

Akira Funahashi

List of Publications by Year in descending order

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Version: 2024-02-01

85
papers

4,605
citations

361296

20
h-index

175177

52
g-index

101
all docs

101
docs citations

101
times ranked

5623
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive pathway map of epidermal growth factor receptor signaling. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0010.	3.2	902
2	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	9.4	828
3	CellDesigner: a process diagram editor for gene-regulatory and biochemical networks. <i>Biosilico</i> , 2003, 1, 159-162.	0.5	562
4	Using process diagrams for the graphical representation of biological networks. <i>Nature Biotechnology</i> , 2005, 23, 961-966.	9.4	429
5	CellDesigner 3.5: A Versatile Modeling Tool for Biochemical Networks. <i>Proceedings of the IEEE</i> , 2008, 96, 1254-1265.	16.4	380
6	Evolving a lingua franca and associated software infrastructure for computational systems biology: the Systems Biology Markup Language (SBML) project. <i>IET Systems Biology</i> , 2004, 1, 41-53.	2.0	187
7	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	3.2	178
8	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	2.4	99
9	Detection of Temperature Difference in Neuronal Cells. <i>Scientific Reports</i> , 2016, 6, 22071.	1.6	93
10	Software support for SBGN maps: SBGN-ML and LibSBGN. <i>Bioinformatics</i> , 2012, 28, 2016-2021.	1.8	74
11	The principles of whole-cell modeling. <i>Current Opinion in Microbiology</i> , 2015, 27, 18-24.	2.3	66
12	Modeling and Simulation Using CellDesigner. <i>Methods in Molecular Biology</i> , 2014, 1164, 121-145.	0.4	60
13	Recursive diagonal torus: an interconnection network for massively parallel computers. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2001, 12, 701-715.	4.0	54
14	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
15	L-turn routing: an adaptive routing in irregular networks. , 2001, , .		48
16	Integration of CellDesigner and SABIO-RK. <i>In Silico Biology</i> , 2007, 7, S81-90.	0.4	47
17	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
18	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. <i>Journal of Biomedical Semantics</i> , 2010, 1, 8.	0.9	31

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19	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
20	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
21	The systems biology simulation core algorithm. <i>BMC Systems Biology</i> , 2013, 7, 55.	3.0	27
22	CellDesigner: A Graphical Biological Network Editor and Workbench Interfacing Simulator. , 2007, , 422-434.		25
23	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
24	CellDesigner: A Modeling Tool for Biochemical Networks. , 2006, , .		19
25	BioPAX support in CellDesigner. <i>Bioinformatics</i> , 2011, 27, 3437-3438.	1.8	18
26	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
27	LibSBMLSim: a reference implementation of fully functional SBML simulator. <i>Bioinformatics</i> , 2013, 29, 1474-1476.	1.8	15
28	Acceleration of discrete stochastic biochemical simulation using GPGPU. <i>Frontiers in Physiology</i> , 2015, 6, 42.	1.3	14
29	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
30	Predicting the future direction of cell movement with convolutional neural networks. <i>PLoS ONE</i> , 2019, 14, e0221245.	1.1	13
31	FPGA Implementation of a Data-Driven Stochastic Biochemical Simulator with the Next Reaction Method. , 2007, , .		12
32	Physiological environment induces quick response “slow exhaustion reactions. <i>Frontiers in Physiology</i> , 2011, 2, 50.	1.3	12
33	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
34	BioSimulators: a central registry of simulation engines and services for recommending specific tools. <i>Nucleic Acids Research</i> , 2022, 50, W108-W114.	6.5	11
35	Mathematical Modeling of Sustainable Synaptogenesis by Repetitive Stimuli Suggests Signaling Mechanisms In Vivo. <i>PLoS ONE</i> , 2012, 7, e51000.	1.1	10
36	ReCSiP: An FPGA-based general-purpose biochemical simulator. <i>Electronics and Communications in Japan</i> , 2007, 90, 1-10.	0.2	9

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37	Software Infrastructure for Effective Communication and Reuse of Computational Models. , 2006, , 355-378.		9
38	An FPGA Implementation of High Throughput Stochastic Simulator for Large-Scale Biochemical Systems. , 2006, , .		8
39	Deduction of intracellular sub-systems from a topological description of the network. Molecular BioSystems, 2007, 3, 523.	2.9	8
40	Routing algorithms based on 2D turn model for irregular networks. , 0, , .		7
41	Efficient scheduling of rate law functions for ODE-based multimodal biochemical simulation on an FPGA. , 0, , .		7
42	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
43	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
44	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, 19698.	1.5	6
45	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
46	Direct Cell Counting Using Macro-Scale Smartphone Images of Cell Aggregates. IEEE Access, 2020, 8, 170033-170043.	2.6	5
47	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
48	An FPGA-Based, Multi-model Simulation Method for Biochemical Systems. , 0, , .		4
49	Framework for ode-based multimodel biochemical simulations on an FPGA. , 0, , .		4
50	Performance Evaluation of an Fpga-Based Biochemical Simulator ReCSip. , 2006, , .		4
51	Practical implementation of a network-based stochastic biochemical simulation system on an FPGA. , 2008, , .		4
52	The design of scalable stochastic biochemical simulator on FPGA. , 0, , .		3
53	Editorial: Quantitative Biology: Dynamics of Living Systems. Frontiers in Physiology, 2016, 7, 196.	1.3	3
54	XitoSBML: A Modeling Tool for Creating Spatial Systems Biology Markup Language Models From Microscopic Images. Frontiers in Genetics, 2019, 10, 1027.	1.1	3

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55	Neural Differentiation Dynamics Controlled by Multiple Feedback Loops in a Comprehensive Molecular Interaction Network. <i>Processes</i> , 2020, 8, 166.	1.3	3
56	SBML Models and MathSBML. , 2007, , 395-421.		3
57	Adaptive routing on the Recursive Diagonal Torus. <i>Lecture Notes in Computer Science</i> , 1997, , 171-182.	1.0	2
58	Configuring area and performance: Empirical evaluation on an FPGA-based biochemical simulator. , 2009, , .		2
59	Automatic Pipeline Construction Focused on Similarity of Rate Law Functions for an FPGA-based Biochemical Simulator. <i>IPSI Transactions on System LSI Design Methodology</i> , 2010, 3, 244-256.	0.5	2
60	Deep Learning for Non-Invasive Determination of the Differentiation Status of Human Neuronal Cells by Using Phase-Contrast Photomicrographs. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 5503.	1.3	2
61	Kinetics of Dimension-Restricted Conditions. , 2007, , 261-281.		2
62	Pipeline Scheduling with Input Port Constraints for an FPGA-Based Biochemical Simulator. <i>Lecture Notes in Computer Science</i> , 2009, , 368-373.	1.0	2
63	Temperature elevation detection in migrating cells. , 2022, 1, 1085.		2
64	A Combining Technique of Rate Law Functions for a Cost-Effective Reconfigurable Biological Simulator. , 2007, , .		1
65	A Framework for Implementing a Network-Based Stochastic Biochemical Simulator on an FPGA. , 2007, , .		1
66	A Modular Approach to Heterogeneous Biochemical Model Simulation on an FPGA. , 2009, , .		1
67	In vivo oriented modeling with consideration of intracellular crowding. , 2013, 2013, 2716-9.		1
68	Assessing uncertainty in model parameters based on sparse and noisy experimental data. <i>Frontiers in Physiology</i> , 2014, 5, 128.	1.3	1
69	Quantitative analysis of sensitivity to a Wnt3a gradient in determination of the pole axis of mitotic cells by using a microfluidic device. <i>FEBS Open Bio</i> , 2018, 8, 1920-1935.	1.0	1
70	Symbolic Integration by Integrating Learning Models With Different Strengths and Weaknesses. <i>IEEE Access</i> , 2022, 10, 47000-47010.	2.6	1
71	3P-239 Effect of molecular crowding on in vivo macromolecular reactions(Mathematical biology,The) Tj ETQq1 1 0.784314 rgBT /Over to	0.0	0
72	LibSBGN: Electronic Processing of SBGN maps. <i>Nature Precedings</i> , 2010, , .	0.1	0

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73	A datapath classification method for FPGA-based scientific application accelerator systems. , 2010, , .		0
74	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2011, , .	0.1	0
75	Physiological Intracellular Crowdedness is Defined by the Perimeter-to-Area Ratio of Sub-Cellular Compartments. Frontiers in Physiology, 2012, 3, 293.	1.3	0
76	Meeting report of the International Workshop on Quantitative Biology 2012: mesoscopic and microscopic worlds meet. Frontiers in Physiology, 2012, 3, 479.	1.3	0
77	Fabrication method to a high resolution control in the space of cell culturing environment with microfluidic system. , 2014, , .		0
78	Requirement of spatiotemporal resolution for imaging intracellular temperature distribution. , 2017, , .		0
79	Electrical Field Chamber with Dinamically Adaptable Stimuli for Myocyte Orientation During Cultivation. , 2021, , .		0
80	SBMLWebApp: Web-Based Simulation, Steady-State Analysis, and Parameter Estimation of Systems Biology Models. Processes, 2021, 9, 1830.	1.3	0
81	Coarse grain parallelization and acceleration of biochemical ODE simulation using GPGPU. IEICE Proceeding Series, 2014, 1, 29-32.	0.0	0
82	Title is missing!. , 2020, 15, e0230218.		0
83	Title is missing!. , 2020, 15, e0230218.		0
84	Title is missing!. , 2020, 15, e0230218.		0
85	Title is missing!. , 2020, 15, e0230218.		0