

Antti HÄÄKkinen

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

583
citations

687363

13
h-index

713466

21
g-index

47
all docs

47
docs citations

47
times ranked

447
citing authors

#	ARTICLE	IF	CITATIONS
1	POIBM: batch correction of heterogeneous RNA-seq datasets through latent sample matching. <i>Bioinformatics</i> , 2022, 38, 2474-2480.	4.1	3
2	QuantISH: RNA in situ hybridization image analysis framework for quantifying cell type-specific target RNA expression and variability. <i>Laboratory Investigation</i> , 2022, 102, 753-761.	3.7	3
3	Longitudinal single-cell RNA-seq analysis reveals stress-promoted chemoresistance in metastatic ovarian cancer. <i>Science Advances</i> , 2022, 8, eabm1831.	10.3	59
4	Agile workflow for interactive analysis of mass cytometry data. <i>Bioinformatics</i> , 2021, 37, 1263-1268.	4.1	8
5	Differential DNA methylation in recovery from shift work disorder. <i>Scientific Reports</i> , 2021, 11, 2895.	3.3	4
6	PRISM: recovering cell-type-specific expression profiles from individual composite RNA-seq samples. <i>Bioinformatics</i> , 2021, 37, 2882-2888.	4.1	17
7	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	13
8	qSNE: quadratic rate t-SNE optimizer with automatic parameter tuning for large datasets. <i>Bioinformatics</i> , 2020, 36, 5086-5092.	4.1	3
9	Anduril 2: upgraded large-scale data integration framework. <i>Bioinformatics</i> , 2019, 35, 3815-3817.	4.1	31
10	Transcription closed and open complex formation coordinate expression of genes with a shared promoter region. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190507.	3.4	4
11	Identifying differentially methylated sites in samples with varying tumor purity. <i>Bioinformatics</i> , 2018, 34, 3078-3085.	4.1	3
12	SCIP: a single-cell image processor toolbox. <i>Bioinformatics</i> , 2018, 34, 4318-4320.	4.1	5
13	iCellFusion. , 2017, , 806-834.		0
14	Dissecting the stochastic transcription initiation process in live <i>Escherichia coli</i> . <i>DNA Research</i> , 2016, 23, 203-214.	3.4	36
15	Increased cytoplasm viscosity hampers aggregate polar segregation in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2016, 99, 686-699.	2.5	21
16	Estimation of kinetic parameters of transcription from temporal single-RNA measurements. <i>Mathematical Biosciences</i> , 2016, 271, 146-153.	1.9	7
17	Characterizing rate limiting steps in transcription from RNA production times in live cells. <i>Bioinformatics</i> , 2016, 32, 1346-1352.	4.1	16
18	Temperature-Dependent Model of Multi-step Transcription Initiation in <i>Escherichia coli</i> Based on Live Single-Cell Measurements. <i>PLoS Computational Biology</i> , 2016, 12, e1005174.	3.2	33

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19	iCellFusion. Advances in Bioinformatics and Biomedical Engineering Book Series, 2016, , 71-99.	0.4	1
20	Estimation of GFP-tagged RNA numbers from temporal fluorescence intensity data. Bioinformatics, 2015, 31, 69-75.	4.1	14
21	Single-cell kinetics of a repressilator when implemented in a single-copy plasmid. Molecular BioSystems, 2015, 11, 1939-1945.	2.9	3
22	Estimation of fluorescence-tagged RNA numbers from spot intensities. Bioinformatics, 2014, 30, 1146-1153.	4.1	18
23	Effects of temperature on the dynamics of the LacI-TetR-CI repressilator. Molecular BioSystems, 2013, 9, 3117.	2.9	10
24	Effects of multimerization on the temporal variability of protein complex abundance. BMC Systems Biology, 2013, 7, S3.	3.0	5
25	CellAging: a tool to study segregation and partitioning in division in cell lineages of Escherichia coli. Bioinformatics, 2013, 29, 1708-1709.	4.1	34
26	Effects of Rate-Limiting Steps in Transcription Initiation on Genetic Filter Motifs. PLoS ONE, 2013, 8, e70439.	2.5	7
27	Asymmetric Disposal of Individual Protein Aggregates in Escherichia coli, One Aggregate at a Time. Journal of Bacteriology, 2012, 194, 1747-1752.	2.2	24
28	Effects of gene length on the dynamics of gene expression. Computational Biology and Chemistry, 2012, 41, 1-9.	2.3	3
29	Detecting sequence dependent transcriptional pauses from RNA and protein number time series. BMC Bioinformatics, 2012, 13, 152.	2.6	0
30	Evolving kinetics of gene expression in stochastic environments. Computational Biology and Chemistry, 2012, 37, 11-16.	2.3	1
31	Dynamics of transcription of closely spaced promoters in Escherichia coli, one event at a time. Journal of Theoretical Biology, 2012, 301, 83-94.	1.7	6
32	Genome wide study of NF-Y type CCAAT boxes in unidirectional and bidirectional promoters in human and mouse. Journal of Theoretical Biology, 2011, 281, 74-83.	1.7	11
33	In vivo kinetics of transcription initiation of the lar promoter in Escherichia coli. Evidence for a sequential mechanism with two rate-limiting steps. BMC Systems Biology, 2011, 5, 149.	3.0	32
34	Evolutionary Dynamics of a Population of Cells with a Toxin Suppressor Gene. Lecture Notes in Computer Science, 2011, , 1-12.	1.3	0
35	Dynamical effects of transcriptional pause-prone sites. Computational Biology and Chemistry, 2010, 34, 143-148.	2.3	14
36	Effects of Transcriptional Pausing on Gene Expression Dynamics. PLoS Computational Biology, 2010, 6, e1000704.	3.2	53

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37	Effects of the promoter open complex formation on gene expression dynamics. <i>Physical Review E</i> , 2010, 81, 011912.	2.1	20
38	Delayed Stochastic Model of Transcription at the Single Nucleotide Level. <i>Journal of Computational Biology</i> , 2009, 16, 539-553.	1.6	39
39	NF-Y influences directionality of transcription from the bidirectional <i>Mrps12/Sarsm</i> promoter in both mouse and human cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 432-442.	1.9	12
40	Quantifying local structure effects in network dynamics. <i>Physical Review E</i> , 2008, 78, 056108.	2.1	6
41	The transcription factor network of <i>E. coli</i> steers global responses to shifts in RNAP concentration. <i>Nucleic Acids Research</i> , 0, , .	14.5	2