Noriko F Hiroi

List of Publications by Year
in descending order

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	Temperature elevation detection in migrating cells. , 2022, 1, 1085.		2
2	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
3	Cellular thermogenesis compensates environmental temperature fluctuations for maintaining intracellular temperature. Biochemical and Biophysical Research Communications, 2020, 533, 70-76.	1.0	5
4	3D convolutional neural networks-based segmentation to acquire quantitative criteria of the nucleus during mouse embryogenesis. Npj Systems Biology and Applications, 2020, 6, 32.	1.4	30
5	Neural Differentiation Dynamics Controlled by Multiple Feedback Loops in a Comprehensive Molecular Interaction Network. Processes, 2020, 8, 166.	1.3	3
6	Identification of a master transcription factor and a regulatory mechanism for desiccation tolerance in the anhydrobiotic cell line Pv11. PLoS ONE, 2020, 15, e0230218.	1.1	11
7	Predicting the future direction of cell movement with convolutional neural networks. PLoS ONE, 2019, 14, e0221245.	1.1	13
8	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
9	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
10	XitoSBML: A Modeling Tool for Creating Spatial Systems Biology Markup Language Models From Microscopic Images. Frontiers in Genetics, 2019, 10, 1027.	1.1	3
11	Transcriptome analysis of the anhydrobiotic cell line Pv11 infers the mechanism of desiccation tolerance and recovery. Scientific Reports, 2018, 8, 17941.	1.6	14
12	Quantitative analysis of sensitivity to a Wnt3a gradient in determination of the pole–to–pole axis of mitotic cells by using a microfluidic device. FEBS Open Bio, 2018, 8, 1920-1935.	1.0	1
13	Requirement of spatiotemporal resolution for imaging intracellular temperature distribution. , 2017, , .		0
14	Editorial: Quantitative Biology: Dynamics of Living Systems. Frontiers in Physiology, 2016, 7, 196.	1.3	3
15	Detection of Temperature Difference in Neuronal Cells. Scientific Reports, 2016, 6, 22071.	1.6	93
16	High-speed microscopy with an electrically tunable lens to image the dynamics ofin vivomolecular complexes. Review of Scientific Instruments, 2015, 86, 013707.	0.6	45
17	A proteomic study of mitotic phase-specific interactors of EB1 reveals a role for SXIP-mediated protein interactions in anaphase onset. Biology Open, 2015, 4, 155-169.	0.6	29
18	Acceleration of discrete stochastic biochemical simulation using GPGPU. Frontiers in Physiology, 2015, 6, 42.	1.3	14

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19	Assessing uncertainty in model parameters based on sparse and noisy experimental data. Frontiers in Physiology, 2014, 5, 128.	1.3	1
20	Fabrication method to a high resolution control in the space of cell culturing environment with microfluidic system. , 2014, , .		0
21	Coarse grain parallelization and acceleration of biochemical ODE simulation using GPGPU. IEICE Proceeding Series, 2014, 1, 29-32.	0.0	0
22	The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55.	3.0	27
23	Automated tracking of mitotic spindle pole positions shows that LGN is required for spindle rotation but not orientation maintenance. Cell Cycle, 2013, 12, 2643-2655.	1.3	22
24	LibSBMLSim: a reference implementation of fully functional SBML simulator. Bioinformatics, 2013, 29, 1474-1476.	1.8	15
25	In vivo oriented modeling with consideration of intracellular crowding. , 2013, 2013, 2716-9.		1
26	Physiological Intracellular Crowdedness is Defined by the Perimeter-to-Area Ratio of Sub-Cellular Compartments. Frontiers in Physiology, 2012, 3, 293.	1.3	0
27	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
28	Mathematical Modeling of Sustainable Synaptogenesis by Repetitive Stimuli Suggests Signaling Mechanisms In Vivo. PLoS ONE, 2012, 7, e51000.	1.1	10
29	Meeting report of the International Workshop on Quantitative Biology 2012: mesoscopic and microscopic worlds meet. Frontiers in Physiology, 2012, 3, 479.	1.3	0
30	Physiological environment induces quick response â€" slow exhaustion reactions. Frontiers in Physiology, 2011, 2, 50.	1.3	12
31	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
32	A datapath classification method for FPGA-based scientific application accelerator systems. , 2010, , .		0
33	A Modular Approach to Heterogeneous Biochemical Model Simulation on an FPGA. , 2009, , .		1
34	Configuring area and performance: Empirical evaluation on an FPGA-based biochemical simulator. , 2009, , .		2
35	3P-239 Effect of molecular crowding on in vivo macromolecular reactions(Mathematical biology,The) Tj ETQq1 1 0.784314 rgBT /Ove	0.0	0
36	Pipeline Scheduling with Input Port Constraints for an FPGA-Based Biochemical Simulator. Lecture Notes in Computer Science, 2009, , 368-373.	1.0	2

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37	Practical implementation of a network-based stochastic biochemical simulation system on an FPGA. , 2008, , .		4
38	A Combining Technique of Rate Law Functions for a Cost-Effective Reconfigurable Biological Simulator. , 2007, , .		1
39	A Framework for Implementing a Network-Based Stochastic Biochemical Simulator on an FPGA. , 2007, , .		1
40	FPGA Implementation of a Data-Driven Stochastic Biochemical Simulator with the Next Reaction Method. , 2007, , .		12
41	Deduction of intracellular sub-systems from a topological description of the network. Molecular BioSystems, 2007, 3, 523.	2.9	8
42	ReCSiP: An FPGA-based general-purpose biochemical simulator. Electronics and Communications in Japan, 2007, 90, 1-10.	0.2	9
43	Kinetics of Dimension-Restricted Conditions. , 2007, , 261-281.		2
44	Performance Evaluation of an Fpga-Based Biochemical Simulator ReCSip. , 2006, , .		4
45	Comparative studies of suppression of malignant cancer cell phenotype by antisense oligo DNA and small interfering RNA. Cancer Gene Therapy, 2006, 13, 7-12.	2.2	15
46	An FPGA Implementation of High Throughput Stochastic Simulator for Large-Scale Biochemical Systems. , 2006, , .		8
47	Mammalian Rcd1 is a novel transcriptional cofactor that mediates retinoic acid-induced cell differentiation. EMBO Journal, 2002, 21, 5235-5244.	3.5	42
48	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
49	An FPGA-Based, Multi-model Simulation Method for Biochemical Systems. , 0, , .		4
50	Efficient scheduling of rate law functions for ODE-based multimodal biochemical simulation on an FPGA. , 0, , .		7
51	The design of scalable stochastic biochemical simulator on FPGA. , 0, , .		3
52	Framework for ode-based multimodel biochemical simulations on an FPGA. , 0, , .		4