

# 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	CoLoRd: compressing long reads. <i>Nature Methods</i> , 2022, 19, 441-444.	19.0	5
2	PHIST: fast and accurate prediction of prokaryotic hosts from metagenomic viral sequences. <i>Bioinformatics</i> , 2022, 38, 1447-1449.	4.1	23
3	VCFShark: how to squeeze a VCF file. <i>Bioinformatics</i> , 2021, 37, 3358-3360.	4.1	2
4	Whisper 2: Indel-sensitive short read mapping. <i>SoftwareX</i> , 2021, 14, 100692.	2.6	1
5	FQsqueezer: k-mer-based compression of sequencing data. <i>Scientific Reports</i> , 2020, 10, 578.	3.3	16
6	Kmer-db: instant evolutionary distance estimation. <i>Bioinformatics</i> , 2019, 35, 133-136.	4.1	26
7	CoMSA: compression of protein multiple sequence alignment files. <i>Bioinformatics</i> , 2019, 35, 227-234.	4.1	9
8	Environmental metagenome classification for constructing a microbiome fingerprint. <i>Biology Direct</i> , 2019, 14, 20.	4.6	16
9	GTShark: genotype compression in large projects. <i>Bioinformatics</i> , 2019, 35, 4791-4793.	4.1	14
10	Whisper: read sorting allows robust mapping of DNA sequencing data. <i>Bioinformatics</i> , 2019, 35, 2043-2050.	4.1	6
11	GTC: how to maintain huge genotype collections in a compressed form. <i>Bioinformatics</i> , 2018, 34, 1834-1840.	4.1	18
12	FaStore: a space-saving solution for raw sequencing data. <i>Bioinformatics</i> , 2018, 34, 2748-2756.	4.1	30
13	Improvements in DNA Reads Correction. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 115-124.	0.6	1
14	DeltaComp: Fast and efficient compression of astronomical timelines. <i>New Astronomy</i> , 2018, 65, 59-66.	1.8	1
15	Even Faster Sorting of (Not Only) Integers. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 481-491.	0.6	4
16	RECKONER: read error corrector based on KMC. <i>Bioinformatics</i> , 2017, 33, 1086-1089.	4.1	24
17	QuickProbs 2: Towards rapid construction of high-quality alignments of large protein families. <i>Scientific Reports</i> , 2017, 7, 41553.	3.3	9
18	KMC 3: counting and manipulating <i>k</i> -mer statistics. <i>Bioinformatics</i> , 2017, 33, 2759-2761.	4.1	407

#	ARTICLE	IF	CITATIONS
19	Sorting Data on Ultra-Large Scale with RADULS. Communications in Computer and Information Science, 2017, , 235-245.	0.5	4
20	FM-index for Dummies. Communications in Computer and Information Science, 2017, , 189-201.	0.5	3
21	FAMSA: Fast and accurate multiple sequence alignment of huge protein families. Scientific Reports, 2016, 6, 33964.	3.3	92
22	Comment on: "ERGC: an efficient referential genome compression algorithm". Bioinformatics, 2016, 32, 1115-1117.	4.1	3
23	CoMeta: Classification of Metagenomes Using k-mers. PLoS ONE, 2015, 10, e0121453.	2.5	28
24	Indexing Arbitrary-Length k-Mers in Sequencing Reads. PLoS ONE, 2015, 10, e0133198.	2.5	14
25	KMC 2: fast and resource-frugal k-mer counting. Bioinformatics, 2015, 31, 1569-1576.	4.1	222
26	GDC 2: Compression of large collections of genomes. Scientific Reports, 2015, 5, 11565.	3.3	46
27	Disk-based compression of data from genome sequencing. Bioinformatics, 2015, 31, 1389-1395.	4.1	57
28	Inter-population Differences in Retrogene Loss and Expression in Humans. PLoS Genetics, 2015, 11, e1005579.	3.5	12
29	Indexes of Large Genome Collections on a PC. PLoS ONE, 2014, 9, e109384.	2.5	33
30	DSRC "Industry-oriented compression of FASTQ files. Bioinformatics, 2014, 30, 2213-2215.	4.1	84
31	Efficient algorithms for the longest common subsequence in k-length substrings. Information Processing Letters, 2014, 114, 634-638.	0.6	5
32	Kalign-LCS "A More Accurate and Faster Variant of Kalign2 Algorithm for the Multiple Sequence Alignment Problem. Advances in Intelligent Systems and Computing, 2014, , 495-502.	0.6	5
33	Fast and Simple Circular Pattern Matching. Advances in Intelligent Systems and Computing, 2014, , 537-544.	0.6	3
34	QuickProbs "A Fast Multiple Sequence Alignment Algorithm Designed for Graphics Processors. PLoS ONE, 2014, 9, e88901.	2.5	14
35	Subcubic Algorithms for the Sequence Excluded LCS Problem. Advances in Intelligent Systems and Computing, 2014, , 503-510.	0.6	0
36	An Effective Way of Storing and Accessing Very Large Transition Matrices Using Multi-core CPU and GPU Architectures. Communications in Computer and Information Science, 2014, , 323-334.	0.5	1

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37	An Improved Algorithm for Fast and Accurate Classification of Sequences. Communications in Computer and Information Science, 2014, , 335-344.	0.5	0
38	Disk-based k-mer counting on a PC. BMC Bioinformatics, 2013, 14, 160.	2.6	61
39	Genome compression: a novel approach for large collections. Bioinformatics, 2013, 29, 2572-2578.	4.1	48
40	BIT-PARALLEL ALGORITHMS FOR THE MERGED LONGEST COMMON SUBSEQUENCE PROBLEM. International Journal of Foundations of Computer Science, 2013, 24, 1281-1298.	1.1	4
41	Data compression for sequencing data. Algorithms for Molecular Biology, 2013, 8, 25.	1.2	82
42	A PARALLEL ALGORITHM FOR THE CONSTRAINED MULTIPLE SEQUENCE ALIGNMENT PROBLEM DESIGNED FOR GPUs. International Journal of Foundations of Computer Science, 2012, 23, 877-901.	1.1	2
43	miRNEST database: an integrative approach in microRNA search and annotation. Nucleic Acids Research, 2012, 40, D198-D204.	14.5	52
44	Quadratic-time algorithm for a string constrained LCS problem. Information Processing Letters, 2012, 112, 423-426.	0.6	25
45	Compression of DNA sequence reads in FASTQ format. Bioinformatics, 2011, 27, 860-862.	4.1	136
46	Robust relative compression of genomes with random access. Bioinformatics, 2011, 27, 2979-2986.	4.1	94
47	A Parallel GPU-Designed Algorithm for the Constrained Multiple Sequence Alignment Problem. Advances in Intelligent and Soft Computing, 2011, , 361-368.	0.2	1
48	Efficient Representation of Transition Matrix in the Markov Process Modeling of Computer Networks. Advances in Intelligent and Soft Computing, 2011, , 457-464.	0.2	11
49	Solving longest common subsequence and related problems on graphical processing units. Software - Practice and Experience, 2010, 40, 673-700.	3.6	3
50	Bit-Parallel Algorithm for the Constrained Longest Common Subsequence Problem. Fundamenta Informaticae, 2010, 99, 409-433.	0.4	10
51	An algorithm for solving the longest increasing circular subsequence problem. Information Processing Letters, 2009, 109, 630-634.	0.6	11
52	Computing the Longest Common Transposition-Invariant Subsequence with GPU. Advances in Intelligent and Soft Computing, 2009, , 551-559.	0.2	1
53	On Two Variants of the Longest Increasing Subsequence Problem. Advances in Intelligent and Soft Computing, 2009, , 541-549.	0.2	1
54	Speeding up transposition-invariant string matching. Information Processing Letters, 2006, 100, 14-20.	0.6	12

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55	Context exhumation after the Burrows-Wheeler transform. Information Processing Letters, 2005, 95, 313-320.	0.6	5
56	Revisiting dictionary-based compression. Software - Practice and Experience, 2005, 35, 1455-1476.	3.6	34
57	Second step algorithms in the Burrows-Wheeler compression algorithm. Software - Practice and Experience, 2002, 32, 99-111.	3.6	60
58	How to squeeze a lexicon. Software - Practice and Experience, 2001, 31, 1077-1090.	3.6	17
59	Improvements to Burrows-Wheeler compression algorithm. Software - Practice and Experience, 2000, 30, 1465-1483.	3.6	31