

# Hiroyuki Kurata

## List of Publications by Year in descending order

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85  
papers

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citations

236612

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h-index

276539

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91  
all docs

91  
docs citations

91  
times ranked

1443  
citing authors

#	ARTICLE	IF	CITATIONS
1	Alternating Covalent Bonding Interactions in a One-Dimensional Chain of a Phenalenyl-Based Singlet Biradical Molecule Having Kekulé Structures. <i>Journal of the American Chemical Society</i> , 2010, 132, 14421-14428.	6.6	162
2	Module-Based Analysis of Robustness Tradeoffs in the Heat Shock Response System. <i>PLoS Computational Biology</i> , 2006, 2, e59.	1.5	89
3	Meta-i6mA: an interspecies predictor for identifying DNA N <sup>6</sup> -methyladenine sites of plant genomes by exploiting informative features in an integrative machine-learning framework. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	86
4	PreAIP: Computational Prediction of Anti-inflammatory Peptides by Integrating Multiple Complementary Features. <i>Frontiers in Genetics</i> , 2019, 10, 129.	1.1	85
5	i4mC-ROSE, a bioinformatics tool for the identification of DNA N <sup>4</sup> -methylcytosine sites in the Rosaceae genome. <i>International Journal of Biological Macromolecules</i> , 2020, 157, 752-758.	3.6	74
6	CADLIVE for constructing a large-scale biochemical network based on a simulation-directed notation and its application to yeast cell cycle. <i>Nucleic Acids Research</i> , 2003, 31, 4071-4084.	6.5	69
7	GPSuc: Global Prediction of Generic and Species-specific Succinylation Sites by aggregating multiple sequence features. <i>PLoS ONE</i> , 2018, 13, e0200283.	1.1	59
8	i6mA-Fuse: improved and robust prediction of DNA 6-ÅmA sites in the Rosaceae genome by fusing multiple feature representation. <i>Plant Molecular Biology</i> , 2020, 103, 225-234.	2.0	59
9	A grid layout algorithm for automatic drawing of biochemical networks. <i>Bioinformatics</i> , 2005, 21, 2036-2042.	1.8	57
10	i4mC-Mouse: Improved identification of DNA N <sup>4</sup> -methylcytosine sites in the mouse genome using multiple encoding schemes. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 906-912.	1.9	57
11	CADLIVE dynamic simulator: Direct link of biochemical networks to dynamic models. <i>Genome Research</i> , 2005, 15, 590-600.	2.4	56
12	Computational identification of protein S-sulfenylation sites by incorporating the multiple sequence features information. <i>Molecular BioSystems</i> , 2017, 13, 2545-2550.	2.9	56
13	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	56
14	Prediction of S-nitrosylation sites by integrating support vector machines and random forest. <i>Molecular Omics</i> , 2019, 15, 451-458.	1.4	48
15	Development of an accurate kinetic model for the central carbon metabolism of <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , 2016, 15, 112.	1.9	42
16	Large-Scale Assessment of Bioinformatics Tools for Lysine Succinylation Sites. <i>Cells</i> , 2019, 8, 95.	1.8	42
17	Deepm5C: A deep-learning-based hybrid framework for identifying human RNA N <sup>5</sup> -methylcytosine sites using a stacking strategy. <i>Molecular Therapy</i> , 2022, 30, 2856-2867.	3.7	40
18	Integration of enzyme activities into metabolic flux distributions by elementary mode analysis. <i>BMC Systems Biology</i> , 2007, 1, 31.	3.0	39

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19	Efficient computational model for identification of antitubercular peptides by integrating amino acid patterns and properties. <i>FEBS Letters</i> , 2019, 593, 3029-3039.	1.3	38
20	Light irradiation causes physiological and metabolic changes for purine alkaloid production by a <i>Coffea arabica</i> cell suspension culture. <i>Plant Science</i> , 1997, 123, 197-203.	1.7	33
21	Proln-Fuse: improved and robust prediction of proinflammatory peptides by fusing of multiple feature representations. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 1229-1236.	1.3	33
22	Computational identification of microbial phosphorylation sites by the enhanced characteristics of sequence information. <i>Scientific Reports</i> , 2019, 9, 8258.	1.6	32
23	Extended CADLIVE: a novel graphical notation for design of biochemical network maps and computational pathway analysis. <i>Nucleic Acids Research</i> , 2007, 35, e134-e134.	6.5	31
24	iLBE for Computational Identification of Linear B-cell Epitopes by Integrating Sequence and Evolutionary Features. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 593-600.	3.0	30
25	Intermittent light irradiation with second- or hour-scale periods controls anthocyanin production by strawberry cells. <i>Enzyme and Microbial Technology</i> , 2000, 26, 621-629.	1.6	29
26	Critical evaluation of web-based DNA N6-methyladenine site prediction tools. <i>Briefings in Functional Genomics</i> , 2021, 20, 258-272.	1.3	29
27	Maximum entropy decomposition of flux distribution at steady state to elementary modes. <i>Journal of Bioscience and Bioengineering</i> , 2009, 107, 84-89.	1.1	28
28	Improved kinetic model of <i>Escherichia coli</i> central carbon metabolism in batch and continuous cultures. <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 251-257.	1.1	27
29	Diffusion Model Based Spectral Clustering for Protein-Protein Interaction Networks. <i>PLoS ONE</i> , 2010, 5, e12623.	1.1	25
30	Ranking network mechanisms by how they fit diverse experiments and deciding on <i>E. coli</i> 's ammonium transport and assimilation network. <i>Npj Systems Biology and Applications</i> , 2019, 5, 14.	1.4	25
31	Evolution of Sequence-based Bioinformatics Tools for Protein-protein Interaction Prediction. <i>Current Genomics</i> , 2020, 21, 454-463.	0.7	25
32	A Comprehensive Review of In silico Analysis for Protein S-sulfenylation Sites. <i>Protein and Peptide Letters</i> , 2018, 25, 815-821.	0.4	23
33	BERT6mA: prediction of DNA N6-methyladenine site using deep learning-based approaches. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	23
34	Immobilized <i>Coffea arabica</i> cell culture using a bubble-column reactor with controlled light intensity. <i>Biotechnology and Bioengineering</i> , 1993, 42, 494-502.	1.7	21
35	Use of maximum entropy principle with Lagrange multipliers extends the feasibility of elementary mode analysis. <i>Journal of Bioscience and Bioengineering</i> , 2010, 110, 254-261.	1.1	21
36	Complementary elementary modes for fast and efficient analysis of metabolic networks. <i>Biochemical Engineering Journal</i> , 2014, 90, 121-130.	1.8	19

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37	Genetic modification of flux for flux prediction of mutants. <i>Bioinformatics</i> , 2009, 25, 1702-1708.	1.8	18
38	iACVP: markedly enhanced identification of anti-coronavirus peptides using a dataset-specific word2vec model. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	17
39	Mathematical Identification of Critical Reactions in the Interlocked Feedback Model. <i>PLoS ONE</i> , 2007, 2, e1103.	1.1	16
40	PredNTS: Improved and Robust Prediction of Nitrotyrosine Sites by Integrating Multiple Sequence Features. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2704.	1.8	16
41	Nonisotropic Scattering Model for Estimation of Light Absorption Rates in a Suspension Culture of <i>Coffea arabica</i> Cells. <i>Biotechnology Progress</i> , 1993, 9, 86-92.	1.3	15
42	Virtual metabolic human dynamic model for pathological analysis and therapy design for diabetes. <i>IScience</i> , 2021, 24, 102101.	1.9	14
43	An integrative and practical evolutionary optimization for a complex, dynamic model of biological networks. <i>Bioprocess and Biosystems Engineering</i> , 2011, 34, 433-446.	1.7	13
44	Biological Design Principles of Complex Feedback Modules in the <i>E. coli</i> Ammonia Assimilation System. <i>Artificial Life</i> , 2011, 18, 53-90.	1.0	12
45	Robust complementary hierarchical clustering for gene expression data analysis by $\hat{l}^2$ -divergence. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 397-407.	1.1	12
46	A prediction model of functional outcome at 6 months using clinical findings of a person with traumatic spinal cord injury at 1 month after injury. <i>Spinal Cord</i> , 2020, 58, 1158-1165.	0.9	12
47	The light/dark cycle operation with an hour-scale period enhances caffeine production by <i>Coffea arabica</i> cells. <i>Enzyme and Microbial Technology</i> , 1998, 23, 518-523.	1.6	11
48	Quasi-multiparameter sensitivity measure for robustness analysis of complex biochemical networks. <i>Journal of Theoretical Biology</i> , 2011, 272, 174-186.	0.8	11
49	A Symmetric Dual Feedback System Provides a Robust and Entrainable Oscillator. <i>PLoS ONE</i> , 2012, 7, e30489.	1.1	11
50	Influence of light irradiation rates and irradiation modes on caffeine production and cell growth in suspension culture of <i>Coffea arabica</i> cells.. <i>Journal of Chemical Engineering of Japan</i> , 1991, 24, 783-788.	0.3	10
51	Two-phase Search (TPS) Method: Nonbiased and High-speed Parameter Search for Dynamic Models of Biochemical Networks. <i>IPSJ Transactions on Bioinformatics</i> , 2009, 2, 2-14.	0.2	9
52	Application of Approximate Pattern Matching in Two Dimensional Spaces to Grid Layout for Biochemical Network Maps. <i>PLoS ONE</i> , 2012, 7, e37739.	1.1	9
53	Recent Development of Bioinformatics Tools for microRNA Target Prediction. <i>Current Medicinal Chemistry</i> , 2022, 29, 865-880.	1.2	9
54	Flux module decomposition for parameter estimation in a multiple-feedback loop model of biochemical networks. <i>Bioprocess and Biosystems Engineering</i> , 2013, 36, 333-344.	1.7	8

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55	PUP-Fuse: Prediction of Protein Pupylation Sites by Integrating Multiple Sequence Representations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2120.	1.8	8
56	Recent Development of Machine Learning Methods in Microbial Phosphorylation Sites. <i>Current Genomics</i> , 2020, 21, 194-203.	0.7	8
57	CADLIVE toolbox for MATLAB: automatic dynamic modeling of biochemical networks with comprehensive system analysis. <i>Bioprocess and Biosystems Engineering</i> , 2014, 37, 1925-1927.	1.7	7
58	Computational Modeling of Lysine Post-Translational Modification: An Overview. <i>Current Synthetic and Systems Biology</i> , 2018, 06, .	0.3	7
59	SIPMA: A Systematic Identification of Protein-Protein Interactions in <i>Zea mays</i> Using Autocorrelation Features in a Machine-Learning Framework. , 2018, , .		6
60	libRCCA: a C library for real-coded genetic algorithms for rapid parameter estimation of kinetic models. <i>IPSI Transactions on Bioinformatics</i> , 2018, 11, 31-40.	0.2	6
61	Self-replenishment cycles generate a threshold response. <i>Scientific Reports</i> , 2019, 9, 17139.	1.6	6
62	Screening for transgenic plant cells that highly express a target gene from genetically mixed cells. <i>Biochemical Engineering Journal</i> , 2002, 10, 175-182.	1.8	5
63	Analytical study of robustness of a negative feedback oscillator by multiparameter sensitivity. <i>BMC Systems Biology</i> , 2014, 8, S1.	3.0	5
64	In vitro evaluation of a combination treatment involving anticancer agents and an aurora kinase B inhibitor. <i>Oncology Letters</i> , 2016, 12, 4263-4269.	0.8	5
65	Metabolic analysis of antibody producing Chinese hamster ovary cell culture under different stresses conditions. <i>Journal of Bioscience and Bioengineering</i> , 2016, 122, 117-124.	1.1	5
66	Mathematical comparison of memory functions between mutual activation and repression networks in a stochastic environment. <i>Journal of Theoretical Biology</i> , 2017, 427, 28-40.	0.8	5
67	iLMS, Computational Identification of Lysine-Malonylation Sites by Combining Multiple Sequence Features. , 2018, , .		5
68	IRC-Fuse: improved and robust prediction of redox-sensitive cysteine by fusing of multiple feature representations. <i>Journal of Computer-Aided Molecular Design</i> , 2021, 35, 315-323.	1.3	5
69	Dynamic Modeling of Metabolic and Gene Regulatory Systems toward Developing Virtual Microbes. <i>Journal of Chemical Engineering of Japan</i> , 2014, 47, 1-9.	0.3	4
70	Coupling protocol of interlocked feedback oscillators in circadian clocks. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200287.	1.5	4
71	Visualizing Global Properties of Large Complex Networks. <i>PLoS ONE</i> , 2008, 3, e2541.	1.1	4
72	Title is missing!. <i>Biotechnology Letters</i> , 1998, 20, 463-468.	1.1	3

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73	CADLIVE Converter for constructing a biochemical network map. <i>Biochemical Engineering Journal</i> , 2011, 54, 200-206.	1.8	3
74	CADLIVE optimizer: web-based parameter estimation for dynamic models. <i>Source Code for Biology and Medicine</i> , 2012, 7, 9.	1.7	3
75	Computer-Aided Rational Design of Efficient NADPH Production System by <i>Escherichia coli</i> pgi Mutant Using a Mixture of Glucose and Xylose. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 277.	2.0	3
76	Mathematical model analyzes light-controlled expression of the CHS promoter in BY-2 cells. <i>Biochemical Engineering Journal</i> , 1999, 4, 65-72.	1.8	2
77	Robustness analysis of the detailed kinetic model of an ErbB signaling network by using dynamic sensitivity. <i>PLoS ONE</i> , 2017, 12, e0178250.	1.1	2
78	RCGAToolbox: A Real-coded Genetic Algorithm Software for Parameter Estimation of Kinetic Models. <i>IPSJ Transactions on Bioinformatics</i> , 2021, 14, 30-35.	0.2	2
79	A gradual update method for simulating the steady-state solution of stiff differential equations in metabolic circuits. <i>Bioprocess and Biosystems Engineering</i> , 2009, 32, 283-288.	1.7	1
80	S-system-based analysis of the robust properties common to many biochemical network models. <i>Bioprocess and Biosystems Engineering</i> , 2016, 39, 735-746.	1.7	1
81	Robust in-phase synchronization in repressor-based coupled gene oscillators. <i>IFAC-PapersOnLine</i> , 2021, 54, 574-579.	0.5	1
82	Software of Living Systems.. <i>Kagaku Kogaku Ronbunshu</i> , 1999, 25, 169-176.	0.1	0
83	Web application for genetic modification flux with database to estimate metabolic fluxes of genetic mutants. <i>Journal of Bioscience and Bioengineering</i> , 2016, 122, 111-116.	1.1	0
84	Syntheses of Partially Brominated Derivatives of Tetra-2-thienylmethane for Three-Dimensionally Extended $\pi$ -Electron Systems. <i>Heterocycles</i> , 2017, 95, 615.	0.4	0
85	Identification of a reliable sacral-sparing examination to assess the ASIA impairment scale in patients with traumatic spinal cord injury. <i>Journal of Spinal Cord Medicine</i> , 2024, 47, 286-292.	0.7	0