Srinivas Aluru

List of Publications by Year
in descending order

46 papers	**5,616** citations	430874 **18** h-index	642732 **23** g-index
51 all docs	**51** docs citations	**51** times ranked	**8032** citing authors

#	Article	IF	Citations
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	12.6	3,612
2	A brassinosteroid transcriptional network revealed by genome‐wide identification of BES1 target genes in *Arabidopsis thaliana*. Plant Journal, 2011, 65, 634-646.	5.7	565
3	A survey of error-correction methods for next-generation sequencing. Briefings in Bioinformatics, 2013, 14, 56-66.	6.5	205
4	RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. Nature Communications, 2017, 8, 14573.	12.8	202
5	Space efficient linear time construction of suffix arrays. Journal of Discrete Algorithms, 2005, 3, 143-156.	0.7	145
6	Reptile: representative tiling for short read error correction. Bioinformatics, 2010, 26, 2526-2533.	4.1	132
7	Efficient clustering of large EST data sets on parallel computers. Nucleic Acids Research, 2003, 31, 2963-2974.	14.5	69
8	Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted genes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12282-12287.	7.1	67
9	Parallel biological sequence comparison using prefix computations. Journal of Parallel and Distributed Computing, 2003, 63, 264-272.	4.1	64
10	Nearly Identical Paralogs: Implications for Maize (*Zea mays* L.) Genome Evolution. Genetics, 2007, 175, 429-439.	2.9	60
11	A Review of Hardware Acceleration for Computational Genomics. IEEE Design and Test, 2014, 31, 19-30.	1.2	59
12	A comprehensive evaluation of long read error correction methods. BMC Genomics, 2020, 21, 889.	2.8	58
13	A strategy for assembling the maize (Zea mays L.) genome. Bioinformatics, 2004, 20, 140-147.	4.1	55
14	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. PLoS Genetics, 2009, 5, e1000728.	3.5	39
15	Parallel Information-Theory-Based Construction of Genome-Wide Gene Regulatory Networks. IEEE Transactions on Parallel and Distributed Systems, 2010, 21, 1721-1733.	5.6	36
16	Space and time efficient parallel algorithms and software for EST clustering. IEEE Transactions on Parallel and Distributed Systems, 2003, 14, 1209-1221.	5.6	26
17	Repeat-aware modeling and correction of short read errors. BMC Bioinformatics, 2011, 12, S52.	2.6	22
18	Parallel Genomic Alignments on the Cell Broadband Engine. IEEE Transactions on Parallel and Distributed Systems, 2009, 20, 1600-1610.	5.6	21

#	ARTICLE	IF	CITATIONS
19	Parallel biological sequence alignments on the Cell Broadband Engine. Parallel and Distributed Processing Symposium (IPDPS), Proceedings of the International Conference on, 2008, , .	1.0	17
20	Parallel Construction of Bidirected String Graphs for Genome Assembly. , 2008, , .		16
21	Accelerating Sequence Alignment to Graphs. , 2019, , .		16
22	Parallel Metagenomic Sequence Clustering Via Sketching and Maximal Quasi-clique Enumeration on Map-Reduce Clouds. , 2011, , .		15
23	Large-Scale Phylogenetic Analysis on Current HPC Architectures. Scientific Programming, 2008, 16, 255-270.	0.7	14
24	Parallel Bayesian Network Structure Learning for Genome-Scale Gene Networks. , 2014, , .		12
25	Accelerating Pairwise Computations on Cell Processors. IEEE Transactions on Parallel and Distributed Systems, 2011, 22, 69-77.	5.6	10
26	Parallel Bayesian network structure learning with application to gene networks. , 2012, , .		9
27	Fast and Accurate Construction of Ultra-Dense Consensus Genetic Maps Using Evolution Strategy Optimization. PLoS ONE, 2015, 10, e0122485.	2.5	9
28	Parallel Discovery of Direct Causal Relations and Markov Boundaries with Applications to Gene Networks. , 2011, , .		8
29	A Parallel Algorithm for Spectrum-based Short Read Error Correction. , 2012, , .		8
30	A Formal Analysis of Space Filling Curves for Parallel Domain Decomposition. , 0, , .		7
31	Constructing Gene Regulatory Networks on Clusters of Cell Processors. , 2009, , .		6
32	A parallel algorithm for exact Bayesian network inference. , 2009, , .		4
33	A MapReduce Style Framework for Computations on Trees. , 2010, , .		4
34	An improved maximum likelihood formulation for accurate genome assembly. , 2011, , .		4
35	In search of perfect reads. BMC Bioinformatics, 2015, 16, S7.	2.6	3
36	Parallel Read Error Correction for Big Genomic Datasets. , 2015, , .		2

#	Article	IF	Citations
37	A Parallel Algorithm for Finding All Pairs Î³-Mismatch Maximal Common Substrings. , 2016, , .		2
38	A Memory and Time Scalable Parallelization of the Reptile Error-Correction Code. , 2016, , .		1
39	Computational biology on parallel computers. , 2003, , .		0
40	Parallel applications employing pairwise computations on emerging architectures. , 2010, , .		0
41	Workshop: Taxonomic clustering of large-scale metagnomic data. , 2012, , .		0
42	Large-scale metagenomic clustering via quasi clique enumeration and read assignment ambiguity resolution. , 2013, , .		0
43	In search of perfect reads. , 2014, , .		0
44	Text Indexing. , 2016, , 2226-2231.		0
45	Sequential and parallel algorithms for all-pair k-mismatch maximal common substrings. Journal of Parallel and Distributed Computing, 2020, 144, 68-79.	4.1	0
46	Text Indexing. , 2008, , 950-954.		0