

# Enno Ohlebusch

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11873067/publications.pdf>

Version: 2024-02-01

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	Replacing suffix trees with enhanced suffix arrays. <i>Journal of Discrete Algorithms</i> , 2004, 2, 53-86.	0.7	544
2	Efficient multiple genome alignment. <i>Bioinformatics</i> , 2002, 18, S312-S320.	4.1	125
3	Modular Termination Proofs for Rewriting Using Dependency Pairs. <i>Journal of Symbolic Computation</i> , 2002, 34, 21-58.	0.8	62
4	An applications-focused review of comparative genomics tools: Capabilities, limitations and future challenges. <i>Briefings in Bioinformatics</i> , 2003, 4, 105-123.	6.5	59
5	Chaining algorithms for multiple genome comparison. <i>Journal of Discrete Algorithms</i> , 2005, 3, 321-341.	0.7	52
6	Computing the longest common prefix array based on the Burrows-Wheeler transform. <i>Journal of Discrete Algorithms</i> , 2013, 18, 22-31.	0.7	50
7	Graphical pan-genome analysis with compressed suffix trees and the Burrows-Wheeler transform. <i>Bioinformatics</i> , 2016, 32, 497-504.	4.1	50
8	On the modularity of termination of term rewriting systems. <i>Theoretical Computer Science</i> , 1994, 136, 333-360.	0.9	41
9	Lempel-Ziv Factorization Revisited. <i>Lecture Notes in Computer Science</i> , 2011, , 15-26.	1.3	41
10	Computing Matching Statistics and Maximal Exact Matches on Compressed Full-Text Indexes. <i>Lecture Notes in Computer Science</i> , 2010, , 347-358.	1.3	36
11	Modular Properties of Composable Term Rewriting Systems. <i>Journal of Symbolic Computation</i> , 1995, 20, 1-41.	0.8	34
12	Sorting by Weighted Reversals, Transpositions, and Inverted Transpositions. <i>Journal of Computational Biology</i> , 2007, 14, 615-636.	1.6	32
13	Bidirectional search in a string with wavelet trees and bidirectional matching statistics. <i>Information and Computation</i> , 2012, 213, 13-22.	0.7	31
14	Compressed suffix trees. <i>Journal of Experimental Algorithmics</i> , 2013, 18, .	1.0	30
15	Termination of Logic Programs: Transformational Methods Revisited. <i>Applicable Algebra in Engineering, Communications and Computing</i> , 2001, 12, 73-116.	0.5	28
16	Linear Time Algorithms for Generalizations of the Longest Common Substring Problem. <i>Algorithmica</i> , 2011, 60, 806-818.	1.3	27
17	CST++. <i>Lecture Notes in Computer Science</i> , 2010, , 322-333.	1.3	25
18	Efficient algorithms for the all-pairs suffix-prefix problem and the all-pairs substring-prefix problem. <i>Information Processing Letters</i> , 2010, 110, 123-128.	0.6	24

#	ARTICLE	IF	CITATIONS
19	CoCoNUT: an efficient system for the comparison and analysis of genomes. BMC Bioinformatics, 2008, 9, 476.	2.6	23
20	Space-Efficient Construction of the Burrows-Wheeler Transform. Lecture Notes in Computer Science, 2013, , 5-16.	1.3	18
21	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
22	A Compressed Enhanced Suffix Array Supporting Fast String Matching. Lecture Notes in Computer Science, 2009, , 51-62.	1.3	17
23	A fast algorithm for the multiple genome rearrangement problem with weighted reversals and transpositions. BMC Bioinformatics, 2008, 9, 516.	2.6	16
24	TALP: A Tool for the Termination Analysis of Logic Programs. Lecture Notes in Computer Science, 2000, , 270-273.	1.3	13
25	Hierarchical termination revisited. Information Processing Letters, 2002, 84, 207-214.	0.6	12
26	A Local Chaining Algorithm and Its Applications in Comparative Genomics. Lecture Notes in Computer Science, 2003, , 1-16.	1.3	12
27	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
28	Space Efficient Computation of Rare Maximal Exact Matches between Multiple Sequences. Journal of Computational Biology, 2008, 15, 357-377.	1.6	12
29	Space-Efficient Computation of Maximal and Supermaximal Repeats in Genome Sequences. Lecture Notes in Computer Science, 2012, , 99-110.	1.3	12
30	Efficient Construction of a Compressed de Bruijn Graph for Pan-Genome Analysis. Lecture Notes in Computer Science, 2015, , 40-51.	1.3	11
31	Transforming Conditional Rewrite Systems with Extra Variables into Unconditional Systems. Lecture Notes in Computer Science, 1999, , 111-130.	1.3	8
32	An improved encoding of genetic variation in a Burrows-Wheeler transform. Bioinformatics, 2020, 36, 1413-1419.	4.1	6
33	GENESIS: genome evolution scenarios. Bioinformatics, 2008, 24, 711-712.	4.1	5
34	Alphabet-independent algorithms for finding context-sensitive repeats in linear time. Journal of Discrete Algorithms, 2015, 34, 23-36.	0.7	4
35	Dynamic construction of pan-genome subgraphs. Open Computer Science, 2020, 10, 82-96.	1.7	4
36	Space-Efficient Parallel Construction of Succinct Representations of Suffix Tree Topologies. Journal of Experimental Algorithmics, 2017, 22, 1-26.	1.0	3

#	ARTICLE	IF	CITATIONS
37	Edge Minimization in de Bruijn Graphs. , 2020, , .		0
38	Edge minimization in de Bruijn graphs. Information and Computation, 2021, , 104795.	0.7	0
39	Coordinate Systems for Pangenome Graphs based on the Level Function and Minimum Path Covers. , 2021, , .		0
40	Alphabet-Independent Algorithms for Finding Context-Sensitive Repeats in Linear Time. Lecture Notes in Computer Science, 2014, , 117-128.	1.3	0
41	On the Computation of Longest Previous Non-overlapping Factors. Lecture Notes in Computer Science, 2019, , 372-381.	1.3	0