

BÄrbel FinkenstÄdt

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,298
citations

516710

16
h-index

501196

28
g-index

32
all docs

32
docs citations

32
times ranked

1818
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Arabidopsis</i> Defense against <i>Botrytis cinerea</i> : Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis. <i>Plant Cell</i> , 2012, 24, 3530-3557.	6.6	337
2	Dynamic Analysis of Stochastic Transcription Cycles. <i>PLoS Biology</i> , 2011, 9, e1000607.	5.6	206
3	Bayesian inference of biochemical kinetic parameters using the linear noise approximation. <i>BMC Bioinformatics</i> , 2009, 10, 343.	2.6	97
4	Time-Series Transcriptomics Reveals That <i>AGAMOUS-LIKE22</i> Affects Primary Metabolism and Developmental Processes in Drought-Stressed <i>Arabidopsis</i> . <i>Plant Cell</i> , 2016, 28, 345-366.	6.6	92
5	Network balance <i>via</i> CRY signalling controls the <i>Arabidopsis</i> circadian clock over ambient temperatures. <i>Molecular Systems Biology</i> , 2013, 9, 650.	7.2	78
6	Reconstruction of transcriptional dynamics from gene reporter data using differential equations. <i>Bioinformatics</i> , 2008, 24, 2901-2907.	4.1	58
7	Bayesian inference for dynamic transcriptional regulation; the Hes1 system as a case study. <i>Bioinformatics</i> , 2007, 23, 2596-2603.	4.1	52
8	Inference on periodicity of circadian time series. <i>Biostatistics</i> , 2013, 14, 792-806.	1.5	50
9	Hidden Markov models for monitoring circadian rhythmicity in telemetric activity data. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170885.	3.4	43
10	Quantifying intrinsic and extrinsic noise in gene transcription using the linear noise approximation: An application to single cell data. <i>Annals of Applied Statistics</i> , 2013, 7, .	1.1	29
11	A stochastic transcriptional switch model for single cell imaging data. <i>Biostatistics</i> , 2015, 16, 655-669.	1.5	29
12	Bayesian inference on stochastic gene transcription from flow cytometry data. <i>Bioinformatics</i> , 2018, 34, i647-i655.	4.1	28
13	Relevance of a Mobile Internet Platform for Capturing Inter- and Intrasubject Variabilities in Circadian Coordination During Daily Routine: Pilot Study. <i>Journal of Medical Internet Research</i> , 2018, 20, e204.	4.3	26
14	Predictability of individual circadian phase during daily routine for medical applications of circadian clocks. <i>JCI Insight</i> , 2019, 4, .	5.0	25
15	Using a Single Fluorescent Reporter Gene to Infer Half-Life of Extrinsic Noise and Other Parameters of Gene Expression. <i>Biophysical Journal</i> , 2010, 98, 2759-2769.	0.5	22
16	Common structure in panels of short ecological time-series. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 2459-2467.	2.6	18
17	Filtering and inference for stochastic oscillators with distributed delays. <i>Bioinformatics</i> , 2019, 35, 1380-1387.	4.1	17
18	Tele-Monitoring of Cancer Patients' Rhythms during Daily Life Identifies Actionable Determinants of Circadian and Sleep Disruption. <i>Cancers</i> , 2020, 12, 1938.	3.7	17

#	ARTICLE	IF	CITATIONS
19	Scalable Bayesian Inference for Coupled Hidden Markov and Semi-Markov Models. Journal of Computational and Graphical Statistics, 2020, 29, 238-249.	1.7	16
20	A temporal switch model for estimating transcriptional activity in gene expression. Bioinformatics, 2013, 29, 1158-1165.	4.1	14
21	Asymmetry between Activation and Deactivation during a Transcriptional Pulse. Cell Systems, 2017, 5, 646-653.e5.	6.2	13
22	$3 \times 10^{-5} \times 10^2$ crosstalk contributes to transcriptional bursting. Genome Biology, 2021, 22, 56.	8.8	11
23	Telemonitored Human Circadian Temperature Dynamics During Daily Routine. Frontiers in Physiology, 2021, 12, 659973.	2.8	8
24	A hierarchical model of transcriptional dynamics allows robust estimation of transcription rates in populations of single cells with variable gene copy number. Bioinformatics, 2013, 29, 1519-1525.	4.1	6
25	Identifying the recurrence of sleep apnea using a harmonic hidden Markov model. Annals of Applied Statistics, 2021, 15, 1171-1193.	1.1	2
26	A spatio-temporal model to reveal oscillator phenotypes in molecular clocks: Parameter estimation elucidates circadian gene transcription dynamics in single-cells. PLoS Computational Biology, 2021, 17, e1009698.	3.2	2
27	ReTrOS: a MATLAB toolbox for reconstructing transcriptional activity from gene and protein expression data. BMC Bioinformatics, 2017, 18, 316.	2.6	1
28	Inferring transcriptional logic from multiple dynamic experiments. Bioinformatics, 2017, 33, 3437-3444.	4.1	1
29	Edgeworthian economies. Proceedings in Applied Mathematics and Mechanics, 2007, 7, 1041305-1041306.	0.2	0