

Noriko F Hiroi

List of Publications by Year in descending order

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52
papers

580
citations

759055

12
h-index

713332

21
g-index

60
all docs

60
docs citations

60
times ranked

999
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of Temperature Difference in Neuronal Cells. <i>Scientific Reports</i> , 2016, 6, 22071.	1.6	93
2	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
3	High-speed microscopy with an electrically tunable lens to image the dynamics of in vivo molecular complexes. <i>Review of Scientific Instruments</i> , 2015, 86, 013707.	0.6	45
4	Mammalian Rcd1 is a novel transcriptional cofactor that mediates retinoic acid-induced cell differentiation. <i>EMBO Journal</i> , 2002, 21, 5235-5244.	3.5	42
5	3D convolutional neural networks-based segmentation to acquire quantitative criteria of the nucleus during mouse embryogenesis. <i>Npj Systems Biology and Applications</i> , 2020, 6, 32.	1.4	30
6	A proteomic study of mitotic phase-specific interactors of EB1 reveals a role for SXIP-mediated protein interactions in anaphase onset. <i>Biology Open</i> , 2015, 4, 155-169.	0.6	29
7	The systems biology simulation core algorithm. <i>BMC Systems Biology</i> , 2013, 7, 55.	3.0	27
8	Automated tracking of mitotic spindle pole positions shows that LGN is required for spindle rotation but not orientation maintenance. <i>Cell Cycle</i> , 2013, 12, 2643-2655.	1.3	22
9	Comparative studies of suppression of malignant cancer cell phenotype by antisense oligo DNA and small interfering RNA. <i>Cancer Gene Therapy</i> , 2006, 13, 7-12.	2.2	15
10	LibSBMLSim: a reference implementation of fully functional SBML simulator. <i>Bioinformatics</i> , 2013, 29, 1474-1476.	1.8	15
11	Acceleration of discrete stochastic biochemical simulation using GPGPU. <i>Frontiers in Physiology</i> , 2015, 6, 42.	1.3	14
12	Transcriptome analysis of the anhydrobiotic cell line Pv11 infers the mechanism of desiccation tolerance and recovery. <i>Scientific Reports</i> , 2018, 8, 17941.	1.6	14
13	Predicting the future direction of cell movement with convolutional neural networks. <i>PLoS ONE</i> , 2019, 14, e0221245.	1.1	13
14	FPGA Implementation of a Data-Driven Stochastic Biochemical Simulator with the Next Reaction Method. , 2007, , .		12
15	Physiological environment induces quick response – slow exhaustion reactions. <i>Frontiers in Physiology</i> , 2011, 2, 50.	1.3	12
16	Identification of a master transcription factor and a regulatory mechanism for desiccation tolerance in the anhydrobiotic cell line Pv11. <i>PLoS ONE</i> , 2020, 15, e0230218.	1.1	11
17	Mathematical Modeling of Sustainable Synaptogenesis by Repetitive Stimuli Suggests Signaling Mechanisms In Vivo. <i>PLoS ONE</i> , 2012, 7, e51000.	1.1	10
18	ReCSiP: An FPGA-based general-purpose biochemical simulator. <i>Electronics and Communications in Japan</i> , 2007, 90, 1-10.	0.2	9

#	ARTICLE	IF	CITATIONS
19	An FPGA Implementation of High Throughput Stochastic Simulator for Large-Scale Biochemical Systems. , 2006, , .		8
20	Deduction of intracellular sub-systems from a topological description of the network. Molecular BioSystems, 2007, 3, 523.	2.9	8
21	Efficient scheduling of rate law functions for ODE-based multimodal biochemical simulation on an FPGA. , 0, , .		7
22	From microscopy data to in silico environments for in vivo-oriented simulations. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 7.	1.4	7
23	Fas-mediated apoptosis in Jurkat cells is suppressed in the pre-G2/M phase. Apoptosis: an International Journal on Programmed Cell Death, 1999, 4, 255-261.	2.2	5
24	Activation of cell migration via morphological changes in focal adhesions depends on shear stress in MYCN-amplified neuroblastoma cells. Journal of the Royal Society Interface, 2019, 16, 20180934.	1.5	5
25	Cellular thermogenesis compensates environmental temperature fluctuations for maintaining intracellular temperature. Biochemical and Biophysical Research Communications, 2020, 533, 70-76.	1.0	5
26	An FPGA-Based, Multi-model Simulation Method for Biochemical Systems. , 0, , .		4
27	Framework for ode-based multimodel biochemical simulations on an FPGA. , 0, , .		4
28	Performance Evaluation of an Fpga-Based Biochemical Simulator ReCSip. , 2006, , .		4
29	Practical implementation of a network-based stochastic biochemical simulation system on an FPGA. , 2008, , .		4
30	The design of scalable stochastic biochemical simulator on FPGA. , 0, , .		3
31	Editorial: Quantitative Biology: Dynamics of Living Systems. Frontiers in Physiology, 2016, 7, 196.	1.3	3
32	XitoSBML: A Modeling Tool for Creating Spatial Systems Biology Markup Language Models From Microscopic Images. Frontiers in Genetics, 2019, 10, 1027.	1.1	3
33	Neural Differentiation Dynamics Controlled by Multiple Feedback Loops in a Comprehensive Molecular Interaction Network. Processes, 2020, 8, 166.	1.3	3
34	Configuring area and performance: Empirical evaluation on an FPGA-based biochemical simulator. , 2009, , .		2
35	Automatic Pipeline Construction Focused on Similarity of Rate Law Functions for an FPGA-based Biochemical Simulator. IPSJ Transactions on System LSI Design Methodology, 2010, 3, 244-256.	0.5	2
36	Deep Learning for Non-Invasive Determination of the Differentiation Status of Human Neuronal Cells by Using Phase-Contrast Photomicrographs. Applied Sciences (Switzerland), 2019, 9, 5503.	1.3	2

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37	Kinetics of Dimension-Restricted Conditions. , 2007, , 261-281.		2
38	Pipeline Scheduling with Input Port Constraints for an FPGA-Based Biochemical Simulator. Lecture Notes in Computer Science, 2009, , 368-373.	1.0	2
39	Temperature elevation detection in migrating cells. , 2022, 1, 1085.		2
40	A Combining Technique of Rate Law Functions for a Cost-Effective Reconfigurable Biological Simulator. , 2007, , .		1
41	A Framework for Implementing a Network-Based Stochastic Biochemical Simulator on an FPGA. , 2007, , .		1
42	A Modular Approach to Heterogeneous Biochemical Model Simulation on an FPGA. , 2009, , .		1
43	In vivo oriented modeling with consideration of intracellular crowding. , 2013, 2013, 2716-9.		1
44	Assessing uncertainty in model parameters based on sparse and noisy experimental data. Frontiers in Physiology, 2014, 5, 128.	1.3	1
45	Quantitative analysis of sensitivity to a Wnt3a gradient in determination of the pole axis of mitotic cells by using a microfluidic device. FEBS Open Bio, 2018, 8, 1920-1935.	1.0	1
46	3P-239 Effect of molecular crowding on in vivo macromolecular reactions(Mathematical biology,The Tj ETQq0 0 0 ggBT /Overlock 10 Tf 0.0		0
47	A datapath classification method for FPGA-based scientific application accelerator systems. , 2010, , .		0
48	Physiological Intracellular Crowdedness is Defined by the Perimeter-to-Area Ratio of Sub-Cellular Compartments. Frontiers in Physiology, 2012, 3, 293.	1.3	0
49	Meeting report of the International Workshop on Quantitative Biology 2012: mesoscopic and microscopic worlds meet. Frontiers in Physiology, 2012, 3, 479.	1.3	0
50	Fabrication method to a high resolution control in the space of cell culturing environment with microfluidic system. , 2014, , .		0
51	Requirement of spatiotemporal resolution for imaging intracellular temperature distribution. , 2017, , .		0
52	Coarse grain parallelization and acceleration of biochemical ODE simulation using GPGPU. IEICE Proceeding Series, 2014, 1, 29-32.	0.0	0