Hiroaki Kitano

List of Publications by Year in descending order

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138 papers 20,009 citations

53 h-index 131 g-index

145 all docs 145
docs citations

145 times ranked 21031 citing authors

#	Article	IF	CITATIONS
1	Toxicity Analysis of Pentachlorophenol Data with a Bioinformatics Tool Set. Methods in Molecular Biology, 2022, 2486, 105-125.	0.4	1
2	Effects of maoto (ma-huang-tang) on host lipid mediator and transcriptome signature in influenza virus infection. Scientific Reports, 2021, 11, 4232.	1.6	5
3	Artificial intelligence-based computational framework for drug-target prioritization and inference of novel repositionable drugs for Alzheimer's disease. Alzheimer's Research and Therapy, 2021, 13, 92.	3.0	29
4	Nobel Turing Challenge: creating the engine for scientific discovery. Npj Systems Biology and Applications, 2021, 7, 29.	1.4	31
5	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
6	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
7	A Geometric Clustering Tool (AGCT) to robustly unravel the inner cluster structures of time-series gene expressions. PLoS ONE, 2020, 15, e0233755.	1.1	3
8	<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
9	Lenvatinib plus anti-PD-1 antibody combination treatment activates CD8+ T cells through reduction of tumor-associated macrophage and activation of the interferon pathway. PLoS ONE, 2019, 14, e0212513.	1.1	294
10	Integrative and theoretical research on the architecture of a biological system and its disorder. Journal of Physiological Sciences, 2019, 69, 433-451.	0.9	1
11	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	1.6	15
12	Multi-dimensional computational pipeline for large-scale deep screening of compound effect assessment: an in silico case study on ageing-related compounds. Npj Systems Biology and Applications, 2019, 5, 42.	1.4	3
13	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. Cell Reports, 2017, 18, 3219-3226.	2.9	28
14	Biological Complexity and the Need for Computational Approaches. History, Philosophy and Theory of the Life Sciences, 2017, , 169-180.	0.4	2
15	Deconstructing the traditional Japanese medicine "Kampo― compounds, metabolites and pharmacological profile of maoto, a remedy for flu-like symptoms. Npj Systems Biology and Applications, 2017, 3, 32.	1.4	25
16	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. Progress in Preventive Medicine (New York, N Y), 2017, 2, e006.	0.7	6
17	Artificial Intelligence to Win the Nobel Prize and Beyond: Creating the Engine for Scientific Discovery. Al Magazine, 2016, 37, 39-49.	1.4	79
18	A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. BMC Genomics, 2016, 17, 1025.	1.2	35

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19	Weighted enrichment method for prediction of transcription regulators from transcriptome and global chromatin immunoprecipitation data. Nucleic Acids Research, 2016, 44, 5010-5021.	6.5	31
20	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. Current Biology, 2016, 26, 3190-3194.	1.8	79
21	Network analyses based on comprehensive molecular interaction maps reveal robust control structures in yeast stress response pathways. Npj Systems Biology and Applications, 2016, 2, 15018.	1.4	27
22	Versatile Modeling Platform for Multilevel Hybrid Modeling of Physiological Systems. Seibutsu Butsuri, 2016, 56, 120-124.	0.0	0
23	systemsDock: a web server for network pharmacology-based prediction and analysis. Nucleic Acids Research, 2016, 44, W507-W513.	6.5	135
24	Digital health revolution: perfect storm or perfect opportunity for pharmaceutical R&D?. Drug Discovery Today, 2016, 21, 900-911.	3.2	42
25	Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. Scientific Reports, 2015, 5, 17209.	1.6	33
26	Elucidation of the molecular mechanisms underlying adverse reactions associated with a kinase inhibitor using systems toxicology. Npj Systems Biology and Applications, 2015, 1, 15005.	1.4	16
27	Accelerating systems biology research and its real world deployment. Npj Systems Biology and Applications, 2015, 1, 15009.	1.4	4
28	Lessons from Toxicology: Developing a 21st-Century Paradigm for Medical Research. Environmental Health Perspectives, 2015, 123, A268-72.	2.8	57
29	An Ultrasensitive Mechanism Regulates Influenza Virus-Induced Inflammation. PLoS Pathogens, 2015, 11, e1004856.	2.1	32
30	Identifying problematic drugs based on the characteristics of their targets. Frontiers in Pharmacology, 2015, 6, 186.	1.6	11
31	Databases for multilevel biophysiology research available at Physiome.jp. Frontiers in Physiology, 2015, 6, 251.	1.3	7
32	VISIONET: intuitive visualisation of overlapping transcription factor networks, with applications in cardiogenic gene discovery. BMC Bioinformatics, 2015, 16, 141.	1.2	6
33	Oscillation of cAMP and Ca2+ in cardiac myocytes: a systems biology approach. Journal of Physiological Sciences, 2015, 65, 195-200.	0.9	15
34	Multi-spectral fluorescent reporter influenza viruses (Color-flu) as powerful tools for in vivo studies. Nature Communications, 2015, 6, 6600.	5.8	98
35	CARFMAP: A Curated Pathway Map of Cardiac Fibroblasts. PLoS ONE, 2015, 10, e0143274.	1.1	19
36	Software Platform for Systems Biology. Drug Delivery System, 2014, 29, 386-396.	0.0	0

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37	A Versatile Platform for Multilevel Modeling of Physiological Systems: SBML-PHML Hybrid Modeling and Simulation. Advanced Biomedical Engineering, 2014, 3, 50-58.	0.4	15
38	Identification of drug-target modules in the human protein–protein interaction network. Artificial Life and Robotics, 2014, 19, 406-413.	0.7	4
39	Influenza Virus-Host Interactome Screen as a Platform for Antiviral Drug Development. Cell Host and Microbe, 2014, 16, 795-805.	5.1	239
40	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. Molecular Neurobiology, 2014, 49, 88-102.	1.9	231
41	Integrative knowledge management to enhance pharmaceutical R&D. Nature Reviews Drug Discovery, 2014, 13, 239-240.	21.5	12
42	Accelerating ODE-Based Simulation of General and Heterogeneous Biophysical Models Using a GPU. IEEE Transactions on Parallel and Distributed Systems, 2014, 25, 1966-1975.	4.0	7
43	Disease Severity Is Associated with Differential Gene Expression at the Early and Late Phases of Infection in Nonhuman Primates Infected with Different H5N1 Highly Pathogenic Avian Influenza Viruses. Journal of Virology, 2014, 88, 8981-8997.	1.5	45
44	Modeling and Simulation Using CellDesigner. Methods in Molecular Biology, 2014, 1164, 121-145.	0.4	60
45	A comprehensive map of the influenza A virus replication cycle. BMC Systems Biology, 2013, 7, 97.	3.0	97
46	Toward an integrated software platform for systems pharmacology. Biopharmaceutics and Drug Disposition, 2013, 34, 508-526.	1.1	18
47	Cancer Systems Biology. , 2013, , 469-479.		0
48	Software Platform for Metabolic Network Reconstruction of Mycobacterium tuberculosis. , 2013, , 21-35.		1
49	Identification of dosage-sensitive genes in <i>Saccharomyces cerevisiae</i> using the genetic tug-of-war method. Genome Research, 2013, 23, 300-311.	2.4	125
50	Adding Protein Context to the Human Protein-Protein Interaction Network to Reveal Meaningful Interactions. PLoS Computational Biology, 2013, 9, e1002860.	1.5	70
51	Harnessing Diversity towards the Reconstructing of Large Scale Gene Regulatory Networks. PLoS Computational Biology, 2013, 9, e1003361.	1.5	32
52	Parallel Real-Time PCR on a Chip for Genetic Tug-of-War (gTOW) Method. Analytical Sciences, 2013, 29, 367-371.	0.8	2
53	Modeling of Rifampicin-Induced CYP3A4 Activation Dynamics for the Prediction of Clinical Drug-Drug Interactions from In Vitro Data. PLoS ONE, 2013, 8, e70330.	1.1	78
54	Combining Machine Learning Systems and Multiple Docking Simulation Packages to Improve Docking Prediction Reliability for Network Pharmacology. PLoS ONE, 2013, 8, e83922.	1.1	268

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55	Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021.	1.8	74
56	Multilevel Modeling of Physiological Systems and Simulation Platform: PhysioDesigner, Flint and Flint K3 Service. , 2012, , .		11
57	A framework for mapping, visualisation and automatic model creation of signalâ€transduction networks. Molecular Systems Biology, 2012, 8, 578.	3.2	54
58	An Open Platform toward Large-Scale Multilevel Modeling and Simulation of Physiological Systems. , 2011, , .		9
59	Software for systems biology: from tools to integrated platforms. Nature Reviews Genetics, 2011, 12, 821-832.	7.7	228
60	Integrated Quantitative Analysis of the Phosphoproteome and Transcriptome in Tamoxifen-resistant Breast Cancer. Journal of Biological Chemistry, 2011, 286, 818-829.	1.6	42
61	Social engineering for virtual 'big science' in systems biology. Nature Chemical Biology, 2011, 7, 323-326.	3.9	35
62	Cancer Robustness and Therapy Strategies. , 2011, , 429-446.		1
63	Violations of robustness tradeâ€offs. Molecular Systems Biology, 2010, 6, 384.	3.2	46
64	Connecting the dots: role of standardization and technology sharing in biological simulation. Drug Discovery Today, 2010, 15, 1024-1031.	3.2	6
65	Visualization of omics data for systems biology. Nature Methods, 2010, 7, S56-S68.	9.0	548
66	Grand challenges in systems physiology. Frontiers in Physiology, 2010, 1, 3.	1.3	31
67	PathText: a text mining integrator for biological pathway visualizations. Bioinformatics, 2010, 26, i374-i381.	1.8	47
68	Payao: a community platform for SBML pathway model curation. Bioinformatics, 2010, 26, 1381-1383.	1.8	50
69	Fragilities Caused by Dosage Imbalance in Regulation of the Budding Yeast Cell Cycle. PLoS Genetics, 2010, 6, e1000919.	1.5	33
70	Large-Scale Analysis of Network Bistability for Human Cancers. PLoS Computational Biology, 2010, 6, e1000851.	1.5	69
71	A comprehensive molecular interaction map of the budding yeast cell cycle. Molecular Systems Biology, 2010, 6, 415.	3.2	62
72	A comprehensive map of the mTOR signaling network. Molecular Systems Biology, 2010, 6, 453.	3.2	201

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73	Robustness and fragility in the yeast high osmolarity glycerol (HOG) signalâ€transduction pathway. Molecular Systems Biology, 2009, 5, 281.	3.2	56
74	Structure of Protein Interaction Networks and Their Implications on Drug Design. PLoS Computational Biology, 2009, 5, e1000550.	1.5	102
75	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	9.4	828
76	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
77	G-Protein Coupled Receptor Signaling Architecture of Mammalian Immune Cells. PLoS ONE, 2009, 4, e4189.	1.1	37
78	CellDesigner 3.5: A Versatile Modeling Tool for Biochemical Networks. Proceedings of the IEEE, 2008, 96, 1254-1265.	16.4	380
79	Regulation of yeast oscillatory dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2241-2246.	3.3	133
80	Towards a theory of biological robustness. Molecular Systems Biology, 2007, 3, 137.	3.2	647
81	Deduction of intracellular sub-systems from a topological description of the network. Molecular BioSystems, 2007, 3, 523.	2.9	8
82	A system for measuring cell division patterns of early <i>Caenorhabditis elegans</i> embryos by using image processing and object tracking. Systems and Computers in Japan, 2007, 38, 12-24.	0.2	7
83	A robustness-based approach to systems-oriented drug design. Nature Reviews Drug Discovery, 2007, 6, 202-210.	21.5	451
84	Scientific Challenges in Systems Biology. , 2007, , 3-13.		4
85	Modeling the impact of store-operated Ca2+ entry on intracellular Ca2+ oscillations. Mathematical Biosciences, 2006, 204, 232-249.	0.9	24
86	Computational cellular dynamics: a network–physics integral. Nature Reviews Molecular Cell Biology, 2006, 7, 163-163.	16.1	14
87	Genome-wide prediction of genetic interactions in a metazoan. BioEssays, 2006, 28, 1087-1090.	1.2	4
88	In Vivo Robustness Analysis of Cell Division Cycle Genes in Saccharomyces cerevisiae. PLoS Genetics, 2006, 2, e111.	1.5	94
89	Self-Extending Symbiosis: A Mechanism for Increasing Robustness Through Evolution. Biological Theory, 2006, 1, 61-66.	0.8	36
90	Robustness tradeâ€offs and host–microbial symbiosis in the immune system. Molecular Systems Biology, 2006, 2, 2006.0022.	3.2	110

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91	A comprehensive map of the tollâ€like receptor signaling network. Molecular Systems Biology, 2006, 2, 2006.0015.	3.2	302
92	Thermal performance of a solar cooker based on an evacuated tube solar collector with a PCM storage unit. Solar Energy, 2005, 78, 416-426.	2.9	249
93	Using process diagrams for the graphical representation of biological networks. Nature Biotechnology, 2005, 23, 961-966.	9.4	429
94	A comprehensive pathway map of epidermal growth factor receptor signaling. Molecular Systems Biology, 2005, 1, 2005.0010.	3.2	902
95	News. IET Systems Biology, 2005, 152, 53.	2.0	1
96	Editorial [Hot Topic: Yeast Systems Biology Special Issue (Guest Editor: Hiroaki Kitano)]. Current Genomics, 2004, 5, 613-613.	0.7	1
97	morph3: a compact-size humanoid robot system capable of acrobatic behavior. Advanced Robotics, 2004, 18, 699-710.	1.1	7
98	Metabolic Syndrome and Robustness Tradeoffs. Diabetes, 2004, 53, S6-S15.	0.3	121
99	Cancer as a robust system: implications for anticancer therapy. Nature Reviews Cancer, 2004, 4, 227-235.	12.8	412
100	Biological robustness. Nature Reviews Genetics, 2004, 5, 826-837.	7.7	1,937
101	Sound and Visual Tracking for Humanoid Robot. Applied Intelligence, 2004, 20, 253-266.	3.3	18
102	Effects of increasing modalities in recognizing three simultaneous speeches. Speech Communication, 2004, 43, 347-359.	1.6	0
103	Title is missing!. Journal of the Robotics Society of Japan, 2004, 22, 847-852.	0.0	0
104	CellDesigner: a process diagram editor for gene-regulatory and biochemical networks. Biosilico, 2003, 1, 159-162.	0.5	562
105	A graphical notation for biochemical networks. Biosilico, 2003, 1, 169-176.	0.5	90
106	Cancer robustness: Tumour tactics. Nature, 2003, 426, 125-125.	13.7	134
107	Human–robot non-verbal interaction empowered by real-time auditory and visual multiple-talker tracking. Advanced Robotics, 2003, 17, 115-130.	1.1	13
108	Next Generation Simulation Tools: The Systems Biology Workbench and BioSPICE Integration. OMICS A Journal of Integrative Biology, 2003, 7, 355-372.	1.0	254

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109	Control design principle of a low-cost humanoid system using a genetic algorithm. Advanced Robotics, 2003, 17, 779-790.	1.1	1
110	A quantitative characterization of the yeast heterotrimeric G protein cycle. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10764-10769.	3.3	169
111	Real-Time Human Tracking by Audio-Visual Integration for Humanoids-Integration of Active Audition and Face Recognition Journal of the Robotics Society of Japan, 2003, 21, 517-525.	0.0	6
112	Issues in Humanoid Audition and Sound Source Localization by Active Audition Transactions of the Japanese Society for Artificial Intelligence, 2003, 18, 104-113.	0.1	1
113	Robustness as a Measure of Plausibility in Models of Biochemical Networks. Journal of Theoretical Biology, 2002, 216, 19-30.	0.8	226
114	Looking beyond the details: a rise in system-oriented approaches in genetics and molecular biology. Current Genetics, 2002, 41, 1-10.	0.8	157
115	Computational systems biology. Nature, 2002, 420, 206-210.	13.7	1,991
116	Systems Biology: A Brief Overview. Science, 2002, 295, 1662-1664.	6.0	3,574
117	Real-time Auditory and Visual Multiple-speaker Tracking For Human-robot Interaction. Journal of Robotics and Mechatronics, 2002, 14, 479-489.	0.5	12
118	History of RoboCup and Prospects for RoboCup-2002. Journal of the Robotics Society of Japan, 2002, 20, 2-6.	0.0	8
119	RoboCup Humanoid League. Journal of the Robotics Society of Japan, 2002, 20, 24-29.	0.0	2
120	Robust Oscillations within the Interlocked Feedback Model of Drosophila Circadian Rhythm. Journal of Theoretical Biology, 2001, 210, 401-406.	0.8	136
121	Perspectives on systems biology. New Generation Computing, 2000, 18, 199-216.	2.5	83
122	RoboCup Rescue project. Advanced Robotics, 2000, 14, 423-425.	1.1	6
123	RoboCup Initiative as a New Research Project. Journal of the Robotics Society of Japan, 2000, 18, 1081-1084.	0.0	2
124	RoboCup and Industry-Government-University Collaboration. Journal of the Robotics Society of Japan, 2000, 18, 641-646.	0.0	0
125	A reconfigurable robot platform. Robotics and Autonomous Systems, 1999, 29, 119-132.	3.0	30
126	The RoboCup Challenge. Robotics and Autonomous Systems, 1999, 29, 3-12.	3.0	24

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127	On interaction and grammar. Pragmatics, 1999, 9, 383-400.	0.4	13
128	Development of an Autonomous Quadruped Robot for Robot Entertainment. Autonomous Robots, 1998, 5, 7-18.	3.2	183
129	The two-process model of cellular aging. Experimental Gerontology, 1998, 33, 393-419.	1.2	15
130	Research program of robocup. Applied Artificial Intelligence, 1998, 12, 117-125.	2.0	6
131	The robocup physical agent challenge: Phase i. Applied Artificial Intelligence, 1998, 12, 251-263.	2.0	29
132	The PerfectC. ELEGANSProject: An Initial Report. Artificial Life, 1998, 4, 141-156.	1.0	15
133	The RoboCup humanoid challenge as the millennium challenge for advanced robotics. Advanced Robotics, 1998, 13, 723-736.	1.1	58
134	Robot Contests. Research Activity and Robot Contest (RoboCup) Journal of the Robotics Society of Japan, 1997, 15, 13-16.	0.0	0
135	A Simple Model of Neurogenesis and Cell Differentiation Based on Evolutionary Large-Scale Chaos. Artificial Life, 1994, 2, 79-99.	1.0	18
136	Neurogenetic learning: an integrated method of designing and training neural networks using genetic algorithms. Physica D: Nonlinear Phenomena, 1994, 75, 225-238.	1.3	72
137	Toward Massively Parallel Spoken Language Translation. Machine Intelligence and Pattern Recognition, 1994, 15, 177-184.	0.2	2
138	?DmDialog: A speech-to-speech dialogue translation system. Machine Translation, 1990, 5, 301-338.	1.3	9