

Gregory Kucherov

List of Publications by Citations

Source: <https://exaly.com/author-pdf/430550/gregory-kucherov-publications-by-citations.pdf>

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85
papers

1,692
citations

20
h-index

39
g-index

95
ext. papers

1,981
ext. citations

2.9
avg, IF

4.83
L-index

#	Paper	IF	Citations
85	mreps: Efficient and flexible detection of tandem repeats in DNA. <i>Nucleic Acids Research</i> , 2003 , 31, 3672-8	20.1	271
84	YASS: enhancing the sensitivity of DNA similarity search. <i>Nucleic Acids Research</i> , 2005 , 33, W540-3	20.1	215
83	NORINE: a database of nonribosomal peptides. <i>Nucleic Acids Research</i> , 2008 , 36, D326-31	20.1	193
82	Diversity of monomers in nonribosomal peptides: towards the prediction of origin and biological activity. <i>Journal of Bacteriology</i> , 2010 , 192, 5143-50	3.5	81
81	A unifying framework for seed sensitivity and its application to subset seeds. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 553-69	1	54
80	Spaced seeds improve k-mer-based metagenomic classification. <i>Bioinformatics</i> , 2015 , 31, 3584-92	7.2	49
79	Using cascading Bloom filters to improve the memory usage for de Bruijn graphs. <i>Algorithms for Molecular Biology</i> , 2014 , 9, 2	1.8	49
78	Reconstructing a Hamiltonian cycle by querying the graph: Application to DNA physical mapping. <i>Discrete Applied Mathematics</i> , 1998 , 88, 147-165	1	42
77	Multiseed lossless filtration. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005 , 2, 51-61	3	41
76	Optimal Reconstruction of Graphs under the Additive Model. <i>Algorithmica</i> , 2000 , 28, 104-124	0.9	39
75	Searching for gapped palindromes. <i>Theoretical Computer Science</i> , 2009 , 410, 5365-5373	1.1	38
74	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020 , 5, 455-464	26.6	37
73	Improved hit criteria for DNA local alignment. <i>BMC Bioinformatics</i> , 2004 , 5, 149	3.6	37
72	Matching a set of strings with variable length don't cares. <i>Theoretical Computer Science</i> , 1997 , 178, 129-154	1.56	35
71	Finding approximate repetitions under Hamming distance. <i>Theoretical Computer Science</i> , 2003 , 303, 135-156	1.56	35
70	On maximal repetitions in words. <i>Lecture Notes in Computer Science</i> , 1999 , 374-385	0.9	25
69	Using Cascading Bloom Filters to Improve the Memory Usage for de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2013 , 364-376	0.9	24

68	Reconsidering the significance of genomic word frequencies. <i>Trends in Genetics</i> , 2007 , 23, 543-6	8.5	22
67	Combinatorial Search on Graphs Motivated by Bioinformatics Applications: A Brief Survey. <i>Lecture Notes in Computer Science</i> , 2005 , 16-27	0.9	21
66	Diversity and structure of PIF/Harbinger-like elements in the genome of <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2007 , 8, 409	4.5	20
65	Linear-time computation of local periods. <i>Theoretical Computer Science</i> , 2004 , 326, 229-240	1.1	20
64	Evolution of biosequence search algorithms: a brief survey. <i>Bioinformatics</i> , 2019 , 35, 3547-3552	7.2	17
63	SIGffRid: a tool to search for sigma factor binding sites in bacterial genomes using comparative approach and biologically driven statistics. <i>BMC Bioinformatics</i> , 2008 , 9, 73	3.6	17
62	Rapid heuristic inference of antibiotic resistance and susceptibility by genomic neighbor typing		17
61	Structural pattern matching of nonribosomal peptides. <i>BMC Structural Biology</i> , 2009 , 9, 15	2.7	16
60	On subset seeds for protein alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009 , 6, 483-94	3	15
59	Optimal Linear Arrangement of Interval Graphs. <i>Lecture Notes in Computer Science</i> , 2006 , 267-279	0.9	14
58	Back-translation for discovering distant protein homologies in the presence of frameshift mutations. <i>Algorithms for Molecular Biology</i> , 2010 , 5, 6	1.8	12
57	On repetition-free binary words of minimal density. <i>Theoretical Computer Science</i> , 1999 , 218, 161-175	1.1	12
56	Decidability of Regularity and Related Properties of Ground Normal Form Languages. <i>Information and Computation</i> , 1995 , 118, 91-100	0.8	12
55	On maximal repetitions of arbitrary exponent. <i>Information Processing Letters</i> , 2010 , 110, 252-256	0.8	11
54	Approximate string matching using a bidirectional index. <i>Theoretical Computer Science</i> , 2016 , 638, 145-158		10
53	Estimating seed sensitivity on homogeneous alignments		10
52	On the combinatorics of suffix arrays. <i>Information Processing Letters</i> , 2013 , 113, 915-920	0.8	9
51	Multi-seed Lossless Filtration. <i>Lecture Notes in Computer Science</i> , 2004 , 297-310	0.9	9

50	Finding repeats with fixed gap		9
49	On relationship between term rewriting systems and regular tree languages. <i>Lecture Notes in Computer Science</i> , 1991 , 299-311	0.9	9
48	Optimal Bounds for Computing (alpha)-gapped Repeats. <i>Lecture Notes in Computer Science</i> , 2016 , 245-255		8
47	Cross-document pattern matching. <i>Journal of Discrete Algorithms</i> , 2014 , 24, 40-47		8
46	Simplitigs as an efficient and scalable representation of de Bruijn graphs		8
45	Absent words in a sliding window with applications. <i>Information and Computation</i> , 2020 , 270, 104461	0.8	7
44	Matching a set of strings with variable length don't cares. <i>Lecture Notes in Computer Science</i> , 1995 , 230-247		7
43	Pattern Matching on Sparse Suffix Trees 2011 ,		6
42	Searching for Gapped Palindromes. <i>Lecture Notes in Computer Science</i> , 2008 , 18-30	0.9	6
41	Minimal Absent Words in a Sliding Window and Applications to On-Line Pattern Matching. <i>Lecture Notes in Computer Science</i> , 2017 , 164-176	0.9	6
40	Simplitigs as an efficient and scalable representation of de Bruijn graphs. <i>Genome Biology</i> , 2021 , 22, 96	18.3	6
39	On-line construction of position heaps. <i>Journal of Discrete Algorithms</i> , 2013 , 20, 3-11		5
38	Designing Efficient Spaced Seeds for SOLiD Read Mapping. <i>Advances in Bioinformatics</i> , 2010 ,	5.5	5
37	Regular language constrained sequence alignment revisited. <i>Journal of Computational Biology</i> , 2011 , 18, 771-81	1.7	5
36	Undecidability of ground reducibility for word rewriting systems with variables. <i>Information Processing Letters</i> , 1995 , 53, 209-215	0.8	5
35	Approximate String Matching Using a Bidirectional Index. <i>Lecture Notes in Computer Science</i> , 2014 , 222-234		5
34	Subset Seed Automaton 2007 , 180-191		5
33	Cross-Documents Pattern Matching. <i>Lecture Notes in Computer Science</i> , 2012 , 196-207	0.9	5

32	A new quasi-reducibility testing algorithm and its application to proofs by induction. <i>Lecture Notes in Computer Science</i> , 1988 , 204-213	0.9	5
31	RNF: a general framework to evaluate NGS read mappers. <i>Bioinformatics</i> , 2016 , 32, 136-9	7.2	4
30	Prefix Table Construction and Conversion. <i>Lecture Notes in Computer Science</i> , 2013 , 41-53	0.9	4
29	Minimally-overlapping words for sequence similarity search. <i>Bioinformatics</i> , 2020 ,	7.2	4
28	Decidability of regularity and related properties of ground normal form languages. <i>Lecture Notes in Computer Science</i> , 1993 , 272-286	0.9	4
27	Improved Filters for the Approximate Suffix-Prefix Overlap Problem. <i>Lecture Notes in Computer Science</i> , 2014 , 139-148	0.9	3
26	A Unifying Framework for Seed Sensitivity and Its Application to Subset Seeds. <i>Lecture Notes in Computer Science</i> , 2005 , 251-263	0.9	3
25	Optimal neighborhood indexing for protein similarity search. <i>BMC Bioinformatics</i> , 2008 , 9, 534	3.6	2
24	Some results on top-context-free tree languages 1994 , 157-171		2
23	Minimally-overlapping words for sequence similarity search		2
22	The complexity of testing ground reducibility for linear word rewriting systems with variables. <i>Lecture Notes in Computer Science</i> , 1995 , 262-275	0.9	2
21	On Maximal Unbordered Factors. <i>Lecture Notes in Computer Science</i> , 2015 , 343-354	0.9	2
20	Computing Discriminating and Generic Words. <i>Lecture Notes in Computer Science</i> , 2012 , 307-317	0.9	2
19	Optimal bounds for computing \mathbb{E} gapped repeats. <i>Information and Computation</i> , 2019 , 268, 104434	0.8	1
18	Algorithms for path-constrained sequence alignment. <i>Journal of Discrete Algorithms</i> , 2014 , 24, 48-58		1
17	Patterns in Words versus Patterns in Trees: A Brief Survey and New Results. <i>Lecture Notes in Computer Science</i> , 2000 , 283-296	0.9	1
16	Efficient Seeding Techniques for Protein Similarity Search. <i>Communications in Computer and Information Science</i> , 2008 , 466-478	0.3	1
15	Seed Design Framework for Mapping SOLiD Reads. <i>Lecture Notes in Computer Science</i> , 2010 , 384-396	0.9	1

14	Computing the Longest Unbordered Substring. <i>Lecture Notes in Computer Science</i> , 2015 , 246-257	0.9	1
13	On-Line Construction of Position Heaps. <i>Lecture Notes in Computer Science</i> , 2011 , 326-337	0.9	1
12	Full-Fledged Real-Time Indexing for Constant Size Alphabets. <i>Lecture Notes in Computer Science</i> , 2013 , 650-660	0.9	1
11	Minimal Discriminating Words Problem Revisited. <i>Lecture Notes in Computer Science</i> , 2013 , 129-140	0.9	1
10	Protein Similarity Search with Subset Seeds on a Dedicated Reconfigurable Hardware 2008 , 1240-1248		0
9	Full-Fledged Real-Time Indexing for Constant Size Alphabets. <i>Algorithmica</i> , 2017 , 79, 387-400	0.9	
8	Efficient alternatives to PSI-BLAST. <i>Bulletin of the Polish Academy of Sciences: Technical Sciences</i> , 2012 , 60, 495-505		
7	Visualization of dynamic automata using Padnon. <i>Lecture Notes in Computer Science</i> , 1998 , 25-28	0.9	
6	The complexity of some complementation problems. <i>Information Processing Letters</i> , 1999 , 71, 159-165	0.8	
5	Back-Translation for Discovering Distant Protein Homologies. <i>Lecture Notes in Computer Science</i> , 2009 , 108-120	0.9	
4	CPM ² 20th Anniversary: A Statistical Retrospective. <i>Lecture Notes in Computer Science</i> , 2009 , 1-11	0.9	
3	Regular Language Constrained Sequence Alignment Revisited. <i>Lecture Notes in Computer Science</i> , 2011 , 404-415	0.9	
2	Special Issue on Computer Science Symposium in Russia (2019). <i>Theory of Computing Systems</i> , 2021 , 65, 441-443	0.6	
1	Space-efficient representation of genomic k-mer count tables.. <i>Algorithms for Molecular Biology</i> , 2022 , 17, 5	1.8	