

# Paul Medvedev

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8685942/publications.pdf>

Version: 2024-02-01

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	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
2	Informed and automated $k$ -mer size selection for genome assembly. <i>Bioinformatics</i> , 2014, 30, 31-37.	4.1	623
3	Computational methods for discovering structural variation with next-generation sequencing. <i>Nature Methods</i> , 2009, 6, S13-S20.	19.0	473
4	Compacting de Bruijn graphs from sequencing data quickly and in low memory. <i>Bioinformatics</i> , 2016, 32, i201-i208.	4.1	170
5	Detecting copy number variation with mated short reads. <i>Genome Research</i> , 2010, 20, 1613-1622.	5.5	150
6	A time- and cost-effective strategy to sequence mammalian Y Chromosomes: an application to the de novo assembly of gorilla Y. <i>Genome Research</i> , 2016, 26, 530-540.	5.5	99
7	Y and W Chromosome Assemblies: Approaches and Discoveries. <i>Trends in Genetics</i> , 2017, 33, 266-282.	6.7	95
8	Error correction enables use of Oxford Nanopore technology for reference-free transcriptome analysis. <i>Nature Communications</i> , 2021, 12, 2.	12.8	94
9	Maximum Likelihood Genome Assembly. <i>Journal of Computational Biology</i> , 2009, 16, 1101-1116.	1.6	87
10	Accurate typing of short tandem repeats from genome-wide sequencing data and its applications. <i>Genome Research</i> , 2015, 25, 736-749.	5.5	87
11	Data structures based on $k$ -mers for querying large collections of sequencing data sets. <i>Genome Research</i> , 2021, 31, 1-12.	5.5	67
12	TwoPaCo: an efficient algorithm to build the compacted de Bruijn graph from many complete genomes. <i>Bioinformatics</i> , 2017, 33, 4024-4032.	4.1	64
13	Paired de Bruijn Graphs: A Novel Approach for Incorporating Mate Pair Information into Genome Assemblers. <i>Journal of Computational Biology</i> , 2011, 18, 1625-1634.	1.6	60
14	De Novo Clustering of Long-Read Transcriptome Data Using a Greedy, Quality Value-Based Algorithm. <i>Journal of Computational Biology</i> , 2020, 27, 472-484.	1.6	55
15	Deciphering highly similar multigene family transcripts from Iso-Seq data with IsoCon. <i>Nature Communications</i> , 2018, 9, 4601.	12.8	54
16	Giraffe genome sequence reveals clues to its unique morphology and physiology. <i>Nature Communications</i> , 2016, 7, 11519.	12.8	47
17	On the Representation of De Bruijn Graphs. <i>Journal of Computational Biology</i> , 2015, 22, 336-352.	1.6	44
18	Scalable multiple whole-genome alignment and locally collinear block construction with SibeliaZ. <i>Nature Communications</i> , 2020, 11, 6327.	12.8	39

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19	Improved representation of sequence bloom trees. <i>Bioinformatics</i> , 2020, 36, 721-727.	4.1	36
20	AllSome Sequence Bloom Trees. <i>Journal of Computational Biology</i> , 2018, 25, 467-479.	1.6	25
21	Toward fast and accurate SNP genotyping from whole genome sequencing data for bedside diagnostics. <i>Bioinformatics</i> , 2019, 35, 415-420.	4.1	24
22	Dynamic evolution of great ape Y chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26273-26280.	7.1	22
23	Safe and Complete Contig Assembly Through Omnitigs. <i>Journal of Computational Biology</i> , 2017, 24, 590-602.	1.6	20
24	Dosage regulation, and variation in gene expression and copy number of human Y chromosome ampliconic genes. <i>PLoS Genetics</i> , 2019, 15, e1008369.	3.5	19
25	kmtricks: efficient and flexible construction of Bloom filters for large sequencing data collections. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	19
26	The Statistics of $k$ -mers from a Sequence Undergoing a Simple Mutation Process Without Spurious Matches. <i>Journal of Computational Biology</i> , 2022, 29, 155-168.	1.6	17
27	Correcting palindromes in long reads after whole-genome amplification. <i>BMC Genomics</i> , 2018, 19, 798.	2.8	16
28	DiscoverY: a classifier for identifying Y chromosome sequences in male assemblies. <i>BMC Genomics</i> , 2019, 20, 641.	2.8	16
29	VarMatch: robust matching of small variant datasets using flexible scoring schemes. <i>Bioinformatics</i> , 2017, 33, 1301-1308.	4.1	15
30	RecoverY: $k$ -mer-based read classification for Y-chromosome-specific sequencing and assembly. <i>Bioinformatics</i> , 2018, 34, 1125-1131.	4.1	15
31	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. <i>Genome Biology and Evolution</i> , 2020, 12, 842-859.	2.5	13
32	Representation of $k$ -mer Sets Using Spectrum-Preserving String Sets. <i>Lecture Notes in Computer Science</i> , 2020, , 152-168.	1.3	12
33	The minimizer Jaccard estimator is biased and inconsistent. <i>Bioinformatics</i> , 2022, 38, i169-i176.	4.1	12
34	De Novo Clustering of Long-Read Transcriptome Data Using a Greedy, Quality-Value Based Algorithm. <i>Lecture Notes in Computer Science</i> , 2019, , 227-242.	1.3	11
35	Modeling biological problems in computer science: a case study in genome assembly. <i>Briefings in Bioinformatics</i> , 2019, 20, 1376-1383.	6.5	11
36	Scalable Pairwise Whole-Genome Homology Mapping of Long Genomes with BubbZ. <i>IScience</i> , 2020, 23, 101224.	4.1	11

#	ARTICLE	IF	CITATIONS
37	Disk compression of k-mer sets. <i>Algorithms for Molecular Biology</i> , 2021, 16, 10.	1.2	8
38	Reprever: resolving low-copy duplicated sequences using template driven assembly. <i>Nucleic Acids Research</i> , 2013, 41, e128-e128.	14.5	7
39	What do Eulerian and Hamiltonian cycles have to do with genome assembly?. <i>PLoS Computational Biology</i> , 2021, 17, e1008928.	3.2	7
40	Improving the Power of Structural Variation Detection by Augmenting the Reference. <i>PLoS ONE</i> , 2015, 10, e0136771.	2.5	6
41	Rearrangement Models and Single-Cut Operations. <i>Journal of Computational Biology</i> , 2010, 17, 1213-1225.	1.6	5
42	A combinatorial approach to the design of vaccines. <i>Journal of Mathematical Biology</i> , 2015, 70, 1327-1358.	1.9	5
43	The plane-width of graphs. <i>Journal of Graph Theory</i> , 2011, 68, 229-245.	0.9	2
44	Recombination Marks the Evolutionary Dynamics of a Recently Endogenized Retrovirus. <i>Molecular Biology and Evolution</i> , 2021, 38, 5423-5436.	8.9	2
45	Ten Simple Rules for writing algorithmic bioinformatics conference papers. <i>PLoS Computational Biology</i> , 2020, 16, e1007742.	3.2	0
46	Markov chains improve the significance computation of overlapping genome annotations. <i>Bioinformatics</i> , 2022, 38, i203-i211.	4.1	0