

# Lucian Ilie

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

1,169  
citations

394421

19  
h-index

395702

33  
g-index

41  
all docs

41  
docs citations

41  
times ranked

648  
citing authors

#	ARTICLE	IF	CITATIONS
1	HiTEC: accurate error correction in high-throughput sequencing data. <i>Bioinformatics</i> , 2011, 27, 295-302.	4.1	111
2	Computing Longest Previous Factor in linear time and applications. <i>Information Processing Letters</i> , 2008, 106, 75-80.	0.6	109
3	Follow automata. <i>Information and Computation</i> , 2003, 186, 140-162.	0.7	102
4	RACER: Rapid and accurate correction of errors in reads. <i>Bioinformatics</i> , 2013, 29, 2490-2493.	4.1	64
5	Repetitions in strings: Algorithms and combinatorics. <i>Theoretical Computer Science</i> , 2009, 410, 5227-5235.	0.9	56
6	A note on the number of squares in a word. <i>Theoretical Computer Science</i> , 2007, 380, 373-376.	0.9	55
7	A Simple Algorithm for Computing the Lempel Ziv Factorization. <i>Proceedings of the Data Compression Conference</i> , 2008, , .	0.0	52
8	Maximal repetitions in strings. <i>Journal of Computer and System Sciences</i> , 2008, 74, 796-807.	1.2	51
9	A simple proof that a word of length $n$ has at most $\frac{n}{2}$ maximal repetitions. <i>Journal of Combinatorics</i> , 2008, 11, 1-17.	0.8	49
10	Multiple spaced seeds for homology search. <i>Bioinformatics</i> , 2007, 23, 2969-2977.	4.1	46
11	SpEED: fast computation of sensitive spaced seeds. <i>Bioinformatics</i> , 2011, 27, 2433-2434.	4.1	46
12	LPF Computation Revisited. <i>Lecture Notes in Computer Science</i> , 2009, , 158-169.	1.3	38
13	Reducing NFAs by invariant equivalences. <i>Theoretical Computer Science</i> , 2003, 306, 373-390.	0.9	36
14	On a conjecture about slender context-free languages. <i>Theoretical Computer Science</i> , 1994, 132, 427-434.	0.9	33
15	The runs conjecture. <i>Theoretical Computer Science</i> , 2011, 412, 2931-2941.	0.9	30
16	Correcting Illumina data. <i>Briefings in Bioinformatics</i> , 2015, 16, 588-599.	6.5	29
17	E-MEM: efficient computation of maximal exact matches for very large genomes. <i>Bioinformatics</i> , 2015, 31, 509-514.	4.1	26
18	A comparison of index-based lempel-ziv LZ77 factorization algorithms. <i>ACM Computing Surveys</i> , 2012, 45, 1-17.	23.0	24

#	ARTICLE	IF	CITATIONS
19	SAGE: String-overlap Assembly of GENomes. BMC Bioinformatics, 2014, 15, 302.	2.6	23
20	Computing the Longest Previous Factor. European Journal of Combinatorics, 2013, 34, 15-26.	0.8	21
21	Towards a Solution to the "Runs" Conjecture. , 2008, , 290-302.		21
22	BOND: Basic OligoNucleotide Design. BMC Bioinformatics, 2013, 14, 69.	2.6	19
23	A characterization of poly-slender context-free languages. RAIRO - Theoretical Informatics and Applications, 2000, 34, 77-86.	0.5	18
24	On lengths of words in context-free languages. Theoretical Computer Science, 2000, 242, 327-359.	0.9	12
25	THE STRUCTURE OF FACTOR ORACLES. International Journal of Foundations of Computer Science, 2007, 18, 781-797.	1.1	12
26	Minimum Unique Substrings and Maximum Repeats. Fundamenta Informaticae, 2011, 110, 183-195.	0.4	12
27	Analysis of Maximal Repetitions in Strings. Lecture Notes in Computer Science, 2007, , 465-476.	1.3	12
28	WORD COMPLEXITY AND REPETITIONS IN WORDS. International Journal of Foundations of Computer Science, 2004, 15, 41-55.	1.1	11
29	Seeds for effective oligonucleotide design. BMC Genomics, 2011, 12, 280.	2.8	9
30	HISEA: Hierarchical SEed Aligner for PacBio data. BMC Bioinformatics, 2017, 18, 564.	2.6	9
31	The Lempel-Ziv Complexity of Fixed Points of Morphisms. SIAM Journal on Discrete Mathematics, 2007, 21, 466-481.	0.8	8
32	On strongly context-free languages. Discrete Applied Mathematics, 2000, 103, 153-165.	0.9	6
33	LASER: Large genome ASsembly EvaluatoR. BMC Research Notes, 2015, 8, 709.	1.4	5
34	Fast computation of neighbor seeds. Bioinformatics, 2009, 25, 822-823.	4.1	4
35	ON GENERALIZED SLENDERNESS OF CONTEXT-FREE LANGUAGES. , 2001, , 189-202.		3
36	SAGE2: parallel human genome assembly. Bioinformatics, 2018, 34, 678-680.	4.1	2

#	ARTICLE	IF	CITATIONS
37	ALeS: adaptive-length spaced-seed design. <i>Bioinformatics</i> , 2021, 37, 1206-1210.	4.1	2
38	Generalized Factors of Words. <i>Fundamenta Informaticae</i> , 1998, 33, 239-247.	0.4	1
39	Uniformly Scattered Factors. , 2000, , 187-198.		1
40	The Lempel-Ziv Complexity of Fixed Points of Morphisms. <i>Lecture Notes in Computer Science</i> , 2006, , 280-291.	1.3	1
41	Periodic and Sturmian languages. <i>Information Processing Letters</i> , 2006, 98, 242-246.	0.6	0