	6.1	12
50	TCLUST: a fast method for clustering genome-scale expression data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2011**, 8, 808-18	3	12
49	Detecting non-adjoining correlations with signals in DNA **1998**,		12
48	Combinatorial Problems Arising in SNP and Haplotype Analysis. *Lecture Notes in Computer Science*, **2003**, 26-47	0.9	11
47	Speeding up tandem mass spectral identification using indexes. *Bioinformatics*, **2012**, 28, 1692-7	7.2	10
46	Ligand-receptor pairing via tree comparison. *Journal of Computational Biology*, **2000**, 7, 59-70	1.7	10
45	Variable number tandem repeats mediate the expression of proximal genes. *Nature Communications*, **2021**, 12, 2075	17.4	10
44	Abstractions for Genomics. *Communications of the ACM*, **2013**, 56, 83-93	2.5	9
43	Extrachromosomal DNA (ecDNA) in cancer pathogenesis. *Current Opinion in Genetics and Development*, **2021**, 66, 78-82	4.9	9
42	Reconstructing breakage fusion bridge architectures using noisy copy numbers. *Journal of Computational Biology*, **2015**, 22, 577-94	1.7	7

41	Improved Recombination Lower Bounds for Haplotype Data. *Lecture Notes in Computer Science*, **2005**, 569-584	0.9	7
40	Compressing Genomic Sequence Fragments Using SlimGene. *Lecture Notes in Computer Science*, **2010**, 310-324	0.9	7
39	Novel insight into the genetic basis of high-altitude pulmonary hypertension in Kyrgyz highlanders. *European Journal of Human Genetics*, **2019**, 27, 150-159	5.3	7
38	The impact of contaminants on the accuracy of genome skimming and the effectiveness of exclusion read filters. *Molecular Ecology Resources*, **2020**, 20, 649	8.4	6
37	Reprever: resolving low-copy duplicated sequences using template driven assembly. *Nucleic Acids Research*, **2013**, 41, e128	20.1	5
36	On the Approximability of Reachability-Preserving Network Orientations. *Internet Mathematics*, **2011**, 7, 209-232	0	5
35	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA.. *Nature*, **2022**,	50.4	5
34	Extrachromosomal DNA: An Emerging Hallmark in Human Cancer. *Annual Review of Pathology: Mechanisms of Disease*, **2021**,	34	5
33	Optimizing PCR assays for DNA-based cancer diagnostics. *Journal of Computational Biology*, **2010**, 17, 369-81	1.7	4
32	Sample reproducibility of genetic association using different multimarker TDTs in genome-wide association studies: characterization and a new approach. *PLoS ONE*, **2012**, 7, e29613	3.7	4
31	Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. *PLoS Computational Biology*, **2021**, 17, e1009449	5	4
30	Shared Peptides in Mass Spectrometry Based Protein Quantification. *Lecture Notes in Computer Science*, **2009**, 356-371	0.9	4
29	Fine-mapping the Favored Mutation in a Positive Selective Sweep		4
28	FaNDOM: Fast nested distance-based seeding of optical maps. *Patterns*, **2021**, 2, 100248	5.1	4
27	Principles of ecDNA random inheritance drive rapid genome change and therapy resistance in human cancers		4
26	The Antibody Repertoire of Colorectal Cancer. *Molecular and Cellular Proteomics*, **2017**, 16, 2111-2124	7.6	3
25	Tests of selection in pooled case-control data: an empirical study. *Frontiers in Genetics*, **2011**, 2, 83	4.5	3
24	EcDNA hubs drive cooperative intermolecular oncogene expression		3

23	Multiple mechanisms drive genomic adaptation to extreme O levels in Drosophila melanogaster. *Nature Communications*, **2021**, 12, 997	17.4	3
22	Extrachromosomal DNA in HPV-Mediated Oropharyngeal Cancer Drives Diverse Oncogene Transcription. *Clinical Cancer Research*, **2021**,	12.9	3
21	Computing the Statistical Significance of Overlap between Genome Annotations with iStat. *Cell Systems*, **2019**, 8, 523-529.e4	10.6	2
20	Structural Alignment of Pseudoknotted RNA. *Lecture Notes in Computer Science*, **2006**, 143-158	0.9	2
19	Variable Number Tandem Repeats mediate the expression of proximal genes		2
18	CONSULT: accurate contamination removal using locality-sensitive hashing. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab071	3.7	2
17	Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT		2
16	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	0.9	1
15	Evaluating genome architecture of a complex region via generalized bipartite matching. *BMC Bioinformatics*, **2013**, 14 Suppl 5, S13	3.6	1
14	Sorting by Reversals: Genome Rearrangements in Plant Organelles and Evolutionary History of X Chromosome. *Molecular Biology and Evolution*, **1995**,	8.3	1
13	Optical genome mapping identifies rare structural variations as predisposition factors associated with severe COVID-19.. *IScience*, **2022**, 103760	6.1	1
12	Targeted profiling of human extrachromosomal DNA by CRISPR-CATCH		1
11	Frequent extrachromosomal oncogene amplification drives aggressive tumors		1
10	AmpliconReconstructor: Integrated analysis of NGS and optical mapping resolves the complex structures of focal amplifications in cancer		1
9	Reconstructing Breakage Fusion Bridge Architectures Using Noisy Copy Numbers. *Lecture Notes in Computer Science*, **2014**, 400-417	0.9	1
8	Assembly-free and alignment-free sample identification using genome skims		1
7	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. *Nucleic Acids Research*, **2016**, 44, e111	20.1	1
6	Plasticity of extrachromosomal and intrachromosomal BRAF amplifications in overcoming targeted therapy dosage challenges.. *Cancer Discovery*, **2021**,	24.4	1

5	Learning Natural Selection from the Site Frequency Spectrum. *Lecture Notes in Computer Science*, **2013**, 230-233	0.9	0
4	Parallel implementation of logic languages. *Lecture Notes in Computer Science*, **1990**, 154-165	0.9	
3	Optimizing PCR Assays for DNA Based Cancer Diagnostics. *Lecture Notes in Computer Science*, **2009**, 220-235	2.9	
2	Uncertainty Quantification Using Subsampling for Assembly-Free Estimates of Genomic Distance and Phylogenetic Relationships. *Lecture Notes in Computer Science*, **2022**, 366-368	0.9	
1	FastViFi: Fast and accurate detection of (Hybrid) Viral DNA and RNA.. *NAR Genomics and Bioinformatics*, **2022**, 4, lqac032	3.7	