

Cheng-Wei Li

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43
papers

311
citations

11
h-index

16
g-index

44
ext. papers

383
ext. citations

3.7
avg, IF

3.75
L-index

#	Paper	IF	Citations
43	Investigation mechanisms between normal, developing and regenerating livers for regenerative liver drug design. <i>Regenerative Medicine</i> , 2019 , 14, 359-387	2.5	
42	Comparing progression molecular mechanisms between lung adenocarcinoma and lung squamous cell carcinoma based on genetic and epigenetic networks: big data mining and genome-wide systems identification. <i>Oncotarget</i> , 2019 , 10, 3760-3806	3.3	8
41	Systems Biology Approaches to Investigate Genetic and Epigenetic Molecular Progression Mechanisms for Identifying Gene Expression Signatures in Papillary Thyroid Cancer. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	6
40	Investigating HIV-Human Interaction Networks to Unravel Pathogenic Mechanism for Drug Discovery: A Systems Biology Approach. <i>Current HIV Research</i> , 2018 , 16, 77-95	1.3	2
39	Investigating genetic-and-epigenetic networks, and the cellular mechanisms occurring in Epstein-Barr virus-infected human B lymphocytes via big data mining and genome-wide two-sided NGS data identification. <i>PLoS ONE</i> , 2018 , 13, e0202537	3.7	5
38	Changes of signal transductivity and robustness of gene regulatory network in the carcinogenesis of leukemic subtypes via microarray sample data. <i>Oncotarget</i> , 2018 , 9, 23636-23660	3.3	
37	Investigating Pathogenic and Hepatocarcinogenic Mechanisms from Normal Liver to HCC by Constructing Genetic and Epigenetic Networks via Big Genetic and Epigenetic Data Mining and Genome-Wide NGS Data Identification. <i>Disease Markers</i> , 2018 , 2018, 8635329	3.2	7
36	Procedure for Exploring Big Mechanisms of Systems Biology Through System Identification and Big Database Mining 2017 , 29-37		
35	Big Offensive and Defensive Mechanisms in Systems Immunity From System Modeling and Big Data Mining 2017 , 249-372		
34	Big Regulatory Mechanisms in the Transcriptional Regulation Control of Gene Expression Using a Stochastic System Model and Genome-Wide Experimental Data 2017 , 87-154		1
33	Big Mechanisms of Aging via System Identification and Big Database Mining 2017 , 671-735		
32	Big Tumorigenesis Mechanisms in Systems Cancer Biology via Big Database Mining and Network Modeling 2017 , 431-526		0
31	Big Mechanisms of Information Flow in Cellular Systems in Response to Environmental Stress Signals via System Identification and Data Mining 2017 , 155-248		
30	Big Drug Design Mechanisms via Systems Biology and Big Database Mining 2017 , 737-845		1
29	System Modeling and System Identification Methods for Big Mechanisms in Biological Systems 2017 , 9-28		
28	Introduction to Big Mechanisms in Systems Biology 2017 , 1-8		0
27	Big Cellular Mechanisms in the Cell Cycle by System Identification and Big Data Mining 2017 , 39-86		

26	Big Regeneration Mechanisms via Systems Biology and Big Database Mining Methods 2017 , 373-430		
25	Investigation of the Cross-talk Mechanism in Caco-2 Cells during Infection through Genetic-and-Epigenetic Interspecies Networks: Big Data Mining and Genome-Wide Identification. <i>Frontiers in Immunology</i> , 2017 , 8, 901	8.4	3
24	Big Evolutionary Mechanisms of Network Robustness and Signaling Transductivity in Aging and Carcinogenic Process by System Modeling and Database Mining 2017 , 527-669		1
23	Investigating core genetic-and-epigenetic cell cycle networks for stemness and carcinogenic mechanisms, and cancer drug design using big database mining and genome-wide next-generation sequencing data. <i>Cell Cycle</i> , 2016 , 15, 2593-2607	4.7	20
22	Constructing an integrated genetic and epigenetic cellular network for whole cellular mechanism using high-throughput next-generation sequencing data. <i>BMC Systems Biology</i> , 2016 , 10, 18	3.5	16
21	Investigating the mechanism of hepatocellular carcinoma progression by constructing genetic and epigenetic networks using NGS data identification and big database mining method. <i>Oncotarget</i> , 2016 , 7, 79453-79473	3.3	13
20	Investigating the specific core genetic-and-epigenetic networks of cellular mechanisms involved in human aging in peripheral blood mononuclear cells. <i>Oncotarget</i> , 2016 , 7, 8556-79	3.3	18
19	Network Biomarkers of Bladder Cancer Based on a Genome-Wide Genetic and Epigenetic Network Derived from Next-Generation Sequencing Data. <i>Disease Markers</i> , 2016 , 2016, 4149608	3.2	10
18	Genetic-and-Epigenetic Interspecies Networks for Cross-Talk Mechanisms in Human Macrophages and Dendritic Cells during MTB Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016 , 6, 124	5.9	8
17	Estimating Sensorimotor Mapping From Stimuli to Behaviors to Infer C. elegans Movements by Neural Transmission Ability Through Connectome Databases. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2016 , 27, 2229-2241	10.3	2
16	Robust sensorimotor control of human arm model under state-dependent noises, control-dependent noises and additive noises. <i>Neurocomputing</i> , 2015 , 167, 61-75	5.4	4
15	Using Nonlinear Stochastic Evolutionary Game Strategy to Model an Evolutionary Biological Network of Organ Carcinogenesis Under a Natural Selection Scheme. <i>Evolutionary Bioinformatics</i> , 2015 , 11, 155-78	1.9	11
14	Multiple target drug cocktail design for attacking the core network markers of four cancers using ligand-based and structure-based virtual screening methods. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 4, S4	3.7	11
13	On the Calculation of System Entropy in Nonlinear Stochastic Biological Networks. <i>Entropy</i> , 2015 , 17, 6801-6833	2.8	11
12	Measuring information flow in cellular networks by the systems biology method through microarray data. <i>Frontiers in Plant Science</i> , 2015 , 6, 390	6.2	8
11	Evolution of network biomarkers from early to late stage bladder cancer samples. <i>BioMed Research International</i> , 2014 , 2014, 159078	3	15
10	Robust observer-based tracking control of hodgkin-huxley neuron systems under environmental disturbances. <i>Neural Computation</i> , 2010 , 22, 3143-78	2.9	6
9	On the noise-enhancing ability of stochastic Hodgkin-Huxley neuron systems. <i>Neural Computation</i> , 2010 , 22, 1737-63	2.9	11

8	On the Interplay between Entropy and Robustness of Gene Regulatory Networks. <i>Entropy</i> , 2010 , 12, 1071-1101	2.8	29
7	Identifying functional mechanisms of gene and protein regulatory networks in response to a broader range of environmental stresses. <i>Comparative and Functional Genomics</i> , 2010 , 408705		12
6	Stochastic Spatio-Temporal Dynamic Model for Gene/Protein Interaction Network in Early Drosophila Development. <i>Gene Regulation and Systems Biology</i> , 2009 , 3, 117762500900300	2	0
5	Stochastic spatio-temporal dynamic model for gene/protein interaction network in early Drosophila development. <i>Gene Regulation and Systems Biology</i> , 2009 , 3, 191-210	2	7
4	Analysing microarray data in drug discovery using systems biology. <i>Expert Opinion on Drug Discovery</i> , 2007 , 2, 755-68	6.2	15
3	Construction and clarification of dynamic gene regulatory network of cancer cell cycle via microarray data. <i>Cancer Informatics</i> , 2007 , 2, 223-41	2.4	5
2	Construction and Clarification of Dynamic Gene Regulatory Network of Cancer Cell Cycle via Microarray Data. <i>Cancer Informatics</i> , 2006 , 2, 117693510600200	2.4	5
1	Quantitative inference of dynamic regulatory pathways via microarray data. <i>BMC Bioinformatics</i> , 2005 , 6, 44	3.6	40