

Jan Fostier

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7178706/publications.pdf>

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	Halvade somatic: Somatic variant calling with Apache Spark. GigaScience, 2022, 11, .	6.4	2
2	Multithreaded variant calling in elPrep 5. PLoS ONE, 2021, 16, e0244471.	2.5	9
3	Dynamic partitioning of search patterns for approximate pattern matching using search schemes. IScience, 2021, 24, 102687.	4.1	3
4	Deep scoping: a breeding strategy to preserve, reintroduce and exploit genetic variation. Theoretical and Applied Genetics, 2021, 134, 3845-3861.	3.6	6
5	GABAC: an arithmetic coding solution for genomic data. Bioinformatics, 2020, 36, 2275-2277.	4.1	6
6	Comparative analysis of somatic variant calling on matched FF and FFPE WGS samples. BMC Medical Genomics, 2020, 13, 94.	1.5	12
7	Computational assessment of the feasibility of protonation-based protein sequencing. PLoS ONE, 2020, 15, e0238625.	2.5	7
8	Accurate determination of node and arc multiplicities in de bruijn graphs using conditional random fields. BMC Bioinformatics, 2020, 21, 402.	2.6	2
9	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
10	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
11	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
12	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
13	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
14	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
15	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
16	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
17	Computational assessment of the feasibility of protonation-based protein sequencing. , 2020, 15, e0238625.		0
18	Illumina error correction near highly repetitive DNA regions improves de novo genome assembly. BMC Bioinformatics, 2019, 20, 298.	2.6	23

#	ARTICLE	IF	CITATIONS
19	elPrep 4: A multithreaded framework for sequence analysis. PLoS ONE, 2019, 14, e0209523.	2.5	17
20	Dynamical anchoring of distant arrhythmia sources by fibrotic regions via restructuring of the activation pattern. PLoS Computational Biology, 2018, 14, e1006637.	3.2	22
21	BrownieAligner: accurate alignment of Illumina sequencing data to de Bruijn graphs. BMC Bioinformatics, 2018, 19, 311.	2.6	22
22	OMSim: a simulator for optical map data. Bioinformatics, 2017, 33, 2740-2742.	4.1	14
23	Evaluation of the impact of Illumina error correction tools on de novo genome assembly. BMC Bioinformatics, 2017, 18, 374.	2.6	49
24	Halvade-RNA: Parallel variant calling from transcriptomic data using MapReduce. PLoS ONE, 2017, 12, e0174575.	2.5	17
25	Performance Analysis of a Parallel, Multi-node Pipeline for DNA Sequencing. Lecture Notes in Computer Science, 2016, , 233-242.	1.3	2
26	Jabba: hybrid error correction for long sequencing reads. Algorithms for Molecular Biology, 2016, 11, 10.	1.2	67
27	Needles: Toward Large-Scale Genomic Prediction with Marker-by-Environment Interaction. Genetics, 2016, 203, 543-555.	2.9	45
28	Solving billions of unknowns using the parallel MLFMA and a Tier 1 supercomputer. , 2015, , .		0
29	Efficient uncertainty quantification of large two-dimensional optical systems with a parallelized stochastic Galerkin method. Optics Express, 2015, 23, 30833.	3.4	3
30	elPrep: High-Performance Preparation of Sequence Alignment/Map Files for Variant Calling. PLoS ONE, 2015, 10, e0132868.	2.5	22
31	Pathway Relevance Ranking for Tumor Samples through Network-Based Data Integration. PLoS ONE, 2015, 10, e0133503.	2.5	24
32	Halvade: scalable sequence analysis with MapReduce. Bioinformatics, 2015, 31, 2482-2488.	4.1	69
33	BLSSpeller: exhaustive comparative discovery of conserved cis-regulatory elements. Bioinformatics, 2015, 31, 3758-3766.	4.1	14
34	Frequency-based haplotype reconstruction from deep sequencing data of bacterial populations. Nucleic Acids Research, 2015, 43, e105-e105.	14.5	45
35	Preconditioner for a scattering solver based on the intrusive stochastic galerkin method accelerated with MLFMM. , 2015, , .		0
36	Jabba: Hybrid Error Correction for Long Sequencing Reads Using Maximal Exact Matches. Lecture Notes in Computer Science, 2015, , 175-188.	1.3	9

#	ARTICLE	IF	CITATIONS
37	Towards Parallel Large-Scale Genomic Prediction by Coupling Sparse and Dense Matrix Algebra. , 2015, , .		2
38	Full-Wave Simulations of Electromagnetic Scattering Problems With Billions of Unknowns. IEEE Transactions on Antennas and Propagation, 2015, 63, 796-799.	5.1	43
39	In-memory, distributed content-based recommender system. Journal of Intelligent Information Systems, 2014, 42, 645-669.	3.9	18
40	DAIRRY-BLUP: A High-Performance Computing Approach to Genomic Prediction. Genetics, 2014, 197, 813-822.	2.9	6
41	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
42	A Parallel, Distributed-Memory Framework for Comparative Motif Discovery. Lecture Notes in Computer Science, 2014, , 268-277.	1.3	1
43	Weak Scalability Analysis of the Distributed-Memory Parallel MLFMA. IEEE Transactions on Antennas and Propagation, 2013, 61, 5567-5574.	5.1	19
44	EPSILON: an eQTL prioritization framework using similarity measures derived from local networks. Bioinformatics, 2013, 29, 1308-1316.	4.1	9
45	Scalable parallel computation of the translation operator in three dimensions. , 2013, , .		0
46	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
47	i-ADHoRe 3.0â€”fast and sensitive detection of genomic homology in extremely large data sets. Nucleic Acids Research, 2012, 40, e11-e11.	14.5	192
48	$O(1)$ Computation of Legendre Polynomials and Gauss-Legendre Nodes and Weights for Parallel Computing. SIAM Journal of Scientific Computing, 2012, 34, C83-C101.	2.8	38
49	Online execution time prediction for computationally intensive applications with periodic progress updates. Journal of Supercomputing, 2012, 62, 768-786.	3.6	7
50	Towards a scalable parallel MLFMA in three dimensions. , 2011, , .		5
51	Simulation of a Luneburg Lens using a broadband Multilevel Fast Multipole Algorithm. Radio Science, 2011, 46, .	1.6	4
52	A fast 2â€”D parallel multilevel fast multipole algorithm solver for oblique plane wave incidence. Radio Science, 2011, 46, .	1.6	9
53	Swiss roll ensemble homogenization by fullâ€”wave simulations. Microwave and Optical Technology Letters, 2011, 53, 2268-2274.	1.4	1
54	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. Bioinformatics, 2011, 27, 749-756.	4.1	24

#	ARTICLE	IF	CITATIONS
55	Design of asynchronous and scalable MLFMA implementations. , 2010, , .		0
56	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
57	Scalability of the parallel MLFMA. Digest / IEEE Antennas and Propagation Society International Symposium, 2009, , .	0.0	0
58	Full-wave electromagnetic scattering at extremely large 2-D objects. Electronics Letters, 2009, 45, 245.	1.0	17
59	An Asynchronous Parallel MLFMA for Scattering at Multiple Dielectric Objects. IEEE Transactions on Antennas and Propagation, 2008, 56, 2346-2355.	5.1	64
60	Accurate wideband evaluation of the shielding effectiveness of complex enclosures using an asynchronous parallel NSPWMLFMA. , 2008, , .		5
61	Recent advances in fast multipole methods to simulate ever larger and more complex structures. , 2008, , .		0
62	Provably scalable parallel multilevel fast multipole algorithm. Electronics Letters, 2008, 44, 1111.	1.0	26
63	A fully scalable, asynchronous parallel MLFMA. , 2008, , .		0
64	An asynchronous parallel multilevel fast multipole algorithm. , 2007, , .		4
65	Fast and accurate evaluation of enclosures with the method of moments by using splay trees. , 2007, , .		2