

Jan F Prins

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

2,329
citations

430874

18
h-index

580821

25
g-index

34
all docs

34
docs citations

34
times ranked

5306
citing authors

#	ARTICLE	IF	CITATIONS
1	NeoSplice: a bioinformatics method for prediction of splice variant neoantigens. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	13
2	Single-Cell Transcriptomic Analyses of Cell Fate Transitions during Human Cardiac Reprogramming. <i>Cell Stem Cell</i> , 2019, 25, 149-164.e9.	11.1	87
3	Single-cell transcriptomics reconstructs fate conversion from fibroblast to cardiomyocyte. <i>Nature</i> , 2017, 551, 100-104.	27.8	168
4	Performance and Scalability Study of FMM Kernels on Novel Multi- and Many-core Architectures. <i>Procedia Computer Science</i> , 2017, 108, 2313-2317.	2.0	1
5	Improving Energy Efficiency in Memory-constrained Applications Using Core-specific Power Control. , 2017, , .		7
6	An Adaptive Core-Specific Runtime for Energy Efficiency. , 2017, , .		18
7	MATCHER: manifold alignment reveals correspondence between single cell transcriptome and epigenome dynamics. <i>Genome Biology</i> , 2017, 18, 138.	8.8	131
8	REC: fast sparse regression-based multicategory classification. <i>Statistics and Its Interface</i> , 2017, 10, 175-185.	0.3	1
9	SLICER: inferring branched, nonlinear cellular trajectories from single cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 106.	8.8	155
10	Selective single cell isolation for genomics using microfluidic arrays. <i>Nucleic Acids Research</i> , 2016, 44, 8292-8301.	14.5	24
11	Asynchronous In Situ Connected-Components Analysis for Complex Fluid flows. , 2016, , .		2
12	Robust detection of alternative splicing in a population of single cells. <i>Nucleic Acids Research</i> , 2016, 44, e73-e73.	14.5	56
13	EnD-Seq and AppEnD: sequencing 3' ends to identify nontemplated tails and degradation intermediates. <i>Rna</i> , 2015, 21, 1375-1389.	3.5	22
14	Pseudogenes transcribed in breast invasive carcinoma show subtype-specific expression and ceRNA potential. <i>BMC Genomics</i> , 2015, 16, 113.	2.8	35
15	Deep Sequencing Shows Multiple Oligouridylations Are Required for 3' to 5' Degradation of Histone mRNAs on Polyribosomes. <i>Molecular Cell</i> , 2014, 53, 1020-1030.	9.7	53
16	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. <i>Genome Research</i> , 2014, 24, 241-250.	5.5	160
17	Petascale Application of a Coupled CPU-GPU Algorithm for Simulation and Analysis of Multiphase Flow Solutions in Porous Medium Systems. , 2014, , .		10
18	Cache-aware asymptotically-optimal sampling-based motion planning. , 2014, 2014, 5804-5810.		0

#	ARTICLE	IF	CITATIONS
19	Power Measurement and Concurrency Throttling for Energy Reduction in OpenMP Programs. , 2013, , .		37
20	A Robust Method for Transcript Quantification with RNA-Seq Data. Journal of Computational Biology, 2013, 20, 167-187.	1.6	13
21	Dynamic Load Balancing of the Adaptive Fast Multipole Method in Heterogeneous Systems. , 2013, , .		4
22	BlackOPS: increasing confidence in variant detection through mappability filtering. Nucleic Acids Research, 2013, 41, e178-e178.	14.5	19
23	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. Nucleic Acids Research, 2013, 41, e39-e39.	14.5	138
24	Characterizing and Mitigating Work Time Inflation in Task Parallel Programs. Scientific Programming, 2013, 21, 123-136.	0.7	1
25	OpenMP task scheduling strategies for multicore NUMA systems. International Journal of High Performance Computing Applications, 2012, 26, 110-124.	3.7	72
26	Characterizing and mitigating work time inflation in task parallel programs. , 2012, , .		25
27	A Robust Method for Transcript Quantification with RNA-seq Data. Lecture Notes in Computer Science, 2012, , 127-147.	1.3	1
28	RNA-Seq Expression Profiling of AML Stem Cells Reveals Differential Expression of Lineage Differentiation Markers and Novel Splice Variants.. Blood, 2012, 120, 2502-2502.	1.4	0
29	FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. Bioinformatics, 2011, 27, 2633-2640.	4.1	50
30	Comparison of OpenMP 3.0 and Other Task Parallel Frameworks on Unbalanced Task Graphs. International Journal of Parallel Programming, 2010, 38, 341-360.	1.5	34
31	A probabilistic framework for aligning paired-end RNA-seq data. Bioinformatics, 2010, 26, 1950-1957.	4.1	23
32	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. Nucleic Acids Research, 2010, 38, e178-e178.	14.5	946
33	Evaluating OpenMP 3.0 Run Time Systems on Unbalanced Task Graphs. Lecture Notes in Computer Science, 2009, , 63-78.	1.3	19
34	Irregular Computations in Fortran â€“ Expression and Implementation Strategies. Scientific Programming, 1999, 7, 313-326.	0.7	4