

# Rayan Chikhi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7707631/publications.pdf>

Version: 2024-02-01

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	Petabase-scale sequence alignment catalyses viral discovery. <i>Nature</i> , 2022, 602, 142-147.	27.8	213
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
3	kmtricks: efficient and flexible construction of Bloom filters for large sequencing data collections. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	19
4	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
5	Comparative genome analysis using sample-specific string detection in accurate long reads. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	5
6	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. <i>Hemato</i> , 2021, 2, 154-166.	0.6	0
7	Disk compression of $k$ -mer sets. <i>Algorithms for Molecular Biology</i> , 2021, 16, 10.	1.2	8
8	Strainberry: automated strain separation in low-complexity metagenomes using long reads. <i>Nature Communications</i> , 2021, 12, 4485.	12.8	25
9	STRONG: metagenomics strain resolution on assembly graphs. <i>Genome Biology</i> , 2021, 22, 214.	8.8	59
10	Minimizer-space de Bruijn graphs: Whole-genome assembly of long reads in minutes on a personal computer. <i>Cell Systems</i> , 2021, 12, 958-968.e6.	6.2	51
11	Bipartite graphs of small readability. <i>Theoretical Computer Science</i> , 2020, 806, 402-415.	0.9	0
12	REINDEER: efficient indexing of $k$ -mer presence and abundance in sequencing datasets. <i>Bioinformatics</i> , 2020, 36, i177-i185.	4.1	40
13	yacd and fpa: upstream tools for long-read genome assembly. <i>Bioinformatics</i> , 2020, 36, 3894-3896.	4.1	47
14	Genome Assembly and Analysis of the North American Mountain Goat ( <i>Oreamnos americanus</i> ) Reveals Species-Level Responses to Extreme Environments. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 437-442.	1.8	11
15	Sparse Dynamic Programming on DAGs with Small Width. <i>ACM Transactions on Algorithms</i> , 2019, 15, 1-21.	1.0	16
16	Using Minimum Path Cover to Boost Dynamic Programming on DAGs: Co-linear Chaining Extended. <i>Lecture Notes in Computer Science</i> , 2018, , 105-121.	1.3	13
17	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
18	DE-kupl: exhaustive capture of biological variation in RNA-seq data through $k$ -mer decomposition. <i>Genome Biology</i> , 2017, 18, 243.	8.8	33

#	ARTICLE	IF	CITATIONS
19	Compacting de Bruijn graphs from sequencing data quickly and in low memory. <i>Bioinformatics</i> , 2016, 32, i201-i208.	4.1	170
20	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
21	On the readability of overlap digraphs. <i>Discrete Applied Mathematics</i> , 2016, 205, 35-44.	0.9	3
22	Giraffe genome sequence reveals clues to its unique morphology and physiology. <i>Nature Communications</i> , 2016, 7, 11519.	12.8	47
23	Reference-free detection of isolated SNPs. <i>Nucleic Acids Research</i> , 2015, 43, e11-e11.	14.5	75
24	On the Representation of De Bruijn Graphs. <i>Journal of Computational Biology</i> , 2015, 22, 336-352.	1.6	44
25	GATB: Genome Assembly & Analysis Tool Box. <i>Bioinformatics</i> , 2014, 30, 2959-2961.	4.1	67
26	Informed and automated $k$ -mer size selection for genome assembly. <i>Bioinformatics</i> , 2014, 30, 31-37.	4.1	623
27	MindTheGap: integrated detection and assembly of short and long insertions. <i>Bioinformatics</i> , 2014, 30, 3451-3457.	4.1	50
28	On the Representation of de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2014, , 35-55.	1.3	67
29	Space-efficient and exact de Bruijn graph representation based on a Bloom filter. <i>Algorithms for Molecular Biology</i> , 2013, 8, 22.	1.2	266
30	DSK: $k$ -mer counting with very low memory usage. <i>Bioinformatics</i> , 2013, 29, 652-653.	4.1	254
31	Real-time ligand binding pocket database search using local surface descriptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2007-2028.	2.6	55