

Veli Antti Tapani MÄäkinen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9314104/publications.pdf>

Version: 2024-02-01

42
papers

1,777
citations

686830

13
h-index

315357

38
g-index

47
all docs

47
docs citations

47
times ranked

1787
citing authors

#	ARTICLE	IF	CITATIONS
1	Compressed full-text indexes. ACM Computing Surveys, 2007, 39, 2.	16.1	545
2	Indexing Graphs for Path Queries with Applications in Genome Research. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 375-388.	1.9	237
3	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737.	5.8	196
4	Storage and Retrieval of Highly Repetitive Sequence Collections. Journal of Computational Biology, 2010, 17, 281-308.	0.8	160
5	Bit-parallel sequence-to-graph alignment. Bioinformatics, 2019, 35, 3599-3607.	1.8	50
6	Space-Efficient Algorithms for Document Retrieval. Lecture Notes in Computer Science, 2007, , 205-215.	1.0	45
7	SNV-PPILP: refined SNV calling for tumor data using perfect phylogenies and ILP. Bioinformatics, 2015, 31, 1133-1135.	1.8	42
8	Versatile Succinct Representations of the Bidirectional Burrows-Wheeler Transform. Lecture Notes in Computer Science, 2013, , 133-144.	1.0	30
9	Towards pan-genome read alignment to improve variation calling. BMC Genomics, 2018, 19, 87.	1.2	29
10	Accurate spliced alignment of long RNA sequencing reads. Bioinformatics, 2021, 37, 4643-4651.	1.8	28
11	Discovery of potential causative mutations in human coding and noncoding genome with the interactive software BasePlayer. Nature Protocols, 2018, 13, 2580-2600.	5.5	27
12	On the complexity of Minimum Path Cover with Subpath Constraints for multi-assembly. BMC Bioinformatics, 2014, 15, S5.	1.2	23
13	Normalized N50 assembly metric using gap-restricted co-linear chaining. BMC Bioinformatics, 2012, 13, 255.	1.2	17
14	Gap Filling as Exact Path Length Problem. Journal of Computational Biology, 2016, 23, 347-361.	0.8	17
15	Bacterial genomic epidemiology with mixed samples. Microbial Genomics, 2021, 7, .	1.0	17
16	Space Efficient String Mining under Frequency Constraints. , 2008, , .		16
17	Repeat- and error-aware comparison of deletions. Bioinformatics, 2015, 31, 2947-2954.	1.8	16
18	Sparse Dynamic Programming on DAGs with Small Width. ACM Transactions on Algorithms, 2019, 15, 1-21.	0.9	16

#	ARTICLE	IF	CITATIONS
19	Fast in-memory XPath search using compressed indexes. <i>Software - Practice and Experience</i> , 2015, 45, 399-434.	2.5	15
20	Using Minimum Path Cover to Boost Dynamic Programming on DAGs: Co-linear Chaining Extended. <i>Lecture Notes in Computer Science</i> , 2018, , 105-121.	1.0	13
21	MIPUP: minimum perfect unmixed phylogenies for multi-sampled tumors via branchings and ILP. <i>Bioinformatics</i> , 2019, 35, 769-777.	1.8	12
22	Graphs Cannot Be Indexed in Polynomial Time for Sub-quadratic Time String Matching, Unless SETH Fails. <i>Lecture Notes in Computer Science</i> , 2021, , 608-622.	1.0	12
23	Evaluating approaches to find exon chains based on long reads. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw137.	3.2	11
24	Explaining a Weighted DAG with Few Paths for Solving Genome-Guided Multi-Assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1345-1354.	1.9	10
25	FLEXIBLE MUSIC RETRIEVAL IN SUBLINEAR TIME. <i>International Journal of Foundations of Computer Science</i> , 2006, 17, 1345-1364.	0.8	9
26	Filtering methods for content-based retrieval on indexed symbolic music databases. <i>Information Retrieval</i> , 2010, 13, 1-21.	1.6	9
27	A framework for space-efficient read clustering in metagenomic samples. <i>BMC Bioinformatics</i> , 2017, 18, 59.	1.2	9
28	Linear time minimum segmentation enables scalable founder reconstruction. <i>Algorithms for Molecular Biology</i> , 2019, 14, 12.	0.3	9
29	The Cycle Switching Graph of the Steiner Triple Systems of Order 19 is Connected. <i>Graphs and Combinatorics</i> , 2011, 27, 539-546.	0.2	8
30	Applying the Positional Burrows-Wheeler Transform to all-pairs Hamming distance. <i>Information Processing Letters</i> , 2019, 146, 17-19.	0.4	7
31	Founder reconstruction enables scalable and seamless pangenomic analysis. <i>Bioinformatics</i> , 2021, 37, 4611-4619.	1.8	7
32	A safe and complete algorithm for metagenomic assembly. <i>Algorithms for Molecular Biology</i> , 2018, 13, 3.	0.3	6
33	Peak alignment using restricted edit distances. <i>New Biotechnology</i> , 2007, 24, 337-342.	2.7	5
34	Linear Time Maximum Segmentation Problems in Column Stream Model. <i>Lecture Notes in Computer Science</i> , 2019, , 322-336.	1.0	4
35	Hardness of Covering Alignment: Phase Transition in Post-Sequence Genomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 23-30.	1.9	3
36	Scalable Reference Genome Assembly from Compressed Pan-Genome Index with Spark. <i>Lecture Notes in Computer Science</i> , 2020, , 68-84.	1.0	2

#	ARTICLE	IF	CITATIONS
37	Variant genotyping with gap filling. PLoS ONE, 2017, 12, e0184608.	1.1	2
38	Linear Time Construction of Indexable Elastic Founder Graphs. Lecture Notes in Computer Science, 2022, , 480-493.	1.0	2
39	Distributed hybrid-indexing of compressed pan-genomes for scalable and fast sequence alignment. PLoS ONE, 2021, 16, e0255260.	1.1	1
40	Editorial: Special Issue on Algorithms for Sequence Analysis and Storage. Algorithms, 2014, 7, 186-187.	1.2	0
41	Editorial: Special Issue on "Combinatorial Algorithms" (IWOCA 2016). Theory of Computing Systems, 2018, 62, 1349-1350.	0.7	0
42	Tailoring r-index for Document Listing Towards Metagenomics Applications. Lecture Notes in Computer Science, 2020, , 291-306.	1.0	0