

Jan Fostier

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

1,051
citations

471509

17
h-index

454955

30
g-index

68
all docs

68
docs citations

68
times ranked

1887
citing authors

#	ARTICLE	IF	CITATIONS
1	i-ADHoRe 3.0 – fast and sensitive detection of genomic homology in extremely large data sets. <i>Nucleic Acids Research</i> , 2012, 40, e11-e11.	14.5	192
2	Halvade: scalable sequence analysis with MapReduce. <i>Bioinformatics</i> , 2015, 31, 2482-2488.	4.1	69
3	Jabba: hybrid error correction for long sequencing reads. <i>Algorithms for Molecular Biology</i> , 2016, 11, 10.	1.2	67
4	An Asynchronous Parallel MLFMA for Scattering at Multiple Dielectric Objects. <i>IEEE Transactions on Antennas and Propagation</i> , 2008, 56, 2346-2355.	5.1	64
5	Evaluation of the impact of Illumina error correction tools on de novo genome assembly. <i>BMC Bioinformatics</i> , 2017, 18, 374.	2.6	49
6	Frequency-based haplotype reconstruction from deep sequencing data of bacterial populations. <i>Nucleic Acids Research</i> , 2015, 43, e105-e105.	14.5	45
7	Needles: Toward Large-Scale Genomic Prediction with Marker-by-Environment Interaction. <i>Genetics</i> , 2016, 203, 543-555.	2.9	45
8	Full-Wave Simulations of Electromagnetic Scattering Problems With Billions of Unknowns. <i>IEEE Transactions on Antennas and Propagation</i> , 2015, 63, 796-799.	5.1	43
9	$O(1)$ Computation of Legendre Polynomials and Gauss–Legendre Nodes and Weights for Parallel Computing. <i>SIAM Journal of Scientific Computing</i> , 2012, 34, C83-C101.	2.8	38
10	Provably scalable parallel multilevel fast multipole algorithm. <i>Electronics Letters</i> , 2008, 44, 1111.	1.0	26
11	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. <i>Bioinformatics</i> , 2011, 27, 749-756.	4.1	24
12	Pathway Relevance Ranking for Tumor Samples through Network-Based Data Integration. <i>PLoS ONE</i> , 2015, 10, e0133503.	2.5	24
13	Illumina error correction near highly repetitive DNA regions improves de novo genome assembly. <i>BMC Bioinformatics</i> , 2019, 20, 298.	2.6	23
14	elPrep: High-Performance Preparation of Sequence Alignment/Map Files for Variant Calling. <i>PLoS ONE</i> , 2015, 10, e0132868.	2.5	22
15	Dynamical anchoring of distant arrhythmia sources by fibrotic regions via restructuring of the activation pattern. <i>PLoS Computational Biology</i> , 2018, 14, e1006637.	3.2	22
16	BrownieAligner: accurate alignment of Illumina sequencing data to de Bruijn graphs. <i>BMC Bioinformatics</i> , 2018, 19, 311.	2.6	22
17	Weak Scalability Analysis of the Distributed-Memory Parallel MLFMA. <i>IEEE Transactions on Antennas and Propagation</i> , 2013, 61, 5567-5574.	5.1	19
18	In-memory, distributed content-based recommender system. <i>Journal of Intelligent Information Systems</i> , 2014, 42, 645-669.	3.9	18

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19	Full-wave electromagnetic scattering at extremely large 2-D objects. Electronics Letters, 2009, 45, 245.	1.0	17
20	An Open-Source Implementation for Full-Wave 2D Scattering by Million-Wavelength-Size Objects. IEEE Antennas and Propagation Magazine, 2010, 52, 23-34.	1.4	17
21	The Index-Based Subgraph Matching Algorithm (ISMA): Fast Subgraph Enumeration in Large Networks Using Optimized Search Trees. PLoS ONE, 2013, 8, e61183.	2.5	17
22	elPrep 4: A multithreaded framework for sequence analysis. PLoS ONE, 2019, 14, e0209523.	2.5	17
23	Halvade-RNA: Parallel variant calling from transcriptomic data using MapReduce. PLoS ONE, 2017, 12, e0174575.	2.5	17
24	BLSSpeller: exhaustive comparative discovery of conserved cis-regulatory elements. Bioinformatics, 2015, 31, 3758-3766.	4.1	14
25	OMSim: a simulator for optical map data. Bioinformatics, 2017, 33, 2740-2742.	4.1	14
26	Comparative analysis of somatic variant calling on matched FF and FFPE WGS samples. BMC Medical Genomics, 2020, 13, 94.	1.5	12
27	A fast parallel multilevel fast multipole algorithm solver for oblique plane wave incidence. Radio Science, 2011, 46, .	1.6	9
28	EPSILON: an eQTL prioritization framework using similarity measures derived from local networks. Bioinformatics, 2013, 29, 1308-1316.	4.1	9
29	Jabba: Hybrid Error Correction for Long Sequencing Reads Using Maximal Exact Matches. Lecture Notes in Computer Science, 2015, , 175-188.	1.3	9
30	Multithreaded variant calling in elPrep 5. PLoS ONE, 2021, 16, e0244471.	2.5	9
31	Online execution time prediction for computationally intensive applications with periodic progress updates. Journal of Supercomputing, 2012, 62, 768-786.	3.6	7
32	Computational assessment of the feasibility of protonation-based protein sequencing. PLoS ONE, 2020, 15, e0238625.	2.5	7
33	DAIRRY-BLUP: A High-Performance Computing Approach to Genomic Prediction. Genetics, 2014, 197, 813-822.	2.9	6
34	GABAC: an arithmetic coding solution for genomic data. Bioinformatics, 2020, 36, 2275-2277.	4.1	6
35	Deep scoping: a breeding strategy to preserve, reintroduce and exploit genetic variation. Theoretical and Applied Genetics, 2021, 134, 3845-3861.	3.6	6
36	Accurate wideband evaluation of the shielding effectiveness of complex enclosures using an asynchronous parallel NSPWMLFMA. , 2008, , .		5

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37	Towards a scalable parallel MLFMA in three dimensions. , 2011, , .		5
38	A Well-Scaling Parallel Algorithm for the Computation of the Translation Operator in the MLFMA. IEEE Transactions on Antennas and Propagation, 2014, 62, 2679-2687.	5.1	5
39	An asynchronous parallel multilevel fast multipole algorithm. , 2007, , .		4
40	Simulation of a Luneburg Lens using a broadband Multilevel Fast Multipole Algorithm. Radio Science, 2011, 46, .	1.6	4
41	BLAMM: BLAS-based algorithm for finding position weight matrix occurrences in DNA sequences on CPUs and GPUs. BMC Bioinformatics, 2020, 21, 81.	2.6	4
42	Efficient uncertainty quantification of large two-dimensional optical systems with a parallelized stochastic Galerkin method. Optics Express, 2015, 23, 30833.	3.4	3
43	Dynamic partitioning of search patterns for approximate pattern matching using search schemes. IScience, 2021, 24, 102687.	4.1	3
44	Fast and accurate evaluation of enclosures with the method of moments by using splay trees. , 2007, , .		2
45	Towards Parallel Large-Scale Genomic Prediction by Coupling Sparse and Dense Matrix Algebra. , 2015, , .		2
46	Performance Analysis of a Parallel, Multi-node Pipeline for DNA Sequencing. Lecture Notes in Computer Science, 2016, , 233-242.	1.3	2
47	Accurate determination of node and arc multiplicities in de bruijn graphs using conditional random fields. BMC Bioinformatics, 2020, 21, 402.	2.6	2
48	Halvade somatic: Somatic variant calling with Apache Spark. GigaScience, 2022, 11, .	6.4	2
49	Swiss roll ensemble homogenization by fullâ€wave simulations. Microwave and Optical Technology Letters, 2011, 53, 2268-2274.	1.4	1
50	A Parallel, Distributed-Memory Framework for Comparative Motif Discovery. Lecture Notes in Computer Science, 2014, , 268-277.	1.3	1
51	Recent advances in fast multipole methods to simulate ever larger and more complex structures. , 2008, , .		0
52	A fully scalable, asynchronous parallel MLFMA. , 2008, , .		0
53	Scalability of the parallel MLFMA. Digest / IEEE Antennas and Propagation Society International Symposium, 2009, , .	0.0	0
54	Design of asynchronous and scalable MLFMA implementations. , 2010, , .		0

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55	Scalable parallel computation of the translation operator in three dimensions. , 2013, , .		0
56	Solving billions of unknowns using the parallel MLFMA and a Tier 1 supercomputer. , 2015, , .		0
57	Preconditioner for a scattering solver based on the intrusive stochastic galerkin method accelerated with MLFMM. , 2015, , .		0
58	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
59	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
60	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
61	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
62	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
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