

Xiong-Hui Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

362
citations

1039406

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h-index

940134

16
g-index

20
all docs

20
docs citations

20
times ranked

508
citing authors

#	ARTICLE	IF	CITATIONS
1	Systems Pharmacology-Based Precision Therapy and Drug Combination Discovery for Breast Cancer. <i>Cancers</i> , 2021, 13, 3586.	1.7	4
2	MNBDR: A Module Network Based Method for Drug Repositioning. <i>Genes</i> , 2021, 12, 25.	1.0	6
3	DNA Methylation Module Network-Based Prognosis and Molecular Typing of Cancer. <i>Genes</i> , 2019, 10, 571.	1.0	16
4	Prediction of Bone Metastasis in Breast Cancer Based on Minimal Driver Gene Set in Gene Dependency Network. <i>Genes</i> , 2019, 10, 466.	1.0	10
5	An Ensemble Strategy to Predict Prognosis in Ovarian Cancer Based on Gene Modules. <i>Frontiers in Genetics</i> , 2019, 10, 366.	1.1	5
6	Identification of Cancer Hallmarks Based on the Gene Co-expression Networks of Seven Cancers. <i>Frontiers in Genetics</i> , 2019, 10, 99.	1.1	12
7	PheWAS-Based Systems Genetics Methods for Anti-Breast Cancer Drug Discovery. <i>Genes</i> , 2019, 10, 154.	1.0	3
8	Identifying cancer prognostic modules by module network analysis. <i>BMC Bioinformatics</i> , 2019, 20, 85.	1.2	11
9	Ensemble Classifier based on gene synergistic network improves breast cancer outcome prediction. , 2019, , .		0
10	Identification of prognostic signature in cancer based on DNA methylation interaction network. <i>BMC Medical Genomics</i> , 2017, 10, 63.	0.7	35
11	Identifying prognostic signature in ovarian cancer using DirGenerank. <i>Oncotarget</i> , 2017, 8, 46398-46413.	0.8	27
12	Functional analysis of long intergenic non-coding RNAs in phosphate-starved rice using competing endogenous RNA network. <i>Scientific Reports</i> , 2016, 6, 20715.	1.6	64
13	Construction and investigation of breastâ€cancerâ€specific ceRNA network based on the mRNA and miRNA expression data. <i>IET Systems Biology</i> , 2014, 8, 96-103.	0.8	110
14	Analysis and classification of DNAâ€binding sites in singleâ€stranded and doubleâ€stranded DNAâ€binding proteins using protein information. <i>IET Systems Biology</i> , 2014, 8, 176-183.	0.8	11
15	A computational model to predict bone metastasis in breast cancer by integrating the dysregulated pathways. <i>BMC Cancer</i> , 2014, 14, 618.	1.1	14
16	Inferring Gene Dependency Network Specific to Phenotypic Alteration Based on Gene Expression Data and Clinical Information of Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e92023.	1.1	9
17	Ensemble classifier based on context specific miRNA regulation modules: a new method for cancer outcome prediction. <i>BMC Bioinformatics</i> , 2013, 14, S6.	1.2	19
18	Predicting distant metastasis in breast cancer using ensemble classifier based on context-specific miRNA regulation modules. , 2012, , .		2

#	ARTICLE	IF	CITATIONS
19	Context-specific miRNA regulation network predicts cancer prognosis. , 2011, , .		2