

# Enno Ohlebusch

## List of Publications by Year in descending order

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41  
papers

1,509  
citations

394421

19  
h-index

315739

38  
g-index

44  
all docs

44  
docs citations

44  
times ranked

1099  
citing authors

#	ARTICLE	IF	CITATIONS
1	Edge minimization in de Bruijn graphs. Information and Computation, 2021, , 104795.	0.7	0
2	Coordinate Systems for Pangenome Graphs based on the Level Function and Minimum Path Covers. , 2021, , .		0
3	An improved encoding of genetic variation in a Burrows-Wheeler transform. Bioinformatics, 2020, 36, 1413-1419.	4.1	6
4	Edge Minimization in de Bruijn Graphs. , 2020, , .		0
5	Dynamic construction of pan-genome subgraphs. Open Computer Science, 2020, 10, 82-96.	1.7	4
6	On the Computation of Longest Previous Non-overlapping Factors. Lecture Notes in Computer Science, 2019, , 372-381.	1.3	0
7	Space-Efficient Parallel Construction of Succinct Representations of Suffix Tree Topologies. Journal of Experimental Algorithmics, 2017, 22, 1-26.	1.0	3
8	A representation of a compressed de Bruijn graph for pan-genome analysis that enables search. Algorithms for Molecular Biology, 2016, 11, 20.	1.2	17
9	Graphical pan-genome analysis with compressed suffix trees and the Burrows-Wheeler transform. Bioinformatics, 2016, 32, 497-504.	4.1	50
10	Efficient Construction of a Compressed de Bruijn Graph for Pan-Genome Analysis. Lecture Notes in Computer Science, 2015, , 40-51.	1.3	11
11	Alphabet-independent algorithms for finding context-sensitive repeats in linear time. Journal of Discrete Algorithms, 2015, 34, 23-36.	0.7	4
12	Alphabet-Independent Algorithms for Finding Context-Sensitive Repeats in Linear Time. Lecture Notes in Computer Science, 2014, , 117-128.	1.3	0
13	Computing the longest common prefix array based on the Burrows-Wheeler transform. Journal of Discrete Algorithms, 2013, 18, 22-31.	0.7	50
14	Compressed suffix trees. Journal of Experimental Algorithmics, 2013, 18, .	1.0	30
15	Space-Efficient Construction of the Burrows-Wheeler Transform. Lecture Notes in Computer Science, 2013, , 5-16.	1.3	18
16	Bidirectional search in a string with wavelet trees and bidirectional matching statistics. Information and Computation, 2012, 213, 13-22.	0.7	31
17	Space-Efficient Computation of Maximal and Supermaximal Repeats in Genome Sequences. Lecture Notes in Computer Science, 2012, , 99-110.	1.3	12
18	Linear Time Algorithms for Generalizations of the Longest Common Substring Problem. Algorithmica, 2011, 60, 806-818.	1.3	27

#	ARTICLE	IF	CITATIONS
19	Lempel-Ziv Factorization Revisited. Lecture Notes in Computer Science, 2011, , 15-26.	1.3	41
20	Efficient algorithms for the all-pairs suffix-prefix problem and the all-pairs substring-prefix problem. Information Processing Letters, 2010, 110, 123-128.	0.6	24
21	CST++. Lecture Notes in Computer Science, 2010, , 322-333.	1.3	25
22	Computing Matching Statistics and Maximal Exact Matches on Compressed Full-Text Indexes. Lecture Notes in Computer Science, 2010, , 347-358.	1.3	36
23	A Compressed Enhanced Suffix Array Supporting Fast String Matching. Lecture Notes in Computer Science, 2009, , 51-62.	1.3	17
24	A space efficient solution to the frequent string mining problem for many databases. Data Mining and Knowledge Discovery, 2008, 17, 24-38.	3.7	12
25	A fast algorithm for the multiple genome rearrangement problem with weighted reversals and transpositions. BMC Bioinformatics, 2008, 9, 516.	2.6	16
26	Space Efficient Computation of Rare Maximal Exact Matches between Multiple Sequences. Journal of Computational Biology, 2008, 15, 357-377.	1.6	12
27	GENESIS: genome evolution scenarios. Bioinformatics, 2008, 24, 711-712.	4.1	5
28	CoCoNUT: an efficient system for the comparison and analysis of genomes. BMC Bioinformatics, 2008, 9, 476.	2.6	23
29	Sorting by Weighted Reversals, Transpositions, and Inverted Transpositions. Journal of Computational Biology, 2007, 14, 615-636.	1.6	32
30	Chaining algorithms for multiple genome comparison. Journal of Discrete Algorithms, 2005, 3, 321-341.	0.7	52
31	Replacing suffix trees with enhanced suffix arrays. Journal of Discrete Algorithms, 2004, 2, 53-86.	0.7	544
32	An applications-focused review of comparative genomics tools: Capabilities, limitations and future challenges. Briefings in Bioinformatics, 2003, 4, 105-123.	6.5	59
33	A Local Chaining Algorithm and Its Applications in Comparative Genomics. Lecture Notes in Computer Science, 2003, , 1-16.	1.3	12
34	Efficient multiple genome alignment. Bioinformatics, 2002, 18, S312-S320.	4.1	125
35	Modular Termination Proofs for Rewriting Using Dependency Pairs. Journal of Symbolic Computation, 2002, 34, 21-58.	0.8	62
36	Hierarchical termination revisited. Information Processing Letters, 2002, 84, 207-214.	0.6	12

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37	Termination of Logic Programs: Transformational Methods Revisited. <i>Applicable Algebra in Engineering, Communications and Computing</i> , 2001, 12, 73-116.	0.5	28
38	TALP: A Tool for the Termination Analysis of Logic Programs. <i>Lecture Notes in Computer Science</i> , 2000, , 270-273.	1.3	13
39	Transforming Conditional Rewrite Systems with Extra Variables into Unconditional Systems. <i>Lecture Notes in Computer Science</i> , 1999, , 111-130.	1.3	8
40	Modular Properties of Composable Term Rewriting Systems. <i>Journal of Symbolic Computation</i> , 1995, 20, 1-41.	0.8	34
41	On the modularity of termination of term rewriting systems. <i>Theoretical Computer Science</i> , 1994, 136, 333-360.	0.9	41