Max A Alekseyev

List of Publications by Year
in descending order

60 papers	23,713 citations	516710 16 h-index	214800 47 g-index
69 all docs	69 docs citations	69 times ranked	30862 citing authors

#	Article	IF	Citations
1	Orienting Ordered Scaffolds: Complexity and Algorithms. SN Computer Science, 2022, 3, .	3.6	0
2	Chromosome-level genome assemblies of the malaria vectors *Anopheles coluzzii* and *Anopheles arabiensis*. GigaScience, 2021, 10, .	6.4	12
3	Computing solutions to the congruence $1n+2n+â‹¯+nnâ‰¡p(\bmod n)$. Discrete Applied Mathematics, 2020, 286, 3-9.	0.9	0
4	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
5	A unified ILP framework for core ancestral genome reconstruction problems. Bioinformatics, 2020, 36, 2993-3003.	4.1	6
6	Linearization of Ancestral Genomes with Duplicated Genes. , 2020, , .		2
7	Linearization of Median Genomes Under the Double-Cut-and-Join-Indel Model. Evolutionary Bioinformatics, 2019, 15, 117693431882053.	1.2	4
8	A Uniform Theory of Adequate Subgraphs for the Genome Median, Halving, and Aliquoting Problems. Lecture Notes in Computer Science, 2019, , 97-111.	1.3	0
9	ON PARTITIONS INTO SQUARES OF DISTINCT INTEGERS WHOSE RECIPROCALS SUM TO 1. , 2019, , 213-221.		1
10	10. Making Walks Count: From Silent Circles to Hamiltonian Cycles. , 2018, , 157-168.		0
11	Implicit Transpositions in DCJ Scenarios. , 2018, , .		0
12	A Rapid Exact Solution for the Guided Genome Halving Problem. , 2018, , .		0
13	On p-Adic Approximation of Sums of Binomial Coefficients. Journal of Mathematical Sciences, 2018, 233, 626-634.	0.4	1
14	Combinatorial Scoring of Phylogenetic Trees and Networks Based on Homoplasy-Free Characters. Journal of Computational Biology, 2018, 25, 1203-1219.	1.6	2
15	Generalized Hultman Numbers and Cycle Structures of Breakpoint Graphs. Journal of Computational Biology, 2017, 24, 93-105.	1.6	3
16	Estimation of the true evolutionary distance under the fragile breakage model. BMC Genomics, 2017, 18, 356.	2.8	8
17	On problem of orienting ordered scaffolds. , 2017, , .		0
18	Implicit Transpositions in DCJ Scenarios. Frontiers in Genetics, 2017, 8, 212.	2.3	2

#	Article	IF	Citations
19	CAMSA: a tool for comparative analysis and merging of scaffold assemblies. BMC Bioinformatics, 2017, 18, 496.	2.6	11
20	A Unified ILP Framework for Genome Median, Halving, and Aliquoting Problems Under DCJ. Lecture Notes in Computer Science, 2017, , 156-178.	1.3	4
21	Comparative genomics meets topology: a novel view on genome median and halving problems. BMC Bioinformatics, 2016, 17, 418.	2.6	5
22	CAMSA: A tool for comparative analysis and merging of scaffold assemblies. , 2016, , .		0
23	5. Solving the Tower of Hanoi with Random Moves. , 2016, , 65-80.		1
24	Transcriptome sequencing based annotation and homologous evidence based scaffolding of Anguilla japonica draft genome. BMC Genomics, 2016, 17, 13.	2.8	9
25	Reconstruction of Ancestral Genomes in Presence of Gene Gain and Loss. Journal of Computational Biology, 2016, 23, 150-164.	1.6	58
26	Combinatorial Scoring of Phylogenetic Networks. Lecture Notes in Computer Science, 2016, , 560-572.	1.3	1
27	On the Minimal Teaching Sets of Two-Dimensional Threshold Functions. SIAM Journal on Discrete Mathematics, 2015, 29, 157-165.	0.8	7
28	A Computational Method for the Rate Estimation of Evolutionary Transpositions. Lecture Notes in Computer Science, 2015, , 471-480.	1.3	8
29	Estimation of the true evolutionary distance under the fragile breakage model. , 2015, , .		3
30	Scaffold assembly based on genome rearrangement analysis. Computational Biology and Chemistry, 2015, 57, 46-53.	2.3	12
31	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
32	TRAIL-Based High Throughput Screening Reveals a Link between TRAIL-Mediated Apoptosis and Glutathione Reductase, a Key Component of Oxidative Stress Response. PLoS ONE, 2015, 10, e0129566.	2.5	13
33	Generalized Hultman Numbers and the Distribution of Multi-break Distances. Lecture Notes in Computer Science, 2015, , 3-12.	1.3	0
34	Solving the Tower of Hanoi with Random Moves. , 2015, , .		0
35	Linearization of Median Genomes under DCJ. Lecture Notes in Computer Science, 2014, , 97-106.	1.3	2
36	BayesHammer: Bayesian clustering for error correction in single-cell sequencing. BMC Genomics, 2013, 14, S7.	2.8	429

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37	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. Lecture Notes in Computer Science, 2013, , 158-170.	1.3	439
38	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. Journal of Computational Biology, 2013, 20, 714-737.	1.6	1,235
39	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. Journal of Computational Biology, 2013, 20, 359-371.	1.6	14
40	Phylogenetic analysis of genome rearrangements among five mammalian orders. Molecular Phylogenetics and Evolution, 2012, 65, 871-882.	2.7	23
41	On pairwise distances and median score of three genomes under DCJ. BMC Bioinformatics, 2012, 13, S1.	2.6	4
42	SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. Journal of Computational Biology, 2012, 19, 455-477.	1.6	20,193
43	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. Lecture Notes in Computer Science, 2012, , 200-212.	1.3	3
44	On the Intersections of Fibonacci, Pell, and Lucas Numbers. Integers, 2011, 11, .	0.3	7
45	On the Number of Two-Dimensional Threshold Functions. SIAM Journal on Discrete Mathematics, 2010, 24, 1617-1631.	0.8	5
46	Comparative genomics reveals birth and death of fragile regions in mammalian evolution. Genome Biology, 2010, 11, R117.	9.6	23
47	Decoding the Genomic Architecture of Mammalian and Plant Genomes: Synteny Blocks and Large-scale Duplications. Communications in Information and Systems, 2010, 10, 1-22.	0.5	2
48	Limited Lifespan of Fragile Regions in Mammalian Evolution. Lecture Notes in Computer Science, 2010, , 198-215.	1.3	0
49	Decoding Synteny Blocks and Large-Scale Duplications in Mammalian and Plant Genomes. Lecture Notes in Computer Science, 2009, , 220-232.	1.3	9
50	Breakpoint graphs and ancestral genome reconstructions. Genome Research, 2009, 19, 943-957.	5.5	111
51	Multi-break rearrangements and chromosomal evolution. Theoretical Computer Science, 2008, 395, 193-202.	0.9	55
52	Multi-Break Rearrangements and Breakpoint Re-Uses: From Circular to Linear Genomes. Journal of Computational Biology, 2008, 15, 1117-1131.	1.6	25
53	Are There Rearrangement Hotspots in the Human Genome?. PLoS Computational Biology, 2007, 3, e209.	3.2	36
54	Colored de Bruijn Graphs and the Genome Halving Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 98-107.	3.0	31

#	Article	IF	Citations
55	Whole Genome Duplications and Contracted Breakpoint Graphs. SIAM Journal on Computing, 2007, 36, 1748-1763.	1.0	18
56	Multi-break Rearrangements: From Circular to Linear Genomes. Lecture Notes in Computer Science, 2007, , 1-15.	1.3	0
57	Genome Halving Problem Revisited. Lecture Notes in Computer Science, 2004, , 1-15.	1.3	1
58	Splicing graphs and EST assembly problem. Bioinformatics, 2002, 18, S181-S188.	4.1	172
59	On Approximation of Groups, Group Actions, and Hopf Algebras. Journal of Mathematical Sciences, 2001, 107, 4305-4332.	0.4	11
60	MAKING WALKS COUNT:. , 0, , 157-168.		0