

Gregory Kucherov

List of Publications by Year in Descending Order

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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	Space-efficient representation of genomic k-mer count tables.. <i>Algorithms for Molecular Biology</i> , 2022 , 17, 5	1.8	
84	Simplitigs as an efficient and scalable representation of de Bruijn graphs. <i>Genome Biology</i> , 2021 , 22, 96	18.3	6
83	Special Issue on Computer Science Symposium in Russia (2019). <i>Theory of Computing Systems</i> , 2021 , 65, 441-443	0.6	
82	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020 , 5, 455-464	26.6	37
81	Absent words in a sliding window with applications. <i>Information and Computation</i> , 2020 , 270, 104461	0.8	7
80	Minimally-overlapping words for sequence similarity search. <i>Bioinformatics</i> , 2020 ,	7.2	4
79	Evolution of biosequence search algorithms: a brief survey. <i>Bioinformatics</i> , 2019 , 35, 3547-3552	7.2	17
78	Optimal bounds for computing ϵ -gapped repeats. <i>Information and Computation</i> , 2019 , 268, 104434	0.8	1
77	Full-Fledged Real-Time Indexing for Constant Size Alphabets. <i>Algorithmica</i> , 2017 , 79, 387-400	0.9	
76	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
75	Optimal Bounds for Computing (α) -gapped Repeats. <i>Lecture Notes in Computer Science</i> , 2016 , 245-255		8
74	Approximate string matching using a bidirectional index. <i>Theoretical Computer Science</i> , 2016 , 638, 145-158		10
73	RNF: a general framework to evaluate NGS read mappers. <i>Bioinformatics</i> , 2016 , 32, 136-9	7.2	4
72	Spaced seeds improve k-mer-based metagenomic classification. <i>Bioinformatics</i> , 2015 , 31, 3584-92	7.2	49
71	Computing the Longest Unbordered Substring. <i>Lecture Notes in Computer Science</i> , 2015 , 246-257	0.9	1
70	On Maximal Unbordered Factors. <i>Lecture Notes in Computer Science</i> , 2015 , 343-354	0.9	2
69	Algorithms for path-constrained sequence alignment. <i>Journal of Discrete Algorithms</i> , 2014 , 24, 48-58		1

68	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
67	Cross-document pattern matching. <i>Journal of Discrete Algorithms</i> , 2014 , 24, 40-47		8
66	Improved Filters for the Approximate Suffix-Prefix Overlap Problem. <i>Lecture Notes in Computer Science</i> , 2014 , 139-148	0.9	3
65	Approximate String Matching Using a Bidirectional Index. <i>Lecture Notes in Computer Science</i> , 2014 , 222-234		5
64	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
63	On the combinatorics of suffix arrays. <i>Information Processing Letters</i> , 2013 , 113, 915-920	0.8	9
62	On-line construction of position heaps. <i>Journal of Discrete Algorithms</i> , 2013 , 20, 3-11		5
61	Prefix Table Construction and Conversion. <i>Lecture Notes in Computer Science</i> , 2013 , 41-53	0.9	4
60	Full-Fledged Real-Time Indexing for Constant Size Alphabets. <i>Lecture Notes in Computer Science</i> , 2013 , 650-660	0.9	1
59	Minimal Discriminating Words Problem Revisited. <i>Lecture Notes in Computer Science</i> , 2013 , 129-140	0.9	1
58	Efficient alternatives to PSI-BLAST. <i>Bulletin of the Polish Academy of Sciences: Technical Sciences</i> , 2012 , 60, 495-505		
57	Cross-Documents Pattern Matching. <i>Lecture Notes in Computer Science</i> , 2012 , 196-207	0.9	5
56	Computing Discriminating and Generic Words. <i>Lecture Notes in Computer Science</i> , 2012 , 307-317	0.9	2
55	Pattern Matching on Sparse Suffix Trees 2011 ,		6
54	Regular language constrained sequence alignment revisited. <i>Journal of Computational Biology</i> , 2011 , 18, 771-81	1.7	5
53	On-Line Construction of Position Heaps. <i>Lecture Notes in Computer Science</i> , 2011 , 326-337	0.9	1
52	Regular Language Constrained Sequence Alignment Revisited. <i>Lecture Notes in Computer Science</i> , 2011 , 404-415	0.9	
51	Designing Efficient Spaced Seeds for SOLiD Read Mapping. <i>Advances in Bioinformatics</i> , 2010 ,	5.5	5

50	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
49	On maximal repetitions of arbitrary exponent. <i>Information Processing Letters</i> , 2010 , 110, 252-256	0.8	11
48	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
47	Seed Design Framework for Mapping SOLiD Reads. <i>Lecture Notes in Computer Science</i> , 2010 , 384-396	0.9	1
46	Searching for gapped palindromes. <i>Theoretical Computer Science</i> , 2009 , 410, 5365-5373	1.1	38
45	Structural pattern matching of nonribosomal peptides. <i>BMC Structural Biology</i> , 2009 , 9, 15	2.7	16
44	On subset seeds for protein alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009 , 6, 483-94	3	15
43	Back-Translation for Discovering Distant Protein Homologies. <i>Lecture Notes in Computer Science</i> , 2009 , 108-120	0.9	
42	CPM ₂ 20th Anniversary: A Statistical Retrospective. <i>Lecture Notes in Computer Science</i> , 2009 , 1-11	0.9	
41	Optimal neighborhood indexing for protein similarity search. <i>BMC Bioinformatics</i> , 2008 , 9, 534	3.6	2
40	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
39	NORINE: a database of nonribosomal peptides. <i>Nucleic Acids Research</i> , 2008 , 36, D326-31	20.1	193
38	Protein Similarity Search with Subset Seeds on a Dedicated Reconfigurable Hardware 2008 , 1240-1248		0
37	Searching for Gapped Palindromes. <i>Lecture Notes in Computer Science</i> , 2008 , 18-30	0.9	6
36	Efficient Seeding Techniques for Protein Similarity Search. <i>Communications in Computer and Information Science</i> , 2008 , 466-478	0.3	1
35	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
34	Reconsidering the significance of genomic word frequencies. <i>Trends in Genetics</i> , 2007 , 23, 543-6	8.5	22
33	Subset Seed Automaton 2007 , 180-191		5

32	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
31	Optimal Linear Arrangement of Interval Graphs. <i>Lecture Notes in Computer Science</i> , 2006 , 267-279	0.9	14
30	YASS: enhancing the sensitivity of DNA similarity search. <i>Nucleic Acids Research</i> , 2005 , 33, W540-3	20.1	215
29	Combinatorial Search on Graphs Motivated by Bioinformatics Applications: A Brief Survey. <i>Lecture Notes in Computer Science</i> , 2005 , 16-27	0.9	21
28	Multiseed lossless filtration. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005 , 2, 51-61	3	41
27	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
26	Improved hit criteria for DNA local alignment. <i>BMC Bioinformatics</i> , 2004 , 5, 149	3.6	37
25	Linear-time computation of local periods. <i>Theoretical Computer Science</i> , 2004 , 326, 229-240	1.1	20
24	Multi-seed Lossless Filtration. <i>Lecture Notes in Computer Science</i> , 2004 , 297-310	0.9	9
23	Finding approximate repetitions under Hamming distance. <i>Theoretical Computer Science</i> , 2003 , 303, 135-156	1.56	35
22	mreps: Efficient and flexible detection of tandem repeats in DNA. <i>Nucleic Acids Research</i> , 2003 , 31, 3672-8	20.1	271
21	Optimal Reconstruction of Graphs under the Additive Model. <i>Algorithmica</i> , 2000 , 28, 104-124	0.9	39
20	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
19	On repetition-free binary words of minimal density. <i>Theoretical Computer Science</i> , 1999 , 218, 161-175	1.1	12
18	The complexity of some complementation problems. <i>Information Processing Letters</i> , 1999 , 71, 159-165	0.8	
17	On maximal repetitions in words. <i>Lecture Notes in Computer Science</i> , 1999 , 374-385	0.9	25
16	Reconstructing a Hamiltonian cycle by querying the graph: Application to DNA physical mapping. <i>Discrete Applied Mathematics</i> , 1998 , 88, 147-165	1	42
15	Visualization of dynamic automata using Padnon. <i>Lecture Notes in Computer Science</i> , 1998 , 25-28	0.9	

14	Matching a set of strings with variable length don't cares. <i>Theoretical Computer Science</i> , 1997 , 178, 129-154		35
13	Decidability of Regularity and Related Properties of Ground Normal Form Languages. <i>Information and Computation</i> , 1995 , 118, 91-100	0.8	12
12	Undecidability of ground reducibility for word rewriting systems with variables. <i>Information Processing Letters</i> , 1995 , 53, 209-215	0.8	5
11	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
10	Matching a set of strings with variable length don't cares. <i>Lecture Notes in Computer Science</i> , 1995 , 230-247		7
9	Some results on top-context-free tree languages 1994 , 157-171		2
8	Decidability of regularity and related properties of ground normal form languages. <i>Lecture Notes in Computer Science</i> , 1993 , 272-286	0.9	4
7	On relationship between term rewriting systems and regular tree languages. <i>Lecture Notes in Computer Science</i> , 1991 , 299-311	0.9	9
6	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
5	Estimating seed sensitivity on homogeneous alignments		10
4	Finding repeats with fixed gap		9
3	Simplitigs as an efficient and scalable representation of de Bruijn graphs		8
2	Minimally-overlapping words for sequence similarity search		2
1	Rapid heuristic inference of antibiotic resistance and susceptibility by genomic neighbor typing		17