

Sebastian Deorowicz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6939507/publications.pdf>

Version: 2024-02-01

59
papers

1,957
citations

361413

20
h-index

289244

40
g-index

76
all docs

76
docs citations

76
times ranked

2036
citing authors

#	ARTICLE	IF	CITATIONS
1	KMC 3: counting and manipulating k -mer statistics. <i>Bioinformatics</i> , 2017, 33, 2759-2761.	4.1	407
2	KMC 2: fast and resource-frugal k -mer counting. <i>Bioinformatics</i> , 2015, 31, 1569-1576.	4.1	222
3	Compression of DNA sequence reads in FASTQ format. <i>Bioinformatics</i> , 2011, 27, 860-862.	4.1	136
4	Robust relative compression of genomes with random access. <i>Bioinformatics</i> , 2011, 27, 2979-2986.	4.1	94
5	FAMSA: Fast and accurate multiple sequence alignment of huge protein families. <i>Scientific Reports</i> , 2016, 6, 33964.	3.3	92
6	DSRC – Industry-oriented compression of FASTQ files. <i>Bioinformatics</i> , 2014, 30, 2213-2215.	4.1	84
7	Data compression for sequencing data. <i>Algorithms for Molecular Biology</i> , 2013, 8, 25.	1.2	82
8	Disk-based k -mer counting on a PC. <i>BMC Bioinformatics</i> , 2013, 14, 160.	2.6	61
9	Second step algorithms in the Burrows-Wheeler compression algorithm. <i>Software - Practice and Experience</i> , 2002, 32, 99-111.	3.6	60
10	Disk-based compression of data from genome sequencing. <i>Bioinformatics</i> , 2015, 31, 1389-1395.	4.1	57
11	miRNEST database: an integrative approach in microRNA search and annotation. <i>Nucleic Acids Research</i> , 2012, 40, D198-D204.	14.5	52
12	Genome compression: a novel approach for large collections. <i>Bioinformatics</i> , 2013, 29, 2572-2578.	4.1	48
13	GDC 2: Compression of large collections of genomes. <i>Scientific Reports</i> , 2015, 5, 11565.	3.3	46
14	Revisiting dictionary-based compression. <i>Software - Practice and Experience</i> , 2005, 35, 1455-1476.	3.6	34
15	Indexes of Large Genome Collections on a PC. <i>PLoS ONE</i> , 2014, 9, e109384.	2.5	33
16	Improvements to Burrows-Wheeler compression algorithm. <i>Software - Practice and Experience</i> , 2000, 30, 1465-1483.	3.6	31
17	FaStore: a space-saving solution for raw sequencing data. <i>Bioinformatics</i> , 2018, 34, 2748-2756.	4.1	30
18	CoMeta: Classification of Metagenomes Using k -mers. <i>PLoS ONE</i> , 2015, 10, e0121453.	2.5	28

#	ARTICLE	IF	CITATIONS
19	Kmer-db: instant evolutionary distance estimation. <i>Bioinformatics</i> , 2019, 35, 133-136.	4.1	26
20	Quadratic-time algorithm for a string constrained LCS problem. <i>Information Processing Letters</i> , 2012, 112, 423-426.	0.6	25
21	RECKONER: read error corrector based on KMC. <i>Bioinformatics</i> , 2017, 33, 1086-1089.	4.1	24
22	PHIST: fast and accurate prediction of prokaryotic hosts from metagenomic viral sequences. <i>Bioinformatics</i> , 2022, 38, 1447-1449.	4.1	23
23	GTC: how to maintain huge genotype collections in a compressed form. <i>Bioinformatics</i> , 2018, 34, 1834-1840.	4.1	18
24	How to squeeze a lexicon. <i>Software - Practice and Experience</i> , 2001, 31, 1077-1090.	3.6	17
25	Environmental metagenome classification for constructing a microbiome fingerprint. <i>Biology Direct</i> , 2019, 14, 20.	4.6	16
26	FQsqueezer: k-mer-based compression of sequencing data. <i>Scientific Reports</i> , 2020, 10, 578.	3.3	16
27	Indexing Arbitrary-Length k-Mers in Sequencing Reads. <i>PLoS ONE</i> , 2015, 10, e0133198.	2.5	14
28	GTShark: genotype compression in large projects. <i>Bioinformatics</i> , 2019, 35, 4791-4793.	4.1	14
29	QuickProbs – A Fast Multiple Sequence Alignment Algorithm Designed for Graphics Processors. <i>PLoS ONE</i> , 2014, 9, e88901.	2.5	14
30	Speeding up transposition-invariant string matching. <i>Information Processing Letters</i> , 2006, 100, 14-20.	0.6	12
31	Inter-population Differences in Retrogene Loss and Expression in Humans. <i>PLoS Genetics</i> , 2015, 11, e1005579.	3.5	12
32	An algorithm for solving the longest increasing circular subsequence problem. <i>Information Processing Letters</i> , 2009, 109, 630-634.	0.6	11
33	Efficient Representation of Transition Matrix in the Markov Process Modeling of Computer Networks. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 457-464.	0.2	11
34	Bit-Parallel Algorithm for the Constrained Longest Common Subsequence Problem. <i>Fundamenta Informaticae</i> , 2010, 99, 409-433.	0.4	10
35	QuickProbs 2: Towards rapid construction of high-quality alignments of large protein families. <i>Scientific Reports</i> , 2017, 7, 41553.	3.3	9
36	CoMSA: compression of protein multiple sequence alignment files. <i>Bioinformatics</i> , 2019, 35, 227-234.	4.1	9

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37	Whisper: read sorting allows robust mapping of DNA sequencing data. <i>Bioinformatics</i> , 2019, 35, 2043-2050.	4.1	6
38	Context exhumation after the Burrows-Wheeler transform. <i>Information Processing Letters</i> , 2005, 95, 313-320.	0.6	5
39	Efficient algorithms for the longest common subsequence in k-length substrings. <i>Information Processing Letters</i> , 2014, 114, 634-638.	0.6	5
40	Kalign-LCS – A More Accurate and Faster Variant of Kalign2 Algorithm for the Multiple Sequence Alignment Problem. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 495-502.	0.6	5
41	CoLoRd: compressing long reads. <i>Nature Methods</i> , 2022, 19, 441-444.	19.0	5
42	BIT-PARALLEL ALGORITHMS FOR THE MERGED LONGEST COMMON SUBSEQUENCE PROBLEM. <i>International Journal of Foundations of Computer Science</i> , 2013, 24, 1281-1298.	1.1	4
43	Sorting Data on Ultra-Large Scale with RADULS. <i>Communications in Computer and Information Science</i> , 2017, , 235-245.	0.5	4
44	Even Faster Sorting of (Not Only) Integers. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 481-491.	0.6	4
45	Solving longest common subsequence and related problems on graphical processing units. <i>Software - Practice and Experience</i> , 2010, 40, 673-700.	3.6	3
46	Comment on: ERGC: an efficient referential genome compression algorithm™. <i>Bioinformatics</i> , 2016, 32, 1115-1117.	4.1	3
47	Fast and Simple Circular Pattern Matching. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 537-544.	0.6	3
48	FM-index for Dummies. <i>Communications in Computer and Information Science</i> , 2017, , 189-201.	0.5	3
49	A PARALLEL ALGORITHM FOR THE CONSTRAINED MULTIPLE SEQUENCE ALIGNMENT PROBLEM DESIGNED FOR GPUs. <i>International Journal of Foundations of Computer Science</i> , 2012, 23, 877-901.	1.1	2
50	VCFShark: how to squeeze a VCF file. <i>Bioinformatics</i> , 2021, 37, 3358-3360.	4.1	2
51	Improvements in DNA Reads Correction. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 115-124.	0.6	1
52	DeltaComp: Fast and efficient compression of astronomical timelines. <i>New Astronomy</i> , 2018, 65, 59-66.	1.8	1
53	Whisper 2: Indel-sensitive short read mapping. <i>SoftwareX</i> , 2021, 14, 100692.	2.6	1
54	A Parallel GPU-Designed Algorithm for the Constrained Multiple Sequence Alignment Problem. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 361-368.	0.2	1

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55	Computing the Longest Common Transposition-Invariant Subsequence with GPU. <i>Advances in Intelligent and Soft Computing</i> , 2009, , 551-559.	0.2	1
56	On Two Variants of the Longest Increasing Subsequence Problem. <i>Advances in Intelligent and Soft Computing</i> , 2009, , 541-549.	0.2	1
57	An Effective Way of Storing and Accessing Very Large Transition Matrices Using Multi-core CPU and GPU Architectures. <i>Communications in Computer and Information Science</i> , 2014, , 323-334.	0.5	1
58	Subcubic Algorithms for the Sequence Excluded LCS Problem. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 503-510.	0.6	0
59	An Improved Algorithm for Fast and Accurate Classification of Sequences. <i>Communications in Computer and Information Science</i> , 2014, , 335-344.	0.5	0