Akira Funahashi

List of Publications by Year
in descending order

85 papers	4,605 citations	361045 20 h-index	174990 52 g-index
101 all docs	101 docs citations	101 times ranked	5623 citing authors

#	Article	IF	Citations
1	High quality genome assembly of the anhydrobiotic midge provides insights on a single chromosome-based emergence of extreme desiccation tolerance. NAR Genomics and Bioinformatics, 2022, 4, lqac029.	1.5	6
2	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
3	Temperature elevation detection in migrating cells. , 2022, 1, 1085.		2
4	Symbolic Integration by Integrating Learning Models With Different Strengths and Weaknesses. IEEE Access, 2022, 10, 47000-47010.	2.6	1
5	Electrical Field Chamber with Dinamically Adaptable Stimuli for Myocyte Orientation During Cultivation. , 2021, , .		0
6	Genome-Wide Role of HSF1 in Transcriptional Regulation of Desiccation Tolerance in the Anhydrobiotic Cell Line, Pv11. International Journal of Molecular Sciences, 2021, 22, 5798.	1.8	6
7	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
8	SBMLWebApp: Web-Based Simulation, Steady-State Analysis, and Parameter Estimation of Systems Biology Models. Processes, 2021, 9, 1830.	1.3	0
9	Cas9-mediated genome editing reveals a significant contribution of calcium signaling pathways to anhydrobiosis in Pv11 cells. Scientific Reports, 2021, 11, 19698.	1.6	5
10	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
11	Direct Cell Counting Using Macro-Scale Smartphone Images of Cell Aggregates. IEEE Access, 2020, 8, 170033-170043.	2.6	5
12	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
13	Neural Differentiation Dynamics Controlled by Multiple Feedback Loops in a Comprehensive Molecular Interaction Network. Processes, 2020, 8, 166.	1.3	3
14	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
15	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
16	Title is missing!. , 2020, 15, e0230218.		0
17	Title is missing!. , 2020, 15, e0230218.		0
18	Title is missing!. , 2020, 15, e0230218.		0

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19	Title is missing!. , 2020, 15, e0230218.		0
20	Predicting the future direction of cell movement with convolutional neural networks. PLoS ONE, 2019, 14, e0221245.	1.1	13
21	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
22	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
23	XitoSBML: A Modeling Tool for Creating Spatial Systems Biology Markup Language Models From Microscopic Images. Frontiers in Genetics, 2019, 10, 1027.	1.1	3
24	Transcriptome analysis of the anhydrobiotic cell line Pv11 infers the mechanism of desiccation tolerance and recovery. Scientific Reports, 2018, 8, 17941.	1.6	14
25	Quantitative analysis of sensitivity to a Wnt3a gradient in determination of the poleâ€toâ€pole axis of mitotic cells by using a microfluidic device. FEBS Open Bio, 2018, 8, 1920-1935.	1.0	1
26	Requirement of spatiotemporal resolution for imaging intracellular temperature distribution. , 2017, , .		0
27	Editorial: Quantitative Biology: Dynamics of Living Systems. Frontiers in Physiology, 2016, 7, 196.	1.3	3
28	Detection of Temperature Difference in Neuronal Cells. Scientific Reports, 2016, 6, 22071.	1.6	93
29	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
30	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
31	Acceleration of discrete stochastic biochemical simulation using GPGPU. Frontiers in Physiology, 2015, 6, 42.	1.3	14
32	The principles of whole-cell modeling. Current Opinion in Microbiology, 2015, 27, 18-24.	2.3	66
33	Assessing uncertainty in model parameters based on sparse and noisy experimental data. Frontiers in Physiology, 2014, 5, 128.	1.3	1
34	Fabrication method to a high resolution control in the space of cell culturing environment with microfluidic system. , 2014, , .		0
35	Modeling and Simulation Using CellDesigner. Methods in Molecular Biology, 2014, 1164, 121-145.	0.4	60
36	Coarse grain parallelization and acceleration of biochemical ODE simulation using GPGPU. IEICE Proceeding Series, 2014, 1, 29-32.	0.0	0

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37	The systems biology simulation core algorithm. BMC Systems Biology, 2013, 7, 55.	3.0	27
38	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
39	LibSBMLSim: a reference implementation of fully functional SBML simulator. Bioinformatics, 2013, 29, 1474-1476.	1.8	15
40	In vivo oriented modeling with consideration of intracellular crowding. , 2013, 2013, 2716-9.		1
41	Physiological Intracellular Crowdedness is Defined by the Perimeter-to-Area Ratio of Sub-Cellular Compartments. Frontiers in Physiology, 2012, 3, 293.	1.3	0
42	Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021.	1.8	74
43	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
44	Mathematical Modeling of Sustainable Synaptogenesis by Repetitive Stimuli Suggests Signaling Mechanisms In Vivo. PLoS ONE, 2012, 7, e51000.	1.1	10
45	Meeting report of the International Workshop on Quantitative Biology 2012: mesoscopic and microscopic worlds meet. Frontiers in Physiology, 2012, 3, 479.	1.3	0
46	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	1.8	18
47	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2011, , .	0.1	0
48	Physiological environment induces quick response â€" slow exhaustion reactions. Frontiers in Physiology, 2011, 2, 50.	1.3	12
49	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
50	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	0.9	31
51	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2010, , .	0.1	0
52	A datapath classification method for FPGA-based scientific application accelerator systems. , 2010, , .		0
53	A Modular Approach to Heterogeneous Biochemical Model Simulation on an FPGA. , 2009, , .		1
54	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828

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55	Configuring area and performance: Empirical evaluation on an FPGA-based biochemical simulator. , 2009, , .		2
56	3P-239 Effect of molecular crowding on in vivo macromolecular reactions(Mathematical biology,The) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.0	0
57	Pipeline Scheduling with Input Port Constraints for an FPGA-Based Biochemical Simulator. Lecture Notes in Computer Science, 2009, , 368-373.	1.0	2
58	CellDesigner 3.5: A Versatile Modeling Tool for Biochemical Networks. Proceedings of the IEEE, 2008, 96, 1254-1265.	16.4	380
59	Practical implementation of a network-based stochastic biochemical simulation system on an FPGA. , 2008, , .		4
60	A Combining Technique of Rate Law Functions for a Cost-Effective Reconfigurable Biological Simulator. , 2007, , .		1
61	A Framework for Implementing a Network-Based Stochastic Biochemical Simulator on an FPGA. , 2007, , .		1
62	FPGA Implementation of a Data-Driven Stochastic Biochemical Simulator with the Next Reaction Method. , 2007, , .		12
63	Deduction of intracellular sub-systems from a topological description of the network. Molecular BioSystems, 2007, 3, 523.	2.9	8
64	ReCSiP: An FPGA-based general-purpose biochemical simulator. Electronics and Communications in Japan, 2007, 90, 1-10.	0.2	9
65	Kinetics of Dimension-Restricted Conditions. , 2007, , 261-281.		2
66	SBML Models and MathSBML. , 2007, , 395-421.		3
67	CellDesigner: A Graphical Biological Network Editor and Workbench Interfacing Simulator. , 2007, , 422-434.		25
68	Integration of CellDesigner and SABIO-RK. In Silico Biology, 2007, 7, S81-90.	0.4	47
69	Performance Evaluation of an Fpga-Based Biochemical Simulator ReCSip. , 2006, , .		4
70	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
71	An FPGA Implementation of High Throughput Stochastic Simulator for Large-Scale Biochemical Systems. , 2006, , .		8
72	Celldesigner: A Modeling Tool for Biochemical Networks. , 2006, , .		19

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73	Software Infrastructure for Effective Communication and Reuse of Computational Models. , 2006, , 355-378.		9
74	Using process diagrams for the graphical representation of biological networks. Nature Biotechnology, 2005, 23, 961-966.	9.4	429
75	A comprehensive pathway map of epidermal growth factor receptor signaling. Molecular Systems Biology, 2005, 1, 2005.0010.	3.2	902
76	Evolving a lingua franca and associated software infrastructure for computational systems biology: the Systems Biology Markup Language (SBML) project. IET Systems Biology, 2004, 1, 41-53.	2.0	187
77	CellDesigner: a process diagram editor for gene-regulatory and biochemical networks. Biosilico, 2003, 1, 159-162.	0.5	562
78	Recursive diagonal torus: an interconnection network for massively parallel computers. IEEE Transactions on Parallel and Distributed Systems, 2001, 12, 701-715.	4.0	54
79	L-turn routing: an adaptive routing in irregular networks. , 2001, , .		48
80	Adaptive routing on the Recursive Diagonal Torus. Lecture Notes in Computer Science, 1997, , 171-182.	1.0	2
81	Routing algorithms based on 2D turn model for irregular networks. , 0, , .		7
82	An FPGA-Based, Multi-model Simulation Method for Biochemical Systems. , 0, , .		4
83	Efficient scheduling of rate law functions for ODE-based multimodal biochemical simulation on an FPGA. , 0, , .		7
84	The design of scalable stochastic biochemical simulator on FPGA. , 0, , .		3
85	Framework for ode-based multimodel biochemical simulations on an FPGA. , 0, , .		4