Rayan Chikhi

List of Publications by Year
in descending order

31 papers	3,262 citations	331670 21 h-index	477307 29 g-index
43 all docs	43 docs citations	43 times ranked	5069 citing authors

#	Article	IF	Citations
1	Critical Assessment of Metagenome Interpretationâ€"a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
2	Informed and automated <i>k</i>-mer size selection for genome assembly. Bioinformatics, 2014, 30, 31-37.	4.1	623
3	Space-efficient and exact de Bruijn graph representation based on a Bloom filter. Algorithms for Molecular Biology, 2013, 8, 22.	1.2	266
4	DSK: <i>k</i>-mer counting with very low memory usage. Bioinformatics, 2013, 29, 652-653.	4.1	254
5	Petabase-scale sequence alignment catalyses viral discovery. Nature, 2022, 602, 142-147.	27.8	213
6	Compacting de Bruijn graphs from sequencing data quickly and in low memory. Bioinformatics, 2016, 32, i201-i208.	4.1	170
7	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
8	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
9	Reference-free detection of isolated SNPs. Nucleic Acids Research, 2015, 43, e11-e11.	14.5	75
10	GATB: Genome Assembly & Analysis Tool Box. Bioinformatics, 2014, 30, 2959-2961.	4.1	67
11	Data structures based on <i>k</i>-mers for querying large collections of sequencing data sets. Genome Research, 2021, 31, 1-12.	5.5	67
12	On the Representation of de Bruijn Graphs. Lecture Notes in Computer Science, 2014, , 35-55.	1.3	67
13	STRONG: metagenomics strain resolution on assembly graphs. Genome Biology, 2021, 22, 214.	8.8	59
14	Real-time ligand binding pocket database search using local surface descriptors. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2007-2028.	2.6	55
15	Minimizer-space de Bruijn graphs: Whole-genome assembly of long reads in minutes on a personal computer. Cell Systems, 2021, 12, 958-968.e6.	6.2	51
16	MindTheGap: integrated detection and assembly of short and long insertions. Bioinformatics, 2014, 30, 3451-3457.	4.1	50
17	Giraffe genome sequence reveals clues to its unique morphology and physiology. Nature Communications, 2016, 7, 11519.	12.8	47
18	yacrd and fpa: upstream tools for long-read genome assembly. Bioinformatics, 2020, 36, 3894-3896.	4.1	47

#	Article	IF	Citations
19	On the Representation of De Bruijn Graphs. Journal of Computational Biology, 2015, 22, 336-352.	1.6	44
20	REINDEER: efficient indexing of *k*-mer presence and abundance in sequencing datasets. Bioinformatics, 2020, 36, i177-i185.	4.1	40
21	DE-kupl: exhaustive capture of biological variation in RNA-seq data through k-mer decomposition. Genome Biology, 2017, 18, 243.	8.8	33
22	Strainberry: automated strain separation in low-complexity metagenomes using long reads. Nature Communications, 2021, 12, 4485.	12.8	25
23	kmtricks: efficient and flexible construction of Bloom filters for large sequencing data collections. Bioinformatics Advances, 2022, 2, .	2.4	19
24	Sparse Dynamic Programming on DAGs with Small Width. ACM Transactions on Algorithms, 2019, 15, 1-21.	1.0	16
25	Using Minimum Path Cover to Boost Dynamic Programming on DAGs: Co-linear Chaining Extended. Lecture Notes in Computer Science, 2018, , 105-121.	1.3	13
26	Genome Assembly and Analysis of the North American Mountain Goat (*Oreamnos americanus*) Reveals Species-Level Responses to Extreme Environments. G3: Genes, Genomes, Genetics, 2020, 10, 437-442.	1.8	11
27	Disk compression of k-mer sets. Algorithms for Molecular Biology, 2021, 16, 10.	1.2	8
28	Comparative genome analysis using sample-specific string detection in accurate long reads. Bioinformatics Advances, 2021, 1, .	2.4	5
29	On the readability of overlap digraphs. Discrete Applied Mathematics, 2016, 205, 35-44.	0.9	3
30	Bipartite graphs of small readability. Theoretical Computer Science, 2020, 806, 402-415.	0.9	0
31	Human Bone Marrow Mesenchymal Stromal Cell-Derived CXCL12, IL-6 and GDF-15 and Their Capacity to Support IgG-Secreting Cells in Culture Are Divergently Affected by Doxorubicin. Hemato, 2021, 2, 154-166.	0.6	0