Paul Medvedev

List of Publications by Year
in descending order

46 papers	3,910 citations	394421 19 h-index	233421 45 g-index
57 all docs	57 docs citations	57 times ranked	5617 citing authors

#	Article	IF	Citations
1	The Statistics ofk-mers from a Sequence Undergoing a Simple Mutation Process Without Spurious Matches. Journal of Computational Biology, 2022, 29, 155-168.	1.6	17
2	Markov chains improve the significance computation of overlapping genome annotations. Bioinformatics, 2022, 38, i203-i211.	4.1	0
3	The minimizer Jaccard estimator is biased and inconsistent. Bioinformatics, 2022, 38, i169-i176.	4.1	12
4	kmtricks: efficient and flexible construction of Bloom filters for large sequencing data collections. Bioinformatics Advances, 2022, 2, .	2.4	19
5	Data structures based on k-mers for querying large collections of sequencing data sets. Genome Research, 2021, 31, 1-12.	5.5	67
6	Error correction enables use of Oxford Nanopore technology for reference-free transcriptome analysis. Nature Communications, 2021, 12, 2.	12.8	94
7	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
8	What do Eulerian and Hamiltonian cycles have to do with genome assembly?. PLoS Computational Biology, 2021, 17, e1008928.	3.2	7
9	Disk compression of k-mer sets. Algorithms for Molecular Biology, 2021, 16, 10.	1.2	8
10	Recombination Marks the Evolutionary Dynamics of a Recently Endogenized Retrovirus. Molecular Biology and Evolution, 2021, 38, 5423-5436.	8.9	2
11	Improved representation of sequence bloom trees. Bioinformatics, 2020, 36, 721-727.	4.1	36
12	Dynamic evolution of great ape Y chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26273-26280.	7.1	22
13	Scalable Pairwise Whole-Genome Homology Mapping of Long Genomes with BubbZ. IScience, 2020, 23, 101224.	4.1	11
14	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. Nature Communications, 2020, 11, 6327.	12.8	39
15	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. Genome Biology and Evolution, 2020, 12, 842-859.	2.5	13
16	De Novo Clustering of Long-Read Transcriptome Data Using a Greedy, Quality Value-Based Algorithm. Journal of Computational Biology, 2020, 27, 472-484.	1.6	55
17	Ten Simple Rules for writing algorithmic bioinformatics conference papers. PLoS Computational Biology, 2020, 16, e1007742.	3.2	0
18	Representation of $$k$$-mer Sets Using Spectrum-Preserving String Sets. Lecture Notes in Computer Science, 2020, , 152-168.	1.3	12

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19	Toward fast and accurate SNP genotyping from whole genome sequencing data for bedside diagnostics. Bioinformatics, 2019, 35, 415-420.	4.1	24
20	DiscoverY: a classifier for identifying Y chromosome sequences in male assemblies. BMC Genomics, 2019, 20, 641.	2.8	16
21	Dosage regulation, and variation in gene expression and copy number ofÂhuman Y chromosome ampliconic genes. PLoS Genetics, 2019, 15, e1008369.	3.5	19
22	De Novo Clustering of Long-Read Transcriptome Data Using a Greedy, Quality-Value Based Algorithm. Lecture Notes in Computer Science, 2019, , 227-242.	1.3	11
23	Modeling biological problems in computer science: a case study in genome assembly. Briefings in Bioinformatics, 2019, 20, 1376-1383.	6.5	11
24	AllSome Sequence Bloom Trees. Journal of Computational Biology, 2018, 25, 467-479.	1.6	25
25	RecoverY: k-mer-based read classification for Y-chromosome-specific sequencing and assembly. Bioinformatics, 2018, 34, 1125-1131.	4.1	15
26	Deciphering highly similar multigene family transcripts from Iso-Seq data with IsoCon. Nature Communications, 2018, 9, 4601.	12.8	54
27	Correcting palindromes in long reads after whole-genome amplification. BMC Genomics, 2018, 19, 798.	2.8	16
28	VarMatch: robust matching of small variant datasets using flexible scoring schemes. Bioinformatics, 2017, 33, 1301-1308.	4.1	15
29	TwoPaCo: an efficient algorithm to build the compacted de Bruijn graph from many complete genomes. Bioinformatics, 2017, 33, 4024-4032.	4.1	64
30	Y and W Chromosome Assemblies: Approaches and Discoveries. Trends in Genetics, 2017, 33, 266-282.	6.7	95
31	Safe and Complete Contig Assembly Through Omnitigs. Journal of Computational Biology, 2017, 24, 590-602.	1.6	20
32	Compacting de Bruijn graphs from sequencing data quickly and in low memory. Bioinformatics, 2016, 32, i201-i208.	4.1	170
33	A time- and cost-effective strategy to sequence mammalian Y Chromosomes: an application to the de novo assembly of gorilla Y. Genome Research, 2016, 26, 530-540.	5.5	99
34	Giraffe genome sequence reveals clues to its unique morphology and physiology. Nature Communications, 2016, 7, 11519.	12.8	47
35	On the Representation of De Bruijn Graphs. Journal of Computational Biology, 2015, 22, 336-352.	1.6	44
36	Accurate typing of short tandem repeats from genome-wide sequencing data and its applications. Genome Research, 2015, 25, 736-749.	5.5	87

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37	A combinatorial approach to the design of vaccines. Journal of Mathematical Biology, 2015, 70, 1327-1358.	1.9	5
38	Improving the Power of Structural Variation Detection by Augmenting the Reference. PLoS ONE, 2015, 10, e0136771.	2.5	6
39	Informed and automated k-mer size selection for genome assembly. Bioinformatics, 2014, 30, 31-37.	4.1	623
40	Reprever: resolving low-copy duplicated sequences using template driven assembly. Nucleic Acids Research, 2013, 41, e128-e128.	14.5	7
41	Paired de Bruijn Graphs: A Novel Approach for Incorporating Mate Pair Information into Genome Assemblers. Journal of Computational Biology, 2011, 18, 1625-1634.	1.6	60
42	The plane-width of graphs. Journal of Graph Theory, 2011, 68, 229-245.	0.9	2
43	Detecting copy number variation with mated short reads. Genome Research, 2010, 20, 1613-1622.	5.5	150
44	Rearrangement Models and Single-Cut Operations. Journal of Computational Biology, 2010, 17, 1213-1225.	1.6	5
45	Computational methods for discovering structural variation with next-generation sequencing. Nature Methods, 2009, 6, S13-S20.	19.0	473
46	Maximum Likelihood Genome Assembly. Journal of Computational Biology, 2009, 16, 1101-1116.	1.6	87