

Jeong Rae Kim

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3957323/publications.pdf>

Version: 2024-02-01

41
papers

1,266
citations

394421

19
h-index

361022

35
g-index

42
all docs

42
docs citations

42
times ranked

1879
citing authors

#	ARTICLE	IF	CITATIONS
1	Network Inference Analysis Identifies SETDB1 as a Key Regulator for Reverting Colorectal Cancer Cells into Differentiated Normal-Like Cells. <i>Molecular Cancer Research</i> , 2020, 18, 118-129.	3.4	23
2	Dynamics of the gene regulatory networks of the inner and rosette leaves in <i>Brassica rapa</i> . <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 317-326.	2.1	1
3	Red Chinese Cabbage Transcriptome Analysis Reveals Structural Genes and Multiple Transcription Factors Regulating Reddish Purple Color. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2901.	4.1	21
4	Stage-Dependent Gene Expression Profiling in Colorectal Cancer. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1685-1692.	3.0	7
5	An IBNR-RBNS insurance risk model with marked Poisson arrivals. <i>Insurance: Mathematics and Economics</i> , 2018, 79, 26-42.	1.2	3
6	Comprehensive analysis of CCCH zinc-finger-type transcription factors in the <i>Brassica rapa</i> genome. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 729-747.	2.1	6
7	Pja2 Inhibits Wnt/ β -catenin Signaling by Reducing the Level of TCF/LEF1. <i>International Journal of Stem Cells</i> , 2018, 11, 242-247.	1.8	12
8	The core regulatory network in human cells. <i>Biochemical and Biophysical Research Communications</i> , 2017, 484, 348-353.	2.1	4
9	Deubiquitinase YOD1 potentiates YAP/TAZ activities through enhancing ITCH stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4691-4696.	7.1	56
10	Identification and characterization of the leaf specific networks of inner and rosette leaves in <i>Brassica rapa</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 821-826.	2.1	4
11	The reverse control of irreversible biological processes. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2016, 8, 366-377.	6.6	26
12	Cover Image, Volume 8, Issue 5. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2016, 8, i-i.	6.6	0
13	Integrative systems analysis of diet-induced obesity identified a critical transition in the transcriptomes of the murine liver and epididymal white adipose tissue. <i>International Journal of Obesity</i> , 2016, 40, 338-345.	3.4	6
14	Identification of Gene Networks with Time Delayed Regulation Based on Temporal Expression Profiles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1161-1168.	3.0	2
15	Analyses of the TCR repertoire of MHC class II-restricted innate CD4+ T cells. <i>Experimental and Molecular Medicine</i> , 2015, 47, e154-e154.	7.7	5
16	Characterization of the Alzheimer's disease-related network based on the dynamic network approach. <i>Journal of Korean Institute of Intelligent Systems</i> , 2015, 25, 529-535.	0.1	1
17	Robustness and Evolvability of the Human Signaling Network. <i>PLoS Computational Biology</i> , 2014, 10, e1003763.	3.2	23
18	Heterozygous mutations in cyclic AMP phosphodiesterase-4D (PDE4D) and protein kinase A (PKA) provide new insights into the molecular pathology of acrodysostosis. <i>Cellular Signalling</i> , 2014, 26, 2446-2459.	3.6	56

#	ARTICLE	IF	CITATIONS
19	Biphasic RLR \rightarrow IFN- β Response Controls the Balance between Antiviral Immunity and Cell Damage. <i>Journal of Immunology</i> , 2013, 190, 1192-1200.	0.8	27
20	The core regulation module of stress-responsive regulatory networks in yeast. <i>Nucleic Acids Research</i> , 2012, 40, 8793-8802.	14.5	18
21	The co-regulation mechanism of transcription factors in the human gene regulatory network. <i>Nucleic Acids Research</i> , 2012, 40, 8849-8861.	14.5	26
22	Cooperative Activation of PI3K by Ras and Rho Family Small GTPases. <i>Molecular Cell</i> , 2012, 47, 281-290.	9.7	146
23	Spatiotemporal network motif reveals the biological traits of developmental gene regulatory networks in <i>Drosophila melanogaster</i> . <i>BMC Systems Biology</i> , 2012, 6, 31.	3.0	20
24	The regulatory circuits for hysteretic switching in cellular signal transduction pathways. <i>FEBS Journal</i> , 2012, 279, 3329-3337.	4.7	6
25	A hidden incoherent switch regulates RCAN1 in the calcineurin \rightarrow NFAT signaling network. <i>Journal of Cell Science</i> , 2011, 124, 82-90.	2.0	45
26	Reduction of Complex Signaling Networks to a Representative Kernel. <i>Science Signaling</i> , 2011, 4, ra35.	3.6	54
27	Dynamic network rewiring determines temporal regulatory functions in <i>Drosophila melanogaster</i> development processes. <i>BioEssays</i> , 2010, 32, 505-513.	2.5	16
28	A system-level investigation into the cellular toxic response mechanism mediated by AhR signal transduction pathway. <i>Bioinformatics</i> , 2010, 26, 2169-2175.	4.1	10
29	A design principle underlying the synchronization of oscillations in cellular systems. <i>Journal of Cell Science</i> , 2010, 123, 537-543.	2.0	55
30	Multiple roles of the NF κ B signaling pathway regulated by coupled negative feedback circuits. <i>FASEB Journal</i> , 2009, 23, 2796-2802.	0.5	20
31	Hub genes with positive feedbacks function as master switches in developmental gene regulatory networks. <i>Bioinformatics</i> , 2009, 25, 1898-1904.	4.1	48
32	The biphasic behavior of incoherent feedforward loops in biomolecular regulatory networks. <i>BioEssays</i> , 2008, 30, 1204-1211.	2.5	93
33	Why have serine/threonine/tyrosine kinases been evolutionarily selected in eukaryotic signaling cascades?. <i>Computational Biology and Chemistry</i> , 2008, 32, 218-221.	2.3	6
34	Coupled Feedback Loops Form Dynamic Motifs of Cellular Networks. <i>Biophysical Journal</i> , 2008, 94, 359-365.	0.5	120
35	Evolutionary design principles of modules that control cellular differentiation: consequences for hysteresis and multistationarity. <i>Bioinformatics</i> , 2008, 24, 1516-1522.	4.1	13
36	Topological Difference of Core Regulatory Networks Induces Different Entrainment Characteristics of Plant and Animal Circadian Clocks. <i>Biophysical Journal</i> , 2007, 93, L01-L03.	0.5	6

#	ARTICLE	IF	CITATIONS
37	Coupled positive and negative feedback circuits form an essential building block of cellular signaling pathways. <i>BioEssays</i> , 2007, 29, 85-90.	2.5	72
38	Reverse engineering of gene regulatory networks. <i>IET Systems Biology</i> , 2007, 1, 149-163.	1.5	100
39	Inferring biomolecular regulatory networks from phase portraits of time-series expression profiles. <i>FEBS Letters</i> , 2006, 580, 3511-3518.	2.8	10
40	Switching feedback mechanisms realize the dual role of MCIP in the regulation of calcineurin activity. <i>FEBS Letters</i> , 2006, 580, 5965-5973.	2.8	34
41	The multi-step phosphorelay mechanism of unorthodox two-component systems in <i>E. coli</i> realizes ultrasensitivity to stimuli while maintaining robustness to noises. <i>Computational Biology and Chemistry</i> , 2006, 30, 438-444.	2.3	65