

Cheng-Wei Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5211762/publications.pdf>

Version: 2024-02-01

44
papers

409
citations

759233

12
h-index

839539

18
g-index

44
all docs

44
docs citations

44
times ranked

567
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation mechanisms between normal, developing and regenerating livers for regenerative liver drug design. <i>Regenerative Medicine</i> , 2019, 14, 353-358.	1.7	1
2	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.	1.8	12
3	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, 2536.	4.1	10
4	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, 1-22.	1.3	19
5	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.	0.5	6
6	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.	2.5	12
7	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.	1.8	0
8	System Modeling and System Identification Methods for Big Mechanisms in Biological Systems. , 2017, , 9-28.		0
9	Introduction to Big Mechanisms in Systems Biology. , 2017, , 1-8.		1
10	Big Cellular Mechanisms in the Cell Cycle by System Identification and Big Data Mining. , 2017, , 39-86.		0
11	Big Regeneration Mechanisms via Systems Biology and Big Database Mining Methods. , 2017, , 373-430.		0
12	Investigation of the Cross-talk Mechanism in Caco-2 Cells during <i>Clostridium difficile</i> Infection through Genetic-and-Epigenetic Interspecies Networks: Big Data Mining and Genome-Wide Identification. <i>Frontiers in Immunology</i> , 2017, 8, 901.	4.8	5
13	Procedure for Exploring Big Mechanisms of Systems Biology Through System Identification and Big Database Mining. , 2017, , 29-37.		0
14	Big Offensive and Defensive Mechanisms in Systems Immunity From System Modeling and Big Data Mining. , 2017, , 249-372.		0
15	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
16	Big Mechanisms of Aging via System Identification and Big Database Mining. , 2017, , 671-735.		0
17	Big Tumorigenesis Mechanisms in Systems Cancer Biology via Big Database Mining and Network Modeling. , 2017, , 431-526.		1
18	Big Mechanisms of Information Flow in Cellular Systems in Response to Environmental Stress Signals via System Identification and Data Mining. , 2017, , 155-248.		0

#	ARTICLE	IF	CITATIONS
19	Big Drug Design Mechanisms via Systems Biology and Big Database Mining. , 2017, , 737-845.		1
20	Big Evolutionary Mechanisms of Network Robustness and Signaling Transductivity in Aging and Carcinogenic Process by System Modeling and Database Mining. , 2017, , 527-669.		1
21	Network Biomarkers of Bladder Cancer Based on a Genome-Wide Genetic and Epigenetic Network Derived from Next-Generation Sequencing Data. Disease Markers, 2016, 2016, 1-18.	1.3	13
22	Genetic-and-Epigenetic Interspecies Networks for Cross-Talk Mechanisms in Human Macrophages and Dendritic Cells during MTB Infection. Frontiers in Cellular and Infection Microbiology, 2016, 6, 124.	3.9	14
23	Estimating Sensorimotor Mapping From Stimuli to Behaviors to Infer <i>C. elegans</i> Movements by Neural Transmission Ability Through Connectome Databases. IEEE Transactions on Neural Networks and Learning Systems, 2016, 27, 2229-2241.	11.3	2
24	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. Cell Cycle, 2016, 15, 2593-2607.	2.6	27
25	Constructing an integrated genetic and epigenetic cellular network for whole cellular mechanism using high-throughput next-generation sequencing data. BMC Systems Biology, 2016, 10, 18.	3.0	21
26	Investigating the mechanism of hepatocellular carcinoma progression by constructing genetic and epigenetic networks using NGS data identification and big database mining method. Oncotarget, 2016, 7, 79453-79473.	1.8	14
27	Investigating the specific core genetic-and-epigenetic networks of cellular mechanisms involved in human aging in peripheral blood mononuclear cells. Oncotarget, 2016, 7, 8556-8579.	1.8	22
28	Using Nonlinear Stochastic Evolutionary Game Strategy to Model an Evolutionary Biological Network of Organ Carcinogenesis under a Natural Selection Scheme. Evolutionary Bioinformatics, 2015, 11, EBO.S26195.	1.2	12
29	Multiple target drug cocktail design for attacking the core network markers of four cancers using ligand-based and structure-based virtual screening methods. BMC Medical Genomics, 2015, 8, S4.	1.5	15
30	On the Calculation of System Entropy in Nonlinear Stochastic Biological Networks. Entropy, 2015, 17, 6801-6833.	2.2	13
31	Measuring information flow in cellular networks by the systems biology method through microarray data. Frontiers in Plant Science, 2015, 6, 390.	3.6	10
32	Robust sensorimotor control of human arm model under state-dependent noises, control-dependent noises and additive noises. Neurocomputing, 2015, 167, 61-75.	5.9	5
33	Evolution of Network Biomarkers from Early to Late Stage Bladder Cancer Samples. BioMed Research International, 2014, 2014, 1-23.	1.9	18
34	Robust Observer-Based Tracking Control of Hodgkin-Huxley Neuron Systems Under Environmental Disturbances. Neural Computation, 2010, 22, 3143-3178.	2.2	7
35	On the Noise-Enhancing Ability of Stochastic Hodgkin-Huxley Neuron Systems. Neural Computation, 2010, 22, 1737-1763.	2.2	14
36	On the Interplay between Entropy and Robustness of Gene Regulatory Networks. Entropy, 2010, 12, 1071-1101.	2.2	33

#	ARTICLE	IF	CITATIONS
37	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, 2010, 1-20.	2.0	15
38	Stochastic Spatio-Temporal Dynamic Model for Gene/Protein Interaction Network in Early Drosophila Development. <i>Gene Regulation and Systems Biology</i> , 2009, 3, 117762500900300.	2.3	1
39	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.	2.3	9
40	Analysing microarray data in drug discovery using systems biology. <i>Expert Opinion on Drug Discovery</i> , 2007, 2, 755-768.	5.0	15
41	Construction and clarification of dynamic gene regulatory network of cancer cell cycle via microarray data. <i>Cancer Informatics</i> , 2007, 2, 223-41.	1.9	6
42	Construction and Clarification of Dynamic Gene Regulatory Network of Cancer Cell Cycle via Microarray Data. <i>Cancer Informatics</i> , 2006, 2, 117693510600200.	1.9	6
43	Quantitative inference of dynamic regulatory pathways via microarray data. <i>BMC Bioinformatics</i> , 2005, 6, 44.	2.6	47
44	Stochastic Game Theory Approach to Robust Synthetic Gene Network Design. , 0, , .		0